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Sir:

Transmitted herewith for filing is the patent application of:

Inventors: Markus Pompejus *et al.*

For: "*Corynebacterium Glutamicum* Genes Encoding Proteins Involved in DNA Replication, Protein Synthesis, and Pathogenesis"

Enclosed are:

- ☒ 63 pages of specification, 5 pages of claims and 1 page of abstract;
- ☒ 6 pages of Table 1;
- ☒ 16 pages of Table 2;
- ☒ 6 pages of Table 3;
- ☒ 14 pages of Table 4;
- ☒ 93 pages of Appendix A;
- ☒ 30 pages of Appendix B;
- ☒ 631 pages of Sequence Listing;
- ☒ Zip Disk Containing Sequence Listing;
- ☒ Transmittal Letter for Zip Disk Containing Sequence Listing;
- ☒ An *unexecuted* Declaration, Petition and Power of Attorney; and
- ☒ A pre-paid acknowledgment postcard.

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***CORYNEBACTERIUM GLUTAMICUM* GENES ENCODING PROTEINS  
INVOLVED IN DNA REPLICATION, PROTEIN SYNTHESIS, AND  
PATHOGENESIS**

5    **Related Applications**

This application claims priority to prior filed U.S. Provisional Patent Application Serial No. 60/144448, filed July 16, 1999, and U.S. Provisional Patent Application Serial No. 60/149402, filed August 17, 1999. The entire contents of both of the above referenced applications is hereby incorporated by this reference.

10

**Background of the Invention**

Certain products and by-products of naturally-occurring metabolic processes in cells have utility in a wide array of industries, including the food, feed, cosmetics, and pharmaceutical industries. These molecules, collectively termed 'fine chemicals', include organic acids, both proteinogenic and non-proteinogenic amino acids, nucleotides and nucleosides, lipids and fatty acids, diols, carbohydrates, aromatic compounds, vitamins and cofactors, and enzymes. Their production is most conveniently performed through the large-scale culture of bacteria developed to produce and secrete large quantities of one or more desired molecules. One particularly useful organism for this purpose is *Corynebacterium glutamicum*, a gram positive bacterium lacking human pathogenicity. Through strain selection, a number of mutant strains have been developed which produce an array of desirable compounds. However, selection of strains improved for the production of a particular molecule is a time-consuming and difficult process.

25

**Summary of the Invention**

The invention provides novel bacterial nucleic acid molecules which have a variety of uses. These uses include the identification of microorganisms which can be used to produce fine chemicals, the modulation of fine chemical production in *C. glutamicum* or related bacteria, the typing or identification of *C. glutamicum* or related bacteria, as reference points for mapping the *C. glutamicum* genome, and as markers for transformation. These novel nucleic acid molecules encode proteins, referred to herein as DNA replication, ribosome and pathogenesis (RRP) proteins.

*C. glutamicum* is a gram positive, aerobic bacterium which is commonly used in industry for the large-scale production of a variety of fine chemicals, and also for the degradation of hydrocarbons (such as in petroleum spills) and for the oxidation of terpenoids. The RRP nucleic acid molecules of the invention, therefore, can be used to

- identify microorganisms which can be used to produce fine chemicals, e.g., by fermentation processes. Modulation of the expression of the RRP nucleic acids of the invention, or modification of the sequence of the RRP nucleic acid molecules of the invention, can be used to modulate the production of one or more fine chemicals from a microorganism (e.g., to improve the yield or production of one or more fine chemicals from a *Corynebacterium* or *Brevibacterium* species).

- The RRP nucleic acids of the invention may also be used to identify an organism as being *Corynebacterium glutamicum* or a close relative thereof, or to identify the presence of *C. glutamicum* or a relative thereof in a mixed population of microorganisms. The invention provides the nucleic acid sequences of a number of *C. glutamicum* genes; by probing the extracted genomic DNA of a culture of a unique or mixed population of microorganisms under stringent conditions with a probe spanning a region of a *C. glutamicum* gene which is unique to this organism, one can ascertain whether this organism is present. Although *Corynebacterium glutamicum* itself is nonpathogenic, it is related to species pathogenic in humans, such as *Corynebacterium diphtheriae* (the causative agent of diphtheria); the detection of such organisms is of significant clinical relevance.

- The RRP nucleic acid molecules of the invention may also serve as reference points for mapping of the *C. glutamicum* genome, or of genomes of related organisms. Similarly, these molecules, or variants or portions thereof, may serve as markers for genetically engineered *Corynebacterium* or *Brevibacterium* species.

- The RRP proteins encoded by the novel nucleic acid molecules of the invention are capable of, for example, performing a function in *C. glutamicum* involved in the replication of DNA, in protein synthesis, or of contributing to the pathogenicity of the microorganism. Given the availability of cloning vectors for use in *Corynebacterium glutamicum*, such as those disclosed in Sinskey *et al.*, U.S. Patent No. 4,649,119, and techniques for genetic manipulation of *C. glutamicum* and the related *Brevibacterium* species (e.g., *lactofermentum*) (Yoshihama *et al.*, *J. Bacteriol.* 162: 591-597 (1985); Katsumata *et al.*, *J. Bacteriol.* 159: 306-311 (1984); and Santamaria *et al.*, *J. Gen. Microbiol.* 130: 2237-2246 (1984)), the nucleic acid molecules of the invention may be utilized in the genetic engineering of this organism to make it a better or more efficient producer of one or more fine chemicals. This improved production or efficiency of production of a fine chemical may be due to a direct effect of manipulation of a gene of the invention, or it may be due to an indirect effect of such manipulation.

- There are a number of mechanisms by which the alteration of an RRP protein of the invention may affect the yield, production, and/or efficiency of production of a fine chemical from a *C. glutamicum* strain incorporating such an altered protein. For

example, by improving the rate at which DNA replication occurs (e.g., by optimizing the activity of one or more DNA polymerase, or by improving the rate at which the topoisomerases or helicases of the invention unwind DNA) it may be possible to increase the rate of cell division, which in turn increases the number of viable fine-chemical-producing *C. glutamicum* cells present in large-scale culture settings.

5 Similarly, by improving the rate at which mRNA is translated to protein (e.g., by optimizing the activity of one or more of the ribosomal proteins) it may be possible to increase the number of proteins in the cell which participate in the synthesis of one or more desired fine chemicals, or in an overall increase in the rate of cell division (due to

10 increased growth and metabolism), both of which should lead to increased production of one or more fine chemicals from large-scale fermentor cultures of these microorganisms. Alterations in the DNA replication proteins of the invention may also permit increased fidelity in the replicative process, thereby increasing the genetic stability and viability of the microorganism and lessening the chance that another

15 engineered mutation improving fine chemical production from the microorganism will not be inadvertently mutagenized by error-prone replication. The RRP proteins of the invention involved in pathogenesis are themselves fine chemicals; by increasing the number or by engineering the corresponding genes such that the expression of these proteins is removed from cellular repression pathways, or by mutagenizing the proteins

20 such that feedback regulatory regions are removed, it may be possible to increase the yield, production, and/or efficiency of production of these proteins from large-scale fermentor culture of organisms containing such mutations.

The invention provides novel nucleic acid molecules which encode proteins, referred to herein as RRP proteins, which are capable of, for example, performing a

25 function in *C. glutamicum* involved in the replication of DNA, in protein synthesis, or of contributing to the pathogenicity of the microorganism. Nucleic acid molecules encoding an RRP protein are referred to herein as RRP nucleic acid molecules. In a preferred embodiment, an RRP protein participates in *C. glutamicum* DNA replication, ribosome function, or in the pathogenesis of the organism, or possesses a *C. glutamicum*

30 enzymatic or proteolytic activity. Examples of such proteins include those encoded by the genes set forth in Table 1.

Accordingly, one aspect of the invention pertains to isolated nucleic acid molecules (e.g., cDNAs, DNAs, or RNAs) comprising a nucleotide sequence encoding an RRP protein or biologically active portions thereof, as well as nucleic acid fragments

35 suitable as primers or hybridization probes for the detection or amplification of RRP-encoding nucleic acids (e.g., DNA or mRNA). In particularly preferred embodiments, the isolated nucleic acid molecule comprises one of the nucleotide sequences set forth in

Appendix A or the coding region or a complement thereof of one of these nucleotide sequences. In other particularly preferred embodiments, the isolated nucleic acid molecule of the invention comprises a nucleotide sequence which hybridizes to or is at least about 50%, preferably at least about 60%, more preferably at least about 70%, 80% or 90%, and even more preferably at least about 95%, 96%, 97%, 98%, 99% or more homologous to a nucleotide sequence set forth in Appendix A, or a portion thereof. In other preferred embodiments, the isolated nucleic acid molecule encodes one of the amino acid sequences set forth in Appendix B. The preferred RRP proteins of the present invention also preferably possess at least one of the RRP activities described herein.

In another embodiment, the isolated nucleic acid molecule encodes a protein or portion thereof wherein the protein or portion thereof includes an amino acid sequence which is sufficiently homologous to an amino acid sequence of Appendix B, e.g., sufficiently homologous to an amino acid sequence of Appendix B such that the protein or portion thereof maintains an RRP activity. Preferably, the protein or portion thereof encoded by the nucleic acid molecule maintains the ability to participate in the replication of DNA, in protein synthesis, or in the pathogenicity of the microorganism. In one embodiment, the protein encoded by the nucleic acid molecule is at least about 50%, preferably at least about 60%, and more preferably at least about 70%, 80%, or 90% and most preferably at least about 95%, 96%, 97%, 98%, or 99% or more homologous to an amino acid sequence of Appendix B (e.g., an entire amino acid sequence selected from those sequences set forth in Appendix B). In another preferred embodiment, the protein is a full length *C. glutamicum* protein which is substantially homologous to an entire amino acid sequence of Appendix B (encoded by an open reading frame shown in Appendix A).

In another preferred embodiment, the isolated nucleic acid molecule is derived from *C. glutamicum* and encodes a protein (e.g., an RRP fusion protein) which includes a biologically active domain which is at least about 50% or more homologous to one of the amino acid sequences of Appendix B and is able to participate in the replication of *C. glutamicum* DNA, in *C. glutamicum* protein synthesis, or may contribute to the pathogenicity of the microorganism, or has one or more of the activities set forth in Table 1, and which also includes heterologous nucleic acid sequences encoding a heterologous polypeptide or regulatory regions.

In another embodiment, the isolated nucleic acid molecule is at least 15 nucleotides in length and hybridizes under stringent conditions to a nucleic acid molecule comprising a nucleotide sequence of Appendix A. Preferably, the isolated nucleic acid molecule corresponds to a naturally-occurring nucleic acid molecule. More

preferably, the isolated nucleic acid encodes a naturally-occurring *C. glutamicum* RRP protein, or a biologically active portion thereof.

- Another aspect of the invention pertains to vectors, e.g., recombinant expression vectors, containing the nucleic acid molecules of the invention, and host cells into which  
5 such vectors have been introduced. In one embodiment, such a host cell is used to produce an RRP protein by culturing the host cell in a suitable medium. The RRP protein can be then isolated from the medium or the host cell.

- Yet another aspect of the invention pertains to a genetically altered microorganism in which an RRP gene has been introduced or altered. In one  
10 embodiment, the genome of the microorganism has been altered by introduction of a nucleic acid molecule of the invention encoding wild-type or mutated RRP sequence as a transgene. In another embodiment, an endogenous RRP gene within the genome of the microorganism has been altered, e.g., functionally disrupted, by homologous recombination with an altered RRP gene. In another embodiment, an endogenous or  
15 introduced RRP gene in a microorganism has been altered by one or more point mutations, deletions, or inversions, but still encodes a functional RRP protein. In still another embodiment, one or more of the regulatory regions (e.g., a promoter, repressor, or inducer) of an RRP gene in a microorganism has been altered (e.g., by deletion, truncation, inversion, or point mutation) such that the expression of the RRP gene is  
20 modulated. In a preferred embodiment, the microorganism belongs to the genus *Corynebacterium* or *Brevibacterium*, with *Corynebacterium glutamicum* being particularly preferred. In a preferred embodiment, the microorganism is also utilized for the production of a desired compound, such as an amino acid, with lysine being particularly preferred.

- 25 In another aspect, the invention provides a method of identifying the presence or activity of *Corynebacterium diphtheriae* in a subject. This method includes detection of one or more of the nucleic acid or amino acid sequences of the invention (e.g., the sequences set forth in Appendix A or Appendix B) in a subject, thereby detecting the presence or activity of *Corynebacterium diphtheriae* in the subject.

- 30 Still another aspect of the invention pertains to an isolated RRP protein or a portion, e.g., a biologically active portion, thereof. In a preferred embodiment, the isolated RRP protein or portion thereof can participate in the replication of *C. glutamicum* DNA, in *C. glutamicum* protein synthesis, or may contribute to the pathogenicity of the microorganism. In another preferred embodiment, the isolated RRP  
35 protein or portion thereof is sufficiently homologous to an amino acid sequence of Appendix B such that the protein or portion thereof maintains the ability to participate in

the replication of *C. glutamicum* DNA, to participate in *C. glutamicum* protein synthesis, or may contribute to the pathogenicity of the microorganism.

- The invention also provides an isolated preparation of an RRP protein. In preferred embodiments, the RRP protein comprises an amino acid sequence of
- 5 Appendix B. In another preferred embodiment, the invention pertains to an isolated full length protein which is substantially homologous to an entire amino acid sequence of Appendix B (encoded by an open reading frame set forth in Appendix A). In yet another embodiment, the protein is at least about 50%, preferably at least about 60%, and more preferably at least about 70%, 80%, or 90%, and most preferably at least about
- 10 95%, 96%, 97%, 98%, or 99% or more homologous to an entire amino acid sequence of Appendix B. In other embodiments, the isolated RRP protein comprises an amino acid sequence which is at least about 50% or more homologous to one of the amino acid sequences of Appendix B and is able to participate in the replication of *C. glutamicum* DNA, to participate in *C. glutamicum* protein synthesis, or may contribute to the
- 15 pathogenicity of the microorganism, or has one or more of the activities set forth in Table 1.

- Alternatively, the isolated RRP protein can comprise an amino acid sequence which is encoded by a nucleotide sequence which hybridizes, *e.g.*, hybridizes under stringent conditions, or is at least about 50%, preferably at least about 60%, more
- 20 preferably at least about 70%, 80%, or 90%, and even more preferably at least about 95%, 96%, 97%, 98%, or 99% or more homologous, to a nucleotide sequence of Appendix B. It is also preferred that the preferred forms of RRP proteins also have one or more of the RRP bioactivities described herein.

- The RRP polypeptide, or a biologically active portion thereof, can be operatively
- 25 linked to a non-RRP polypeptide to form a fusion protein. In preferred embodiments, this fusion protein has an activity which differs from that of the RRP protein alone. In other preferred embodiments, this fusion protein participates in the replication of *C. glutamicum* DNA, participates in *C. glutamicum* protein synthesis, or contributes to the pathogenicity of the microorganism. In particularly preferred embodiments, integration
- 30 of this fusion protein into a host cell modulates production of a desired compound from the cell.

- In another aspect, the invention provides methods for screening molecules which modulate the activity of an RRP protein, either by interacting with the protein itself or a substrate or binding partner of the RRP protein, or by modulating the transcription or
- 35 translation of an RRP nucleic acid molecule of the invention.

Another aspect of the invention pertains to a method for producing a fine chemical. This method involves the culturing of a cell containing a vector directing the

expression of an RRP nucleic acid molecule of the invention, such that a fine chemical is produced. In a preferred embodiment, this method further includes the step of obtaining a cell containing such a vector, in which a cell is transfected with a vector directing the expression of an RRP nucleic acid. In another preferred embodiment, this method further includes the step of recovering the fine chemical from the culture. In a particularly preferred embodiment, the cell is from the genus *Corynebacterium* or *Brevibacterium*, or is selected from those strains set forth in Table 3.

Another aspect of the invention pertains to methods for modulating production of a molecule from a microorganism. Such methods include contacting the cell with an agent which modulates RRP protein activity or RRP nucleic acid expression such that a cell associated activity is altered relative to this same activity in the absence of the agent. In a preferred embodiment, the cell is modulated for one or more *C. glutamicum* processes involved in the replication of *C. glutamicum* DNA, in *C. glutamicum* protein synthesis, or in the pathogenicity of the microorganism. The agent which modulates RRP protein activity can be an agent which stimulates RRP protein activity or RRP nucleic acid expression. Examples of agents which stimulate RRP protein activity or RRP nucleic acid expression include small molecules, active RRP proteins, and nucleic acids encoding RRP proteins that have been introduced into the cell. Examples of agents which inhibit RRP activity or expression include small molecules and antisense RRP nucleic acid molecules.

Another aspect of the invention pertains to methods for modulating yields of a desired compound from a cell, involving the introduction of a wild-type or mutant RRP gene into a cell, either maintained on a separate plasmid or integrated into the genome of the host cell. If integrated into the genome, such integration can be random, or it can take place by homologous recombination such that the native gene is replaced by the introduced copy, causing the production of the desired compound from the cell to be modulated. In a preferred embodiment, said yields are increased. In another preferred embodiment, said chemical is a fine chemical. In a particularly preferred embodiment, said fine chemical is an amino acid. In especially preferred embodiments, said amino acid is L-lysine.

#### **Detailed Description of the Invention**

The present invention provides RRP nucleic acid and protein molecules which are involved in *C. glutamicum* DNA replication, protein synthesis, or pathogenesis. The molecules of the invention may be utilized in the modulation of production of fine chemicals from microorganisms, such as *C. glutamicum*, either directly (e.g., where increased activity of a ribosome permits increased production of fine chemical

- biosynthetic proteins, which may result in increased yields, production, or efficiency of production of one or more fine chemicals from the modified *C. glutamicum*), or may have an indirect impact which nonetheless results in an increase of yield, production, and/or efficiency of production of the desired compound (e.g., where modulation of the activity or number of copies of a *C. glutamicum* DNA synthesis protein results in an increase in the rate of *C. glutamicum* cell division, resulting in greater numbers of viable cells in culture, which in turn permits increased production in a large-scale culture setting). Aspects of the invention are further explicated below.

## 10 I. Fine Chemicals

- The term "fine chemical" is art-recognized and includes molecules produced by an organism which have applications in various industries, such as, but not limited to, the pharmaceutical, agriculture, and cosmetics industries. Such compounds include organic acids, such as tartaric acid, itaconic acid, and diaminopimelic acid, both
- 15 proteinogenic and non-proteinogenic amino acids, purine and pyrimidine bases, nucleosides, and nucleotides (as described e.g. in Kuninaka, A. (1996) Nucleotides and related compounds, p. 561-612, in Biotechnology vol. 6, Rehm *et al.*, eds. VCH: Weinheim, and references contained therein), lipids, both saturated and unsaturated fatty acids (e.g., arachidonic acid), diols (e.g., propane diol, and butane diol), carbohydrates
- 20 (e.g., hyaluronic acid and trehalose), aromatic compounds (e.g., aromatic amines, vanillin, and indigo), vitamins and cofactors (as described in Ullmann's Encyclopedia of Industrial Chemistry, vol. A27, "Vitamins", p. 443-613 (1996) VCH: Weinheim and references therein; and Ong, A.S., Niki, E. & Packer, L. (1995) "Nutrition, Lipids, Health, and Disease" Proceedings of the UNESCO/Confederation of Scientific and
- 25 Technological Associations in Malaysia, and the Society for Free Radical Research – Asia, held Sept. 1-3, 1994 at Penang, Malaysia, AOCs Press, (1995)), enzymes, polyketides (Cane *et al.* (1998) *Science* 282: 63-68), toxins, and all other chemicals described in Gutcho (1983) Chemicals by Fermentation, Noyes Data Corporation, ISBN: 0818805086 and references therein. The metabolism and uses of certain of these
- 30 fine chemicals are further explicated below.

### A. Amino Acid Metabolism and Uses

- Amino acids comprise the basic structural units of all proteins, and as such are essential for normal cellular functioning in all organisms. The term "amino acid" is art-
- 35 recognized. The proteinogenic amino acids, of which there are 20 species, serve as structural units for proteins, in which they are linked by peptide bonds, while the nonproteinogenic amino acids (hundreds of which are known) are not normally found in



proteins (see Ulmann's Encyclopedia of Industrial Chemistry, vol. A2, p. 57-97 VCH: Weinheim (1985)). Amino acids may be in the D- or L- optical configuration, though L-amino acids are generally the only type found in naturally-occurring proteins.

- Biosynthetic and degradative pathways of each of the 20 proteinogenic amino acids
- 5 have been well characterized in both prokaryotic and eukaryotic cells (see, for example, Stryer, L. Biochemistry, 3<sup>rd</sup> edition, pages 578-590 (1988)). The 'essential' amino acids (histidine, isoleucine, leucine, lysine, methionine, phenylalanine, threonine, tryptophan, and valine), so named because they are generally a nutritional requirement due to the complexity of their biosyntheses, are readily converted by simple biosynthetic pathways
- 10 to the remaining 11 'nonessential' amino acids (alanine, arginine, asparagine, aspartate, cysteine, glutamate, glutamine, glycine, proline, serine, and tyrosine). Higher animals do retain the ability to synthesize some of these amino acids, but the essential amino acids must be supplied from the diet in order for normal protein synthesis to occur.

- Aside from their function in protein biosynthesis, these amino acids are
- 15 interesting chemicals in their own right, and many have been found to have various applications in the food, feed, chemical, cosmetics, agriculture, and pharmaceutical industries. Lysine is an important amino acid in the nutrition not only of humans, but also of monogastric animals such as poultry and swine. Glutamate is most commonly used as a flavor additive (mono-sodium glutamate, MSG) and is widely used throughout
- 20 the food industry, as are aspartate, phenylalanine, glycine, and cysteine. Glycine, L-methionine and tryptophan are all utilized in the pharmaceutical industry. Glutamine, valine, leucine, isoleucine, histidine, arginine, proline, serine and alanine are of use in both the pharmaceutical and cosmetics industries. Threonine, tryptophan, and D/L-methionine are common feed additives. (Leuchtenberger, W. (1996) Amino acids - technical production and use, p. 466-502 in Rehm *et al.* (eds.) Biotechnology vol. 6, chapter 14a, VCH: Weinheim). Additionally, these amino acids have been found to be
- 25 useful as precursors for the synthesis of synthetic amino acids and proteins, such as N-acetylcysteine, S-carboxymethyl-L-cysteine, (S)-5-hydroxytryptophan, and others described in Ulmann's Encyclopedia of Industrial Chemistry, vol. A2, p. 57-97, VCH: Weinheim, 1985.
- 30

- The biosynthesis of these natural amino acids in organisms capable of producing them, such as bacteria, has been well characterized (for review of bacterial amino acid biosynthesis and regulation thereof, see Umbarger, H.E. (1978) *Ann. Rev. Biochem.* 47: 533-606). Glutamate is synthesized by the reductive amination of  $\alpha$ -ketoglutarate, an intermediate in the citric acid cycle. Glutamine, proline, and arginine
- 35 are each subsequently produced from glutamate. The biosynthesis of serine is a three-step process beginning with 3-phosphoglycerate (an intermediate in glycolysis), and

resulting in this amino acid after oxidation, transamination, and hydrolysis steps. Both cysteine and glycine are produced from serine; the former by the condensation of homocysteine with serine, and the latter by the transferal of the side-chain  $\beta$ -carbon atom to tetrahydrofolate, in a reaction catalyzed by serine transhydroxymethylase.

- 5 Phenylalanine, and tyrosine are synthesized from the glycolytic and pentose phosphate pathway precursors erythrose 4-phosphate and phosphoenolpyruvate in a 9-step biosynthetic pathway that differ only at the final two steps after synthesis of prephenate. Tryptophan is also produced from these two initial molecules, but its synthesis is an 11-step pathway. Tyrosine may also be synthesized from phenylalanine, in a reaction
- 10 catalyzed by phenylalanine hydroxylase. Alanine, valine, and leucine are all biosynthetic products of pyruvate, the final product of glycolysis. Aspartate is formed from oxaloacetate, an intermediate of the citric acid cycle. Asparagine, methionine, threonine, and lysine are each produced by the conversion of aspartate. Isoleucine is formed from threonine. A complex 9-step pathway results in the production of histidine
- 15 from 5-phosphoribosyl-1-pyrophosphate, an activated sugar.

- Amino acids in excess of the protein synthesis needs of the cell cannot be stored, and are instead degraded to provide intermediates for the major metabolic pathways of the cell (for review see Stryer, L. *Biochemistry* 3<sup>rd</sup> ed. Ch. 21 "Amino Acid Degradation and the Urea Cycle" p. 495-516 (1988)). Although the cell is able to convert unwanted
- 20 amino acids into useful metabolic intermediates, amino acid production is costly in terms of energy, precursor molecules, and the enzymes necessary to synthesize them. Thus it is not surprising that amino acid biosynthesis is regulated by feedback inhibition, in which the presence of a particular amino acid serves to slow or entirely stop its own production (for overview of feedback mechanisms in amino acid biosynthetic pathways,
- 25 see Stryer, L. *Biochemistry*, 3<sup>rd</sup> ed. Ch. 24: "Biosynthesis of Amino Acids and Heme" p. 575-600 (1988)). Thus, the output of any particular amino acid is limited by the amount of that amino acid present in the cell.

#### *B. Vitamin, Cofactor, and Nutraceutical Metabolism and Uses*

- 30 Vitamins, cofactors, and nutraceuticals comprise another group of molecules which the higher animals have lost the ability to synthesize and so must ingest, although they are readily synthesized by other organisms such as bacteria. These molecules are either bioactive substances themselves, or are precursors of biologically active substances which may serve as electron carriers or intermediates in a variety of
- 35 metabolic pathways. Aside from their nutritive value, these compounds also have significant industrial value as coloring agents, antioxidants, and catalysts or other processing aids. (For an overview of the structure, activity, and industrial applications

of these compounds, see, for example, Ullman's Encyclopedia of Industrial Chemistry, "Vitamins" vol. A27, p. 443-613, VCH: Weinheim, 1996.) The term "vitamin" is art-recognized, and includes nutrients which are required by an organism for normal functioning, but which that organism cannot synthesize by itself. The group of vitamins  
5 may encompass cofactors and nutraceutical compounds. The language "cofactor" includes nonproteinaceous compounds required for a normal enzymatic activity to occur. Such compounds may be organic or inorganic; the cofactor molecules of the invention are preferably organic. The term "nutraceutical" includes dietary supplements having health benefits in plants and animals, particularly humans. Examples of such  
10 molecules are vitamins, antioxidants, and also certain lipids (*e.g.*, polyunsaturated fatty acids).

The biosynthesis of these molecules in organisms capable of producing them, such as bacteria, has been largely characterized (Ullman's Encyclopedia of Industrial Chemistry, "Vitamins" vol. A27, p. 443-613, VCH: Weinheim, 1996; Michal, G. (1999)  
15 Biochemical Pathways: An Atlas of Biochemistry and Molecular Biology, John Wiley & Sons; Ong, A.S., Niki, E. & Packer, L. (1995) "Nutrition, Lipids, Health, and Disease" Proceedings of the UNESCO/Confederation of Scientific and Technological Associations in Malaysia, and the Society for Free Radical Research - Asia, held Sept. 1-3, 1994 at Penang, Malaysia, AOCs Press: Champaign, IL X, 374 S).

20 Thiamin (vitamin B<sub>1</sub>) is produced by the chemical coupling of pyrimidine and thiazole moieties. Riboflavin (vitamin B<sub>2</sub>) is synthesized from guanosine-5'-triphosphate (GTP) and ribose-5'-phosphate. Riboflavin, in turn, is utilized for the synthesis of flavin mononucleotide (FMN) and flavin adenine dinucleotide (FAD). The family of compounds collectively termed 'vitamin B<sub>6</sub>' (*e.g.*, pyridoxine, pyridoxamine, pyridoxa-  
25 5'-phosphate, and the commercially used pyridoxin hydrochloride) are all derivatives of the common structural unit, 5-hydroxy-6-methylpyridine. Pantothenate (pantothenic acid, (R)-(+)-N-(2,4-dihydroxy-3,3-dimethyl-1-oxobutyl)- $\beta$ -alanine) can be produced either by chemical synthesis or by fermentation. The final steps in pantothenate biosynthesis consist of the ATP-driven condensation of  $\beta$ -alanine and pantoic acid. The  
30 enzymes responsible for the biosynthesis steps for the conversion to pantoic acid, to  $\beta$ -alanine and for the condensation to pantothenic acid are known. The metabolically active form of pantothenate is Coenzyme A, for which the biosynthesis proceeds in 5 enzymatic steps. Pantothenate, pyridoxal-5'-phosphate, cysteine and ATP are the precursors of Coenzyme A. These enzymes not only catalyze the formation of  
35 pantothenate, but also the production of (R)-pantoic acid, (R)-pantolacton, (R)-panthenol (provitamin B<sub>5</sub>), pantetheine (and its derivatives) and coenzyme A.

Biotin biosynthesis from the precursor molecule pimeloyl-CoA in microorganisms has been studied in detail and several of the genes involved have been identified. Many of the corresponding proteins have been found to also be involved in Fe-cluster synthesis and are members of the nifs class of proteins. Lipoic acid is derived from octanoic acid, and serves as a coenzyme in energy metabolism, where it becomes part of the pyruvate dehydrogenase complex and the  $\alpha$ -ketoglutarate dehydrogenase complex. The folates are a group of substances which are all derivatives of folic acid, which is turn is derived from L-glutamic acid, p-amino-benzoic acid and 6-methylpterin. The biosynthesis of folic acid and its derivatives, starting from the metabolism intermediates guanosine-5'-triphosphate (GTP), L-glutamic acid and p-amino-benzoic acid has been studied in detail in certain microorganisms.

Corrinoids (such as the cobalamines and particularly vitamin B<sub>12</sub>) and porphyrines belong to a group of chemicals characterized by a tetrapyrrole ring system. The biosynthesis of vitamin B<sub>12</sub> is sufficiently complex that it has not yet been completely characterized, but many of the enzymes and substrates involved are now known. Nicotinic acid (nicotinate), and nicotinamide are pyridine derivatives which are also termed 'niacin'. Niacin is the precursor of the important coenzymes NAD (nicotinamide adenine dinucleotide) and NADP (nicotinamide adenine dinucleotide phosphate) and their reduced forms.

The large-scale production of these compounds has largely relied on cell-free chemical syntheses, though some of these chemicals have also been produced by large-scale culture of microorganisms, such as riboflavin, Vitamin B<sub>6</sub>, pantothenate, and biotin. Only Vitamin B<sub>12</sub> is produced solely by fermentation, due to the complexity of its synthesis. *In vitro* methodologies require significant inputs of materials and time, often at great cost.

#### *C. Purine, Pyrimidine, Nucleoside and Nucleotide Metabolism and Uses*

Purine and pyrimidine metabolism genes and their corresponding proteins are important targets for the therapy of tumor diseases and viral infections. The language "purine" or "pyrimidine" includes the nitrogenous bases which are constituents of nucleic acids, co-enzymes, and nucleotides. The term "nucleotide" includes the basic structural units of nucleic acid molecules, which are comprised of a nitrogenous base, a pentose sugar (in the case of RNA, the sugar is ribose; in the case of DNA, the sugar is D-deoxyribose), and phosphoric acid. The language "nucleoside" includes molecules which serve as precursors to nucleotides, but which are lacking the phosphoric acid moiety that nucleotides possess. By inhibiting the biosynthesis of these molecules, or their mobilization to form nucleic acid molecules, it is possible to inhibit RNA and DNA

synthesis; by inhibiting this activity in a fashion targeted to cancerous cells, the ability of tumor cells to divide and replicate may be inhibited. Additionally, there are nucleotides which do not form nucleic acid molecules, but rather serve as energy stores (*i.e.*, AMP) or as coenzymes (*i.e.*, FAD and NAD).

- 5        Several publications have described the use of these chemicals for these medical indications, by influencing purine and/or pyrimidine metabolism (*e.g.* Christopherson, R.I. and Lyons, S.D. (1990) "Potent inhibitors of *de novo* pyrimidine and purine biosynthesis as chemotherapeutic agents." *Med. Res. Reviews* 10: 505-548). Studies of enzymes involved in purine and pyrimidine metabolism have been focused on the
- 10    development of new drugs which can be used, for example, as immunosuppressants or anti-proliferants (Smith, J.L., (1995) "Enzymes in nucleotide synthesis." *Curr. Opin. Struct. Biol.* 5: 752-757; (1995) *Biochem Soc. Transact.* 23: 877-902). However, purine and pyrimidine bases, nucleosides and nucleotides have other utilities: as intermediates in the biosynthesis of several fine chemicals (*e.g.*, thiamine, S-adenosyl-methionine,
- 15    folates, or riboflavin), as energy carriers for the cell (*e.g.*, ATP or GTP), and for chemicals themselves, commonly used as flavor enhancers (*e.g.*, IMP or GMP) or for several medicinal applications (see, for example, Kuninaka, A. (1996) *Nucleotides and Related Compounds in Biotechnology* vol. 6, Rehm *et al.*, eds. VCH: Weinheim, p. 561-612). Also, enzymes involved in purine, pyrimidine, nucleoside, or nucleotide
- 20    metabolism are increasingly serving as targets against which chemicals for crop protection, including fungicides, herbicides and insecticides, are developed.

- The metabolism of these compounds in bacteria has been characterized (for reviews see, for example, Zalkin, H. and Dixon, J.E. (1992) "*de novo* purine nucleotide biosynthesis", in: *Progress in Nucleic Acid Research and Molecular Biology*, vol. 42, Academic Press:, p. 259-287; and Michal, G. (1999) "Nucleotides and Nucleosides",
- 25    Chapter 8 in: *Biochemical Pathways: An Atlas of Biochemistry and Molecular Biology*, Wiley: New York). Purine metabolism has been the subject of intensive research, and is essential to the normal functioning of the cell. Impaired purine metabolism in higher animals can cause severe disease, such as gout. Purine nucleotides are synthesized from
- 30    ribose-5-phosphate, in a series of steps through the intermediate compound inosine-5'-phosphate (IMP), resulting in the production of guanosine-5'-monophosphate (GMP) or adenosine-5'-monophosphate (AMP), from which the triphosphate forms utilized as nucleotides are readily formed. These compounds are also utilized as energy stores, so their degradation provides energy for many different biochemical processes in the cell.
- 35    Pyrimidine biosynthesis proceeds by the formation of uridine-5'-monophosphate (UMP) from ribose-5-phosphate. UMP, in turn, is converted to cytidine-5'-triphosphate (CTP). The deoxy- forms of all of these nucleotides are produced in a one step reduction

reaction from the diphosphate ribose form of the nucleotide to the diphosphate deoxyribose form of the nucleotide. Upon phosphorylation, these molecules are able to participate in DNA synthesis.

5 *D. Trehalose Metabolism and Uses*

Trehalose consists of two glucose molecules, bound in  $\alpha$ ,  $\alpha$ -1,1 linkage. It is commonly used in the food industry as a sweetener, an additive for dried or frozen foods, and in beverages. However, it also has applications in the pharmaceutical, cosmetics and biotechnology industries (see, for example, Nishimoto *et al.*, (1998) U.S. Patent No. 5,759,610; Singer, M.A. and Lindquist, S. (1998) *Trends Biotech.* 16: 460-467; Paiva, C.L.A. and Panek, A.D. (1996) *Biotech. Ann. Rev.* 2: 293-314; and Shiosaka, M. (1997) *J. Japan* 172: 97-102). Trehalose is produced by enzymes from many microorganisms and is naturally released into the surrounding medium, from which it can be collected using methods known in the art.

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II. Activities of the Genes of the Invention

In order for a population of a particular type of bacterial cells to survive in an environment, at least three activities are necessary. First, the cells must be able to divide efficiently, such that the population is at least maintained, if not increased. Second, the cells must be able to efficiently express those genes encoding proteins necessary for normal cellular functioning. Finally, the cells must be able to influence their interaction with the surrounding environment, either by adaptation to the prevailing environmental conditions, by physical movement to preferred surroundings, or by directly altering the surrounding environment such that their own viability is improved. Critical processes involved in each of the aforementioned activities include replication of the bacterial genome, the action of the ribosome in protein synthesis, and anticellular or cell lytic activities (such as those involved in the pathogenesis of an organism).

*A. DNA Replication*

In order for a cell (*e.g.*, a bacterial cell) to divide to form viable progeny cells, the cellular genome must be replicated. This is a multistep process, in which the tightly packaged DNA must first be locally freed from topological constraints, the two strands of the double helix must be unwound, a DNA polymerase must synthesize a new strand of DNA complementary to one of the original strands, and both the old and the new strands must be repackaged. Each of these steps is described in greater detail in the following section (see, *e.g.*, Michal, G. (1999) *Biochemical Pathways: An Atlas of Biochemistry and Molecular Biology*, Wiley: New York, and references therein; and

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Griffiths, A.J.F. *et al.*, (1993) *An Introduction to Genetic Analysis*, 5<sup>th</sup> ed., Freeman: New York p. 304-332 and references therein).

The general structure of genomic DNA in bacterial cells has been characterized. Bacterial chromosomes are usually circular in nature, and bacterial cells may also  
5 contain one or more different types of plasmids (also circular pieces of DNA, although usually significantly smaller in size than the bacterial chromosome) which may be replicated and incorporated into the daughter cell simultaneously with the chromosome. Replication of either of these circular pieces of genetic information typically begins at a single designated origin of replication (*ori*). Replication of the DNA may then take place  
10 either in one direction around the circle (rolling circle replication) until the origin is again reached, or it may occur in both directions simultaneously ( $\theta$ -mechanism).

The *ori* site has a particular structure which permits the initiation of replication. First, the *ori* region typically contains multiple sequences which serve as binding sites for initiator proteins. The binding of the initiator proteins (*e.g.*, DnaA in *E. coli*) to these  
15 binding sites at the origin takes place in an ATP-dependent fashion. Upon ATP hydrolysis, the DNA bends around these DNA-associated molecules, and the two strands of DNA at the site separate, forming an open complex.

The molecule responsible for the actual synthesis of the new DNA molecule is a DNA polymerase. For replication purposes, the DNA polymerase utilized by the cell is  
20 the DNA polymerase III (Pol III) holoenzyme. This complex comprises 10 molecules, each of which has a different function in the complex. For example, the dimeric  $\gamma$  subunit acts to associate the  $\beta$  subunit with a primed DNA template in an ATP-dependent fashion. The  $\beta$  subunit is the 'processivity factor' – the portion of the holoenzyme which specifically associates with the DNA template and which permits the  
25 template to 'slide' along the DNA due to its ring-like structure. The  $\alpha$  subunit catalyzes the reaction which adds the new dNTP to the nascent nucleotide strand, and the  $\epsilon$  subunit contains the 3'-5' exonuclease activity.

A significant topological barrier to DNA synthesis exists due to the structure of a DNA molecule and to that of the bacterial chromosome. Not only must the double helix  
30 of the DNA molecule be split such that a single strand may be replicated, but this unwinding process results in increased positive supercoiling of the chromosome. Two types of enzymes permit these processes to occur despite the topological constraints: helicase unwinds the double helix in an ATP-dependent fashion, introducing positive supercoils into the bacterial chromosome. Gyrase introduces negative supercoils into  
35 the bacterial genome (in an ATP-dependent fashion), counteracting the positive supercoils introduced by the helicase. The result of their combined is a replication fork: a split between the two strands of DNA in which replication of each strand of the DNA

can occur. Single-stranded binding proteins (SSBs) bind to the unwound DNA molecules to prevent them from reassociating.

In order for Pol III to initiate DNA synthesis, it must have a sequence from which to prime synthesis. Primase (*E. coli* DnaG) synthesizes RNA primers as starting  
5 sequences for Pol III. The Pol III complex gamma subunit associates with the newly synthesized primers and subsequently associates with the dimeric beta Pol III subunits, initiating DNA synthesis. Replication of each strand takes place simultaneously, but because Pol III polymerizes dNTPs only in the 5'-3' direction, only one strand (the 3'-5' leading strand) can be continuously replicated. The other strand (the complementary  
10 lagging strand) is replicated in short fragments (Okazaki fragments), due to the lack of progressivity of the polymerase in this direction. These fragments are subsequently ligated by DNA ligase to form a single strand. Incorrectly added bases are excised by the 3'-5' exonuclease activity of Pol III and the nick sealed by DNA ligase.

Bacterial DNA replication is terminated at a site opposite to the origin at which  
15 terminator proteins bind. The association of these proteins with the DNA prevents the replication fork from progressing. The RNA primer used to initiate DNA synthesis is degraded by DNA polymerase I (Pol I) or ribonuclease H (RnaseH), and Pol I adds the appropriate dNTPs to the gap. Finally, DNA ligase seals the nicks. To achieve  
semiconservative replication, the two strands of the parental bacterial chromosome are  
20 separated by topoisomerases and are each paired with the complementary daughter strand.

#### *B. Protein Synthesis*

Protein synthesis is a multistep process which converts mRNA to the corresponding  
25 polypeptide chain (see, e.g., Michal, G. (1999) *Biochemical Pathways: An Atlas of Biochemistry and Molecular Biology*, Wiley: New York, and references therein; and Griffiths, A.J.F. *et al.*, (1993) *An Introduction to Genetic Analysis*, 5<sup>th</sup> ed., Freeman: New York p. 391-398 and references therein). As the initiator codon (AUG, encoding methionine) first becomes accessible after being transcribed from the DNA by RNA  
30 polymerase, a translation initiation complex forms. This complex is comprised of the mRNA molecule itself, an initiation tRNA molecule (charged with methionine, corresponding to the first AUG codon of the mRNA molecule, and which has also been formylated to form the N-terminus of the nascent polypeptide), initiation factors, and the ribosome itself.

35 The bacterial ribosome (the 70S ribosome) contains two subunits. The first subunit is large (50S) while the second is small (30S). Each subunit contains a complex of RNA and protein molecules which assemble soon after or during their synthesis.



These complexes are globular in shape, and the large subunit contains a long channel through which it is believed that the nascent polypeptide chain leaves the ribosome. There are at least three known sites of activity in the bacterial ribosome: one to bind a charged tRNA (aminoacyl tRNA), one to bind a tRNA associated with the nascent polypeptide chain, and the third to expel the uncharged tRNA from the complex. Ribosomes may occur singly or in groups, termed 'polyribosomes' or 'polysomes'. These complexes are plentiful within the cell; one *E. coli* cell may contain as many as 15,000 ribosomes, constituting up to one quarter of the total biomass of the cell.

Upon the binding of the initiator tRNA<sup>met</sup> in complex with the initiation factor IF-2 and GTP, the 30S ribosomal subunit binds such that the tRNA anticodon is associated with the peptidyl site in this molecule. The binding of the 50S subunit to this complex causes hydrolysis of the bound GTP, with concomitant release of the initiation factors. The amino-acid-charged tRNA corresponding to the second codon of the mRNA is positioned in the aminoacyl tRNA site in the ribosome (by the action of the elongation factor EF-Tu). The methionine attached to the tRNA in the peptidyl site and the amino acid bound to the tRNA in the aminoacyl site react to form a peptide bond, catalyzed by the peptidyltransferase activity of the 23S rRNA in the complex. Two simultaneous translocation steps subsequently occur in a GTP-dependent fashion: the nascent polypeptide-bound (peptidyl) tRNA remaining in the aminoacyl site is translocated to the peptidyl site of the ribosome (with concomitant displacement of the now uncharged tRNA in the peptidyl site to the ejection site), and the mRNA moves one codon site relative to the ribosome such that the next codon is exposed to the aminoacyl-tRNA site on the ribosome.

This cycle of amino acid addition and elongation of the peptide chain continues until a stop codon (UAA, UGA, UAG) is reached. There do not exist tRNA molecules specific for these stop codons; thus, no amino acid can be added. Instead, one of two release factors (specific to the particular codon in question) binds to the mRNA at the stop codon in a complex with release factor 3 and GTP. The release of the nascent polypeptide chain is accomplished by the hydrolysis of this GTP, and the remaining bound ribosomal subunits are dissociated through the activity of the ribosomal recycling factor.

### C. Pathogenesis

Bacteria possess numerous mechanisms by which they are able to survive and even to adapt to environments with suboptimal growth conditions. These include protective elements (e.g., the cell wall, which prevents osmotic lysis), the ability to switch to the utilization of different nutrient sources (e.g., inorganic compounds, or

carbon sources), and the ability to adjust to different stresses (e.g., temperature stress, osmotic stress, pH stress, or oxygen stress) by the activation of a sigma factor regulatory cascade. Under growth conditions in a complex environment containing cells other than the bacterium, many bacteria are capable of another survival mechanism: pathogenesis.

- 5 In order to survive in a host (e.g., a plant, animal, or human host), bacteria must be able to not only defend themselves against killing or removal by host immune systems, but also to proliferate. Many bacteria have developed multiple mechanisms by which each goal may be accomplished (see, e.g., Stanier *et al.* (1986) *The Microbial World* 5<sup>th</sup> ed., Prentice Hall: Englewood Cliffs and references therein; and Hacker, J.
- 10 (1999) "Prokaryotes in Medicine" in "Biology of the Prokaryotes, Lengeler *et al.*, eds., Thieme Verlag: Stuttgart, p. 815-849, and references therein). Many bacteria produce peptide or protein toxins (e.g., hemolysins, or diphtheria toxin from *Corynebacterium diphtheriae*) which act to specifically or nonspecifically destroy host cells. Frequently these toxins are directed to immune cells which would otherwise act to remove the
- 15 bacteria from the host. Such toxins may exert their lethal effect in a variety of ways, including by inhibition of protein synthesis in the target cell (e.g., exotoxin A from *Pseudomonas aeruginosa* or diphtheria toxin), by interfering with cellular signal transduction in the target cell (e.g., anthrax lethal toxin, cholera toxin), or by simply creating holes in the target cell membrane which lead to cell lysis (e.g., hemolysins).
- 20 These toxic activities manifest as a disease, for example, diphtheria, tuberculosis (*Mycobacterium bovis* or *M. tuberculosis*), anthrax (*Bacillus anthracis*).

Proliferation (i.e., colonization) of the bacterial cells depends on special factors termed adhesion factors or adhesins. These frequently proteinaceous molecules at the cell surface of the bacterium permit the bacterium to bind to one or more specific host

25 cells or surfaces. This not only permits the bacterium to not be removed by circulatory and excretory processes, but it also limits the exposure of the bacterium to the host immune system, since the bacteria remain stationary and sometimes even inaccessible once adhered to a surface.

- Corynebacterium glutamicum* is a soil bacterium not known to be pathogenic,
- 30 but its genome surprisingly includes several genes which are typically associated with bacterial pathogenesis, but the expression of which has never been observed. Similar situations have been observed in other bacteria: a bacterial species may have stains which are virulent (disease causing) and avirulent (nonpathogenic). A classic example of this is *E. coli*, from which both virulent (e.g., enteropathogenic species) and avirulent
- 35 (e.g., K-12 strains) are well known. Certain bacteria are typically not pathogenic, but may still contain within their genome genes encoding proteins involved in pathogenicity, such as adhesins or toxins. These may be a evolutionary remnant, or may

simply only be expressed under specific conditions which the bacterium rarely encounters.

### III. Elements and Methods of the Invention

5       The present invention is based, at least in part, on the discovery of novel molecules, referred to herein as RRP nucleic acid and protein molecules, which participate in *C. glutamicum* DNA replication, protein synthesis, or pathogenesis. In one embodiment, the RRP molecules participate in the replication of *C. glutamicum* DNA, in *C. glutamicum* ribosome activity, or in the pathogenicity of the microorganism. In a  
10       preferred embodiment, the activity of the RRP molecules of the present invention with regard to DNA replication, protein synthesis, or pathogenesis has an impact on the production of a desired fine chemical by this organism. In a particularly preferred embodiment, the RRP molecules of the invention are modulated in activity, such that the *C. glutamicum* cellular processes in which the RRP molecules participate (e.g., DNA  
15       replication, protein synthesis, or pathogenesis) are also altered in activity, resulting either directly or indirectly in a modulation of the yield, production, and/or efficiency of production of a desired fine chemical by *C. glutamicum*.

      The language, "RRP protein" or "RRP polypeptide" includes proteins which participate in a number of cellular processes related to *C. glutamicum* DNA replication, protein synthesis, or pathogenesis. For example, an RRP protein may be involved in the  
20       replication of *C. glutamicum* DNA, in *C. glutamicum* ribosome activity, or in the pathogenicity of the microorganism. Examples of RRP proteins include those encoded by the RRP genes set forth in Table 1 and Appendix A. The terms "RRP gene" or "RRP nucleic acid sequence" include nucleic acid sequences encoding an RRP protein, which  
25       consist of a coding region and also corresponding untranslated 5' and 3' sequence regions. Examples of RRP genes include those set forth in Table 1. The terms "production" or "productivity" are art-recognized and include the concentration of the fermentation product (for example, the desired fine chemical) formed within a given time and a given fermentation volume (e.g., kg product per hour per liter). The term  
30       "efficiency of production" includes the time required for a particular level of production to be achieved (for example, how long it takes for the cell to attain a particular rate of output of a fine chemical). The term "yield" or "product/carbon yield" is art-recognized and includes the efficiency of the conversion of the carbon source into the product (i.e., fine chemical). This is generally written as, for example, kg product per kg carbon  
35       source. By increasing the yield or production of the compound, the quantity of recovered molecules, or of useful recovered molecules of that compound in a given amount of culture over a given amount of time is increased. The terms "biosynthesis" or

a "biosynthetic pathway" are art-recognized and include the synthesis of a compound, preferably an organic compound, by a cell from intermediate compounds in what may be a multistep and highly regulated process. The terms "degradation" or a "degradation pathway" are art-recognized and include the breakdown of a compound, preferably an organic compound, by a cell to degradation products (generally speaking, smaller or less complex molecules) in what may be a multistep and highly regulated process. The language "metabolism" is art-recognized and includes the totality of the biochemical reactions that take place in an organism. The metabolism of a particular compound, then, (e.g., the metabolism of an amino acid such as glycine) comprises the overall biosynthetic, modification, and degradation pathways in the cell related to this compound. The language "pathogenicity" or "pathogenesis" is art-recognized and includes the activity of an organism, such as a bacterial organism, to bring about a disease state in a host (e.g., cholera, diphtheria, or anthrax). Such disease states are typically the result of cell lytic activity of the organism, which may occur through the expression and release of cytotoxins (e.g., cholera toxin, diphtheria toxin, or anthrax toxin). Other bacterial proteins or peptides not pertaining specifically to cell lysis but contributing to the colonization of the host by the bacterium may also be considered pathogenesis proteins, such as, but not limited to, adhesins. The term "DNA replication" is art-recognized and includes all of the activities associated with the replication of DNA *in vivo* or *in vitro*, and for the purposes of the invention, particularly within bacterial cells. These activities include but are not limited to the assembly of DNA polymerases, the unwinding of DNA, the incorporation of new dNTPs into the nascent DNA strand, the excision and replacement of erroneous bases, and the termination of replication. The term "protein synthesis" is art-recognized and includes the process of converting mRNA codons into amino acids in a growing polypeptide chain, as catalyzed by the ribosome. The term "ribosome function" or "ribosome activity" is art-recognized and includes all of the functions of a ribosome, including, but not limited to, the binding of mRNA, the binding of an aminoacyl-tRNA and a peptidyl-tRNA, and the catalysis of the addition of the next amino acid to the growing polypeptide chain.

In another embodiment, the RRP molecules of the invention are capable of modulating the production of a desired molecule, such as a fine chemical, in a microorganism such as *C. glutamicum*. There are a number of mechanisms by which the alteration of an RRP protein of the invention may affect the yield, production, and/or efficiency of production of a fine chemical from a *C. glutamicum* strain incorporating such an altered protein. For example, by improving the rate at which DNA replication occurs (e.g., by optimizing the activity of one or more DNA polymerase, or by

improving the rate at which the topoisomerases or helicases of the invention unwind DNA) it may be possible to increase the rate of cell division, which in turn increases the number of viable fine-chemical-producing *C. glutamicum* cells present in large-scale culture settings. Similarly, by improving the rate at which mRNA is translated to protein (e.g., by optimizing the activity of one or more of the ribosomal proteins) it may be possible to increase the number of proteins in the cell which participate in the synthesis of one or more desired fine chemicals, or in an overall increase in the rate of cell division (due to increased growth and metabolism), both of which should lead to increased production of one or more fine chemicals from large-scale fermentor cultures of these microorganisms. Alterations in the DNA replication proteins of the invention may also permit increased fidelity in the replicative process, thereby increasing the genetic stability and viability of the microorganism and lessening the chance that another engineered mutation improving fine chemical production will not be inadvertently mutagenized by error-prone replication. The RRP proteins of the invention involved in pathogenesis are themselves fine chemicals; by increasing the number or by engineering the corresponding genes such that the expression of these proteins is removed from cellular repression pathways, or by mutagenizing the proteins such that feedback regulatory regions are removed, it may be possible to increase the yield, production, and/or efficiency of production of these proteins from large-scale fermentor culture of organisms containing such mutations.

The isolated nucleic acid sequences of the invention are contained within the genome of a *Corynebacterium glutamicum* strain available through the American Type Culture Collection, given designation ATCC 13032. The nucleotide sequence of the isolated *C. glutamicum* RRP DNAs and the predicted amino acid sequences of the *C. glutamicum* RRP proteins are shown in Appendices A and B, respectively. Computational analyses were performed which classified and/or identified these nucleotide sequences as sequences which encode proteins that participate in the replication of *C. glutamicum* DNA, in *C. glutamicum* ribosome activity, or in the pathogenicity of this microorganism.

The present invention also pertains to proteins which have an amino acid sequence which is substantially homologous to an amino acid sequence of Appendix B. As used herein, a protein which has an amino acid sequence which is substantially homologous to a selected amino acid sequence is least about 50% homologous to the selected amino acid sequence, e.g., the entire selected amino acid sequence. A protein which has an amino acid sequence which is substantially homologous to a selected amino acid sequence can also be least about 50-60%, preferably at least about 60-70%, and more preferably at least about 70-80%, 80-90%, or 90-95%, and most preferably at

least about 96%, 97%, 98%, 99% or more homologous to the selected amino acid sequence.

- The RRP protein or a biologically active portion or fragment thereof of the invention can participate in *C. glutamicum* DNA replication, in *C. glutamicum* protein synthesis, or in the pathogenicity of this microorganism, or have one or more of the activities set forth in Table 1.

Various aspects of the invention are described in further detail in the following subsections.

#### 10 A. Isolated Nucleic Acid Molecules

- One aspect of the invention pertains to isolated nucleic acid molecules that encode RRP polypeptides or biologically active portions thereof, as well as nucleic acid fragments sufficient for use as hybridization probes or primers for the identification or amplification of RRP-encoding nucleic acid (e.g., RRP DNA). As used herein, the term "nucleic acid molecule" is intended to include DNA molecules (e.g., cDNA or genomic DNA) and RNA molecules (e.g., mRNA) and analogs of the DNA or RNA generated using nucleotide analogs. This term also encompasses untranslated sequence located at both the 3' and 5' ends of the coding region of the gene: at least about 100 nucleotides of sequence upstream from the 5' end of the coding region and at least about 20 nucleotides of sequence downstream from the 3' end of the coding region of the gene. The nucleic acid molecule can be single-stranded or double-stranded, but preferably is double-stranded DNA. An "isolated" nucleic acid molecule is one which is separated from other nucleic acid molecules which are present in the natural source of the nucleic acid. Preferably, an "isolated" nucleic acid is free of sequences which naturally flank the nucleic acid (i.e., sequences located at the 5' and 3' ends of the nucleic acid) in the genomic DNA of the organism from which the nucleic acid is derived. For example, in various embodiments, the isolated RRP nucleic acid molecule can contain less than about 5 kb, 4kb, 3kb, 2kb, 1 kb, 0.5 kb or 0.1 kb of nucleotide sequences which naturally flank the nucleic acid molecule in genomic DNA of the cell from which the nucleic acid is derived (e.g., a *C. glutamicum* cell). Moreover, an "isolated" nucleic acid molecule, such as a DNA molecule, can be substantially free of other cellular material, or culture medium when produced by recombinant techniques, or chemical precursors or other chemicals when chemically synthesized.

- A nucleic acid molecule of the present invention, e.g., a nucleic acid molecule having a nucleotide sequence of Appendix A, or a portion thereof, can be isolated using standard molecular biology techniques and the sequence information provided herein. For example, a *C. glutamicum* RRP DNA can be isolated from a *C. glutamicum* library

- using all or portion of one of the sequences of Appendix A as a hybridization probe and standard hybridization techniques (e.g., as described in Sambrook, J., Fritsh, E. F., and Maniatis, T. *Molecular Cloning: A Laboratory Manual. 2nd, ed., Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989*).
- 5 Moreover, a nucleic acid molecule encompassing all or a portion of one of the sequences of Appendix A can be isolated by the polymerase chain reaction using oligonucleotide primers designed based upon this sequence (e.g., a nucleic acid molecule encompassing all or a portion of one of the sequences of Appendix A can be isolated by the polymerase chain reaction using oligonucleotide primers designed based upon this same sequence of
- 10 Appendix A). For example, mRNA can be isolated from normal endothelial cells (e.g., by the guanidinium-thiocyanate extraction procedure of Chirgwin *et al.* (1979) *Biochemistry* 18: 5294-5299) and DNA can be prepared using reverse transcriptase (e.g., Moloney MLV reverse transcriptase, available from Gibco/BRL, Bethesda, MD; or AMV reverse transcriptase, available from Seikagaku America, Inc., St. Petersburg, FL).
- 15 Synthetic oligonucleotide primers for polymerase chain reaction amplification can be designed based upon one of the nucleotide sequences shown in Appendix A. A nucleic acid of the invention can be amplified using cDNA or, alternatively, genomic DNA, as a template and appropriate oligonucleotide primers according to standard PCR amplification techniques. The nucleic acid so amplified can be cloned into an
- 20 appropriate vector and characterized by DNA sequence analysis. Furthermore, oligonucleotides corresponding to an RRP nucleotide sequence can be prepared by standard synthetic techniques, e.g., using an automated DNA synthesizer.

In a preferred embodiment, an isolated nucleic acid molecule of the invention comprises one of the nucleotide sequences shown in Appendix A. The sequences of

25 Appendix A correspond to the *Corynebacterium glutamicum* RRP DNAs of the invention. This DNA comprises sequences encoding RRP proteins (*i.e.*, the "coding region", indicated in each sequence in Appendix A), as well as 5' untranslated sequences and 3' untranslated sequences, also indicated in Appendix A. Alternatively, the nucleic acid molecule can comprise only the coding region of any of the sequences in Appendix

30 A.

For the purposes of this application, it will be understood that each of the sequences set forth in Appendix A has an identifying RXA or RXN number having the designation "RXA", or "RXN" followed by 5 digits (*i.e.*, RXA00823 or RXN00625). Each of these sequences comprises up to three parts: a 5' upstream region, a coding

35 region, and a downstream region. Each of these three regions is identified by the same RXA or RXN designation to eliminate confusion. The recitation "one of the sequences in Appendix A", then, refers to any of the sequences in Appendix A, which may be

distinguished by their differing RXA or RXN designations. The coding region of each of these sequences is translated into a corresponding amino acid sequence, which is set forth in Appendix B. The sequences of Appendix B are identified by the same RXA or RXN designations as Appendix A, such that they can be readily correlated. For example, the amino acid sequences in Appendix B designated RXA00823 and RXN00625 are translations of the coding regions of the nucleotide sequence of nucleic acid molecules RXA00823 and RXN00625, respectively, in Appendix A. Each of the RXA and RXN nucleotide and amino acid sequences of the invention has also been assigned a SEQ ID NO, as indicated in Table 1. For example, as set forth in Table 1, the nucleic acid sequence of RXA01064 is SEQ ID NO:13, and the amino acid sequence of RXA01064 is SEQ ID NO:14.

Several of the genes of the invention are "F-designated genes". An F-designated gene includes those genes set forth in Table 1 which have an 'F' in front of the RXA or RXN designation. For example, SEQ ID NO:3, designated, as indicated on Table 1, as "F RXA00625", is an F-designated gene, as are SEQ ID NOs: 7, 17, and 25 (designated on Table 1 as "F RXA00538", "F RXA01594", and "F RXA00562", respectively).

In one embodiment, the nucleic acid molecules of the present invention are not intended to include those compiled in Table 2. In the case of the *dapD* gene, a sequence for this gene was published in Wehrmann, A., *et al.* (1998) *J. Bacteriol.* 180(12): 3159-3165. However, the sequence obtained by the inventors of the present application is significantly longer than the published version. It is believed that the published version relied on an incorrect start codon, and thus represents only a fragment of the actual coding region.

In another preferred embodiment, an isolated nucleic acid molecule of the invention comprises a nucleic acid molecule which is a complement of one of the nucleotide sequences shown in Appendix A, or a portion thereof. A nucleic acid molecule which is complementary to one of the nucleotide sequences shown in Appendix A is one which is sufficiently complementary to one of the nucleotide sequences shown in Appendix A such that it can hybridize to one of the nucleotide sequences shown in Appendix A, thereby forming a stable duplex.

In still another preferred embodiment, an isolated nucleic acid molecule of the invention comprises a nucleotide sequence which is at least about 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, or 60%, preferably at least about 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, or 70%, more preferably at least about 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, or 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, or 90%, or 91%, 92%, 93%, 94%, and even more preferably at least about 95%, 96%, 97%, 98%, 99% or more homologous to a nucleotide sequence shown



in Appendix A, or a portion thereof. Ranges and identity values intermediate to the above-recited ranges, (e.g., 70-90% identical or 80-95% identical) are also intended to be encompassed by the present invention. For example, ranges of identity values using a combination of any of the above values recited as upper and/or lower limits are intended to be included. In an additional preferred embodiment, an isolated nucleic acid molecule of the invention comprises a nucleotide sequence which hybridizes, e.g., hybridizes under stringent conditions, to one of the nucleotide sequences shown in Appendix A, or a portion thereof.

Moreover, the nucleic acid molecule of the invention can comprise only a portion of the coding region of one of the sequences in Appendix A, for example a fragment which can be used as a probe or primer or a fragment encoding a biologically active portion of an RRP protein. The nucleotide sequences determined from the cloning of the RRP genes from *C. glutamicum* allows for the generation of probes and primers designed for use in identifying and/or cloning RRP homologues in other cell types and organisms, as well as RRP homologues from other *Corynebacteria* or related species. The probe/primer typically comprises substantially purified oligonucleotide. The oligonucleotide typically comprises a region of nucleotide sequence that hybridizes under stringent conditions to at least about 12, preferably about 25, more preferably about 40, 50 or 75 consecutive nucleotides of a sense strand of one of the sequences set forth in Appendix A, an anti-sense sequence of one of the sequences set forth in Appendix A, or naturally occurring mutants thereof. Primers based on a nucleotide sequence of Appendix A can be used in PCR reactions to clone RRP homologues. Probes based on the RRP nucleotide sequences can be used to detect transcripts or genomic sequences encoding the same or homologous proteins. In preferred embodiments, the probe further comprises a label group attached thereto, e.g. the label group can be a radioisotope, a fluorescent compound, an enzyme, or an enzyme co-factor. Such probes can be used as a part of a diagnostic test kit for identifying cells which misexpress an RRP protein, such as by measuring a level of an RRP-encoding nucleic acid in a sample of cells, e.g., detecting RRP mRNA levels or determining whether a genomic RRP gene has been mutated or deleted.

In one embodiment, the nucleic acid molecule of the invention encodes a protein or portion thereof which includes an amino acid sequence which is sufficiently homologous to an amino acid sequence of Appendix B such that the protein or portion thereof maintains the ability to participate in the replication of *C. glutamicum* DNA, in *C. glutamicum* protein synthesis, or in the pathogenicity of this microorganism. As used herein, the language "sufficiently homologous" refers to proteins or portions thereof which have amino acid sequences which include a minimum number of identical or

equivalent (e.g., an amino acid residue which has a similar side chain as an amino acid residue in one of the sequences of Appendix B) amino acid residues to an amino acid sequence of Appendix B such that the protein or portion thereof is able to participate in the replication of *C. glutamicum* DNA, in *C. glutamicum* protein synthesis, or in the pathogenicity of this microorganism. Proteins involved in *C. glutamicum* DNA replication, in ribosome function/activity, or in the pathogenesis of this microorganism, as described herein, may play a role in the production and secretion of one or more fine chemicals. Examples of such activities are also described herein. Thus, "the function of an RRP protein" contributes either directly or indirectly to the yield, production, and/or efficiency of production of one or more fine chemicals. Examples of RRP protein activities are set forth in Table 1.

In another embodiment, the protein is at least about 50-60%, preferably at least about 60-70%, and more preferably at least about 70-80%, 80-90%, 90-95%, and most preferably at least about 96%, 97%, 98%, 99% or more homologous to an entire amino acid sequence of Appendix B.

Portions of proteins encoded by the RRP nucleic acid molecules of the invention are preferably biologically active portions of one of the RRP proteins. As used herein, the term "biologically active portion of an RRP protein" is intended to include a portion, e.g., a domain/motif, of an RRP protein that can participate in the replication of *C. glutamicum* DNA, in *C. glutamicum* protein synthesis, or in the pathogenicity of this microorganism, or has an activity as set forth in Table 1. To determine whether an RRP protein or a biologically active portion thereof can participate in the replication of *C. glutamicum* DNA, in *C. glutamicum* protein synthesis, or in the pathogenicity of this microorganism, an assay of enzymatic/protein activity may be performed. Such assay methods are well known to those of ordinary skill in the art, as detailed in Example 8 of the Exemplification.

Additional nucleic acid fragments encoding biologically active portions of an RRP protein can be prepared by isolating a portion of one of the sequences in Appendix B, expressing the encoded portion of the RRP protein or peptide (e.g., by recombinant expression *in vitro*) and assessing the activity of the encoded portion of the RRP protein or peptide.

The invention further encompasses nucleic acid molecules that differ from one of the nucleotide sequences shown in Appendix A (and portions thereof) due to degeneracy of the genetic code and thus encode the same RRP protein as that encoded by the nucleotide sequences shown in Appendix A. In another embodiment, an isolated nucleic acid molecule of the invention has a nucleotide sequence encoding a protein having an amino acid sequence shown in Appendix B. In a still further embodiment, the nucleic

acid molecule of the invention encodes a full length *C. glutamicum* protein which is substantially homologous to an amino acid sequence of Appendix B (encoded by an open reading frame shown in Appendix A).

- It will be understood by one of ordinary skill in the art that in one embodiment
- 5 the sequences of the invention are not meant to include the sequences of the prior art, such as those Genbank sequences set forth in Tables 2 or 4 which were available prior to the present invention. In one embodiment, the invention includes nucleotide and amino acid sequences having a percent identity to a nucleotide or amino acid sequence of the invention which is greater than that of a sequence of the prior art (e.g., a Genbank
- 10 sequence (or the protein encoded by such a sequence) set forth in Tables 2 or 4). For example, the invention includes a nucleotide sequence which is greater than and/or at least 38% identical to the nucleotide sequence designated RXA00823 (SEQ ID NO:9), a nucleotide sequence which is greater than and/or at least 40% identical to the nucleotide sequence designated RXA01064 (SEQ ID NO:13), and a nucleotide sequence which is
- 15 greater than and/or at least 45% identical to the nucleotide sequence designated RXA02363 (SEQ ID NO:35). One of ordinary skill in the art would be able to calculate the lower threshold of percent identity for any given sequence of the invention by examining the GAP-calculated percent identity scores set forth in Table 4 for each of the three top hits for the given sequence, and by subtracting the highest GAP-calculated
- 20 percent identity from 100 percent. One of ordinary skill in the art will also appreciate that nucleic acid and amino acid sequences having percent identities greater than the lower threshold so calculated (e.g., at least 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, or 60%, preferably at least about 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, or 70%, more preferably at least about 71%, 72%, 73%, 74%, 75%,
- 25 76%, 77%, 78%, 79%, or 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, or 90%, or 91%, 92%, 93%, 94%, and even more preferably at least about 95%, 96%, 97%, 98%, 99% or more identical) are also encompassed by the invention.

- In addition to the *C. glutamicum* RRP nucleotide sequences shown in Appendix A, it will be appreciated by those of ordinary skill in the art that DNA sequence
- 30 polymorphisms that lead to changes in the amino acid sequences of RRP proteins may exist within a population (e.g., the *C. glutamicum* population). Such genetic polymorphism in the RRP gene may exist among individuals within a population due to natural variation. As used herein, the terms "gene" and "recombinant gene" refer to nucleic acid molecules comprising an open reading frame encoding an RRP protein,
- 35 preferably a *C. glutamicum* RRP protein. Such natural variations can typically result in 1-5% variance in the nucleotide sequence of the RRP gene. Any and all such nucleotide variations and resulting amino acid polymorphisms in RRP that are the result of natural

variation and that do not alter the functional activity of RRP proteins are intended to be within the scope of the invention.

Nucleic acid molecules corresponding to natural variants and non-*C. glutamicum* homologues of the *C. glutamicum* RRP DNA of the invention can be isolated based on their homology to the *C. glutamicum* RRP nucleic acid disclosed herein using the *C. glutamicum* DNA, or a portion thereof, as a hybridization probe according to standard hybridization techniques under stringent hybridization conditions. Accordingly, in another embodiment, an isolated nucleic acid molecule of the invention is at least 15 nucleotides in length and hybridizes under stringent conditions to the nucleic acid molecule comprising a nucleotide sequence of Appendix A. In other embodiments, the nucleic acid is at least 30, 50, 100, 250 or more nucleotides in length. As used herein, the term "hybridizes under stringent conditions" is intended to describe conditions for hybridization and washing under which nucleotide sequences at least 60% homologous to each other typically remain hybridized to each other. Preferably, the conditions are such that sequences at least about 65%, more preferably at least about 70%, and even more preferably at least about 75% or more homologous to each other typically remain hybridized to each other. Such stringent conditions are known to those of ordinary skill in the art and can be found in *Current Protocols in Molecular Biology*, John Wiley & Sons, N.Y. (1989), 6.3.1-6.3.6. A preferred, non-limiting example of stringent hybridization conditions are hybridization in 6X sodium chloride/sodium citrate (SSC) at about 45°C, followed by one or more washes in 0.2 X SSC, 0.1% SDS at 50-65°C. Preferably, an isolated nucleic acid molecule of the invention that hybridizes under stringent conditions to a sequence of Appendix A corresponds to a naturally-occurring nucleic acid molecule. As used herein, a "naturally-occurring" nucleic acid molecule refers to an RNA or DNA molecule having a nucleotide sequence that occurs in nature (e.g., encodes a natural protein). In one embodiment, the nucleic acid encodes a natural *C. glutamicum* RRP protein.

In addition to naturally-occurring variants of the RRP sequence that may exist in the population, the one of ordinary skill in the art will further appreciate that changes can be introduced by mutation into a nucleotide sequence of Appendix A, thereby leading to changes in the amino acid sequence of the encoded RRP protein, without altering the functional ability of the RRP protein. For example, nucleotide substitutions leading to amino acid substitutions at "non-essential" amino acid residues can be made in a sequence of Appendix A. A "non-essential" amino acid residue is a residue that can be altered from the wild-type sequence of one of the RRP proteins (Appendix B) without altering the activity of said RRP protein, whereas an "essential" amino acid residue is required for RRP protein activity. Other amino acid residues, however, (e.g.,

those that are not conserved or only semi-conserved in the domain having RRP activity) may not be essential for activity and thus are likely to be amenable to alteration without altering RRP activity.

- Accordingly, another aspect of the invention pertains to nucleic acid molecules
- 5 encoding RRP proteins that contain changes in amino acid residues that are not essential for RRP activity. Such RRP proteins differ in amino acid sequence from a sequence contained in Appendix B yet retain at least one of the RRP activities described herein. In one embodiment, the isolated nucleic acid molecule comprises a nucleotide sequence encoding a protein, wherein the protein comprises an amino acid sequence at least about
- 10 50% homologous to an amino acid sequence of Appendix B and is capable of participating in the replication of *C. glutamicum* DNA, in *C. glutamicum* protein synthesis, or in the pathogenicity of this microorganism, or has one or more of the activities set forth in Table 1. Preferably, the protein encoded by the nucleic acid molecule is at least about 50-60% homologous to one of the sequences in Appendix B,
- 15 more preferably at least about 60-70% homologous to one of the sequences in Appendix B, even more preferably at least about 70-80%, 80-90%, 90-95% homologous to one of the sequences in Appendix B, and most preferably at least about 96%, 97%, 98%, or 99% homologous to one of the sequences in Appendix B.

- To determine the percent homology of two amino acid sequences (e.g., one of
- 20 the sequences of Appendix B and a mutant form thereof) or of two nucleic acids, the sequences are aligned for optimal comparison purposes (e.g., gaps can be introduced in the sequence of one protein or nucleic acid for optimal alignment with the other protein or nucleic acid). The amino acid residues or nucleotides at corresponding amino acid positions or nucleotide positions are then compared. When a position in one sequence
- 25 (e.g., one of the sequences of Appendix B) is occupied by the same amino acid residue or nucleotide as the corresponding position in the other sequence (e.g., a mutant form of the sequence selected from Appendix B), then the molecules are homologous at that position (i.e., as used herein amino acid or nucleic acid "homology" is equivalent to amino acid or nucleic acid "identity"). The percent homology between the two
- 30 sequences is a function of the number of identical positions shared by the sequences (i.e., % homology = # of identical positions/total # of positions x 100).

- An isolated nucleic acid molecule encoding an RRP protein homologous to a protein sequence of Appendix B can be created by introducing one or more nucleotide substitutions, additions or deletions into a nucleotide sequence of Appendix A such that
- 35 one or more amino acid substitutions, additions or deletions are introduced into the encoded protein. Mutations can be introduced into one of the sequences of Appendix A by standard techniques, such as site-directed mutagenesis and PCR-mediated

mutagenesis. Preferably, conservative amino acid substitutions are made at one or more predicted non-essential amino acid residues. A "conservative amino acid substitution" is one in which the amino acid residue is replaced with an amino acid residue having a similar side chain. Families of amino acid residues having similar side chains have been defined in the art. These families include amino acids with basic side chains (*e.g.*, lysine, arginine, histidine), acidic side chains (*e.g.*, aspartic acid, glutamic acid), uncharged polar side chains (*e.g.*, glycine, asparagine, glutamine, serine, threonine, tyrosine, cysteine), nonpolar side chains (*e.g.*, alanine, valine, leucine, isoleucine, proline, phenylalanine, methionine, tryptophan), beta-branched side chains (*e.g.*, threonine, valine, isoleucine) and aromatic side chains (*e.g.*, tyrosine, phenylalanine, tryptophan, histidine). Thus, a predicted nonessential amino acid residue in an RRP protein is preferably replaced with another amino acid residue from the same side chain family. Alternatively, in another embodiment, mutations can be introduced randomly along all or part of an RRP coding sequence, such as by saturation mutagenesis, and the resultant mutants can be screened for an RRP activity described herein to identify mutants that retain RRP activity. Following mutagenesis of one of the sequences of Appendix A, the encoded protein can be expressed recombinantly and the activity of the protein can be determined using, for example, assays described herein (see Example 8 of the Exemplification).

In addition to the nucleic acid molecules encoding RRP proteins described above, another aspect of the invention pertains to isolated nucleic acid molecules which are antisense thereto. An "antisense" nucleic acid comprises a nucleotide sequence which is complementary to a "sense" nucleic acid encoding a protein, *e.g.*, complementary to the coding strand of a double-stranded DNA molecule or complementary to an mRNA sequence. Accordingly, an antisense nucleic acid can hydrogen bond to a sense nucleic acid. The antisense nucleic acid can be complementary to an entire RRP coding strand, or to only a portion thereof. In one embodiment, an antisense nucleic acid molecule is antisense to a "coding region" of the coding strand of a nucleotide sequence encoding an RRP protein. The term "coding region" refers to the region of the nucleotide sequence comprising codons which are translated into amino acid residues (*e.g.*, the entire coding region of SEQ ID NO:5 (RXN02943) comprises nucleotides 1 to 1668). In another embodiment, the antisense nucleic acid molecule is antisense to a "noncoding region" of the coding strand of a nucleotide sequence encoding RRP. The term "noncoding region" refers to 5' and 3' sequences which flank the coding region that are not translated into amino acids (*i.e.*, also referred to as 5' and 3' untranslated regions).

Given the coding strand sequences encoding RRP disclosed herein (e.g., the sequences set forth in Appendix A), antisense nucleic acids of the invention can be designed according to the rules of Watson and Crick base pairing. The antisense nucleic acid molecule can be complementary to the entire coding region of RRP mRNA, but more preferably is an oligonucleotide which is antisense to only a portion of the coding or noncoding region of RRP mRNA. For example, the antisense oligonucleotide can be complementary to the region surrounding the translation start site of RRP mRNA. An antisense oligonucleotide can be, for example, about 5, 10, 15, 20, 25, 30, 35, 40, 45 or 50 nucleotides in length. An antisense nucleic acid of the invention can be constructed using chemical synthesis and enzymatic ligation reactions using procedures known in the art. For example, an antisense nucleic acid (e.g., an antisense oligonucleotide) can be chemically synthesized using naturally occurring nucleotides or variously modified nucleotides designed to increase the biological stability of the molecules or to increase the physical stability of the duplex formed between the antisense and sense nucleic acids, e.g., phosphorothioate derivatives and acridine substituted nucleotides can be used. Examples of modified nucleotides which can be used to generate the antisense nucleic acid include 5-fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, xanthine, 4-acetylcytosine, 5-(carboxyhydroxymethyl) uracil, 5-carboxymethylaminomethyl-2-thiouridine, 5-carboxymethylaminomethyluracil, dihydrouracil, beta-D-galactosylqueosine, inosine, N6-isopentenyladenine, 1-methylguanine, 1-methylinosine, 2,2-dimethylguanine, 2-methyladenine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N6-adenine, 7-methylguanine, 5-methylaminomethyluracil, 5-methoxyaminomethyl-2-thiouracil, beta-D-mannosylqueosine, 5'-methoxycarboxymethyluracil, 5-methoxyuracil, 2-methylthio-N6-isopentenyladenine, uracil-5-oxyacetic acid (v), wybutoxosine, pseudouracil, queosine, 2-thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, uracil-5-oxyacetic acid methylester, uracil-5-oxyacetic acid (v), 5-methyl-2-thiouracil, 3-(3-amino-3-N-2-carboxypropyl) uracil, (acp3)w, and 2,6-diaminopurine. Alternatively, the antisense nucleic acid can be produced biologically using an expression vector into which a nucleic acid has been subcloned in an antisense orientation (i.e., RNA transcribed from the inserted nucleic acid will be of an antisense orientation to a target nucleic acid of interest, described further in the following subsection).

The antisense nucleic acid molecules of the invention are typically administered to a cell or generated *in situ* such that they hybridize with or bind to cellular mRNA and/or genomic DNA encoding an RRP protein to thereby inhibit expression of the protein, e.g., by inhibiting transcription and/or translation. The hybridization can be by conventional nucleotide complementarity to form a stable duplex, or, for example, in the

case of an antisense nucleic acid molecule which binds to DNA duplexes, through specific interactions in the major groove of the double helix. The antisense molecule can be modified such that it specifically binds to a receptor or an antigen expressed on a selected cell surface, e.g., by linking the antisense nucleic acid molecule to a peptide or an antibody which binds to a cell surface receptor or antigen. The antisense nucleic acid molecule can also be delivered to cells using the vectors described herein. To achieve sufficient intracellular concentrations of the antisense molecules, vector constructs in which the antisense nucleic acid molecule is placed under the control of a strong prokaryotic, viral, or eukaryotic promoter are preferred.

10 In yet another embodiment, the antisense nucleic acid molecule of the invention is an  $\alpha$ -anomeric nucleic acid molecule. An  $\alpha$ -anomeric nucleic acid molecule forms specific double-stranded hybrids with complementary RNA in which, contrary to the usual  $\beta$ -units, the strands run parallel to each other (Gaultier *et al.* (1987) *Nucleic Acids Res.* 15:6625-6641). The antisense nucleic acid molecule can also comprise a 2'-o-methylribonucleotide (Inoue *et al.* (1987) *Nucleic Acids Res.* 15:6131-6148) or a  
15 chimeric RNA-DNA analogue (Inoue *et al.* (1987) *FEBS Lett.* 215:327-330).

In still another embodiment, an antisense nucleic acid of the invention is a ribozyme. Ribozymes are catalytic RNA molecules with ribonuclease activity which are capable of cleaving a single-stranded nucleic acid, such as an mRNA, to which they  
20 have a complementary region. Thus, ribozymes (e.g., hammerhead ribozymes (described in Haselhoff and Gerlach (1988) *Nature* 334:585-591)) can be used to catalytically cleave RRP mRNA transcripts to thereby inhibit translation of RRP mRNA. A ribozyme having specificity for an RRP-encoding nucleic acid can be designed based upon the nucleotide sequence of an RRP DNA molecule disclosed  
25 herein (i.e., SEQ ID NO:9 (RXA00823 in Appendix A)). For example, a derivative of a *Tetrahymena* L-19 IVS RNA can be constructed in which the nucleotide sequence of the active site is complementary to the nucleotide sequence to be cleaved in an RRP-encoding mRNA. See, e.g., Cech *et al.* U.S. Patent No. 4,987,071 and Cech *et al.* U.S. Patent No. 5,116,742. Alternatively, RRP mRNA can be used to select a catalytic RNA  
30 having a specific ribonuclease activity from a pool of RNA molecules. See, e.g., Bartel, D. and Szostak, J.W. (1993) *Science* 261:1411-1418.

Alternatively, RRP gene expression can be inhibited by targeting nucleotide sequences complementary to the regulatory region of an RRP nucleotide sequence (e.g., an RRP promoter and/or enhancers) to form triple helical structures that prevent  
35 transcription of an RRP gene in target cells. See generally, Helene, C. (1991) *Anticancer Drug Des.* 6(6):569-84; Helene, C. *et al.* (1992) *Ann. N.Y. Acad. Sci.* 660:27-36; and Maher, L.J. (1992) *Bioassays* 14(12):807-15.



*B. Recombinant Expression Vectors and Host Cells*

Another aspect of the invention pertains to vectors, preferably expression vectors, containing a nucleic acid encoding an RRP protein (or a portion thereof). As used herein, the term "vector" refers to a nucleic acid molecule capable of transporting another nucleic acid to which it has been linked. One type of vector is a "plasmid", which refers to a circular double stranded DNA loop into which additional DNA segments can be ligated. Another type of vector is a viral vector, wherein additional DNA segments can be ligated into the viral genome. Certain vectors are capable of autonomous replication in a host cell into which they are introduced (e.g., bacterial vectors having a bacterial origin of replication and episomal mammalian vectors). Other vectors (e.g., non-episomal mammalian vectors) are integrated into the genome of a host cell upon introduction into the host cell, and thereby are replicated along with the host genome. Moreover, certain vectors are capable of directing the expression of genes to which they are operatively linked. Such vectors are referred to herein as "expression vectors". In general, expression vectors of utility in recombinant DNA techniques are often in the form of plasmids. In the present specification, "plasmid" and "vector" can be used interchangeably as the plasmid is the most commonly used form of vector. However, the invention is intended to include such other forms of expression vectors, such as viral vectors (e.g., replication defective retroviruses, adenoviruses and adeno-associated viruses), which serve equivalent functions.

The recombinant expression vectors of the invention comprise a nucleic acid of the invention in a form suitable for expression of the nucleic acid in a host cell, which means that the recombinant expression vectors include one or more regulatory sequences, selected on the basis of the host cells to be used for expression, which are operatively linked to the nucleic acid sequence to be expressed. Within a recombinant expression vector, "operably linked" is intended to mean that the nucleotide sequence of interest is linked to the regulatory sequence(s) in a manner which allows for expression of the nucleotide sequence (e.g., in an *in vitro* transcription/translation system or in a host cell when the vector is introduced into the host cell). The term "regulatory sequence" is intended to include promoters, enhancers and other expression control elements (e.g., polyadenylation signals). Such regulatory sequences are described, for example, in Goeddel; *Gene Expression Technology: Methods in Enzymology* 185, Academic Press, San Diego, CA (1990). Regulatory sequences include those which direct constitutive expression of a nucleotide sequence in many types of host cell and those which direct expression of the nucleotide sequence only in certain host cells. Preferred regulatory sequences are, for example, promoters such as cos-, tac-, trp-, tet-, trp-tet-, lpp-, lac-, lpp-lac-, lacI<sup>q</sup>-, T7-, T5-, T3-, gal-, trc-, ara-, SP6-, army, SPO2, λ-P<sub>R</sub>-

or  $\lambda$  P<sub>L</sub>, which are used preferably in bacteria. Additional regulatory sequences are, for example, promoters from yeasts and fungi, such as ADC1, Mfa, AC, P-60, CYC1, GAPDH, TEF, rp28, ADH, promoters from plants such as CaMV/35S, SSU, OCS, lib4, usp, STL1, B33, nos or ubiquitin- or phaseolin-promoters. It is also possible to use artificial promoters. It will be appreciated by one of ordinary skill in the art that the design of the expression vector can depend on such factors as the choice of the host cell to be transformed, the level of expression of protein desired, etc. The expression vectors of the invention can be introduced into host cells to thereby produce proteins or peptides, including fusion proteins or peptides, encoded by nucleic acids as described herein (e.g., RRP proteins, mutant forms of RRP proteins, fusion proteins, etc.).

The recombinant expression vectors of the invention can be designed for expression of RRP proteins in prokaryotic or eukaryotic cells. For example, RRP genes can be expressed in bacterial cells such as *C. glutamicum*, insect cells (using baculovirus expression vectors), yeast and other fungal cells (see Romanos, M.A. *et al.* (1992) "Foreign gene expression in yeast: a review", *Yeast* 8: 423-488; van den Hondel, C.A.M.J.J. *et al.* (1991) "Heterologous gene expression in filamentous fungi" in: More Gene Manipulations in Fungi, J.W. Bennet & L.L. Lasure, eds., p. 396-428: Academic Press: San Diego; and van den Hondel, C.A.M.J.J. & Punt, P.J. (1991) "Gene transfer systems and vector development for filamentous fungi, in: Applied Molecular Genetics of Fungi, Peberdy, J.F. *et al.*, eds., p. 1-28, Cambridge University Press: Cambridge), algae and multicellular plant cells (see Schmidt, R. and Willmitzer, L. (1988) High efficiency *Agrobacterium tumefaciens* -mediated transformation of *Arabidopsis thaliana* leaf and cotyledon explants" *Plant Cell Rep.*: 583-586), or mammalian cells. Suitable host cells are discussed further in Goeddel, *Gene Expression Technology: Methods in Enzymology* 185, Academic Press, San Diego, CA (1990). Alternatively, the recombinant expression vector can be transcribed and translated *in vitro*, for example using T7 promoter regulatory sequences and T7 polymerase.

Expression of proteins in prokaryotes is most often carried out with vectors containing constitutive or inducible promoters directing the expression of either fusion or non-fusion proteins. Fusion vectors add a number of amino acids to a protein encoded therein, usually to the amino terminus of the recombinant protein but also to the C-terminus or fused within suitable regions in the proteins. Such fusion vectors typically serve three purposes: 1) to increase expression of recombinant protein; 2) to increase the solubility of the recombinant protein; and 3) to aid in the purification of the recombinant protein by acting as a ligand in affinity purification. Often, in fusion expression vectors, a proteolytic cleavage site is introduced at the junction of the fusion moiety and the recombinant protein to enable separation of the recombinant protein

from the fusion moiety subsequent to purification of the fusion protein. Such enzymes, and their cognate recognition sequences, include Factor Xa, thrombin and enterokinase.

- Typical fusion expression vectors include pGEX (Pharmacia Biotech Inc; Smith, D.B. and Johnson, K.S. (1988) *Gene* 67:31-40), pMAL (New England Biolabs, Beverly, MA) and pRIT5 (Pharmacia, Piscataway, NJ) which fuse glutathione S-transferase (GST), maltose E binding protein, or protein A, respectively, to the target recombinant protein. In one embodiment, the coding sequence of the RRP protein is cloned into a pGEX expression vector to create a vector encoding a fusion protein comprising, from the N-terminus to the C-terminus, GST-thrombin cleavage site-X protein. The fusion protein can be purified by affinity chromatography using glutathione-agarose resin. Recombinant RRP protein unfused to GST can be recovered by cleavage of the fusion protein with thrombin.

- Examples of suitable inducible non-fusion *E. coli* expression vectors include pTrc (Amann *et al.*, (1988) *Gene* 69:301-315) pLG338, pACYC184, pBR322, pUC18, pUC19, pKC30, pRep4, pHS1, pHS2, pPLC236, pMBL24, pLG200, pUR290, pIN-III113-B1,  $\lambda$ gt11, pBdCl, and pET 11d (Studier *et al.*, *Gene Expression Technology: Methods in Enzymology* 185, Academic Press, San Diego, California (1990) 60-89; and Pouwels *et al.*, eds. (1985) *Cloning Vectors*. Elsevier: New York ISBN 0 444 904018). Target gene expression from the pTrc vector relies on host RNA polymerase transcription from a hybrid trp-lac fusion promoter. Target gene expression from the pET 11d vector relies on transcription from a T7 gn10-lac fusion promoter mediated by a coexpressed viral RNA polymerase (T7 gn1). This viral polymerase is supplied by host strains BL21(DE3) or HMS174(DE3) from a resident  $\lambda$  prophage harboring a T7 gn1 gene under the transcriptional control of the lacUV 5 promoter. For transformation of other varieties of bacteria, appropriate vectors may be selected. For example, the plasmids pIJ101, pIJ364, pIJ702 and pIJ361 are known to be useful in transforming *Streptomyces*, while plasmids pUB110, pC194, or pBD214 are suited for transformation of *Bacillus* species. Several plasmids of use in the transfer of genetic information into *Corynebacterium* include pHM1519, pBL1, pSA77, or pAJ667 (Pouwels *et al.*, eds. (1985) *Cloning Vectors*. Elsevier: New York ISBN 0 444 904018). One strategy to maximize recombinant protein expression is to express the protein in a host bacteria with an impaired capacity to proteolytically cleave the recombinant protein (Gottesman, S., *Gene Expression Technology: Methods in Enzymology* 185, Academic Press, San Diego, California (1990) 119-128). Another strategy is to alter the nucleic acid sequence of the nucleic acid to be inserted into an expression vector so that the individual codons for each amino acid are those preferentially utilized in the bacterium chosen for expression, such as *C. glutamicum* (Wada *et al.* (1992) *Nucleic Acids Res.*

20: 2111-2118). Such alteration of nucleic acid sequences of the invention can be carried out by standard DNA synthesis techniques.

- In another embodiment, the RRP protein expression vector is a yeast expression vector. Examples of vectors for expression in yeast *S. cerevisiae* include pYepSec1 (Baldari, *et al.*, (1987) *Embo J.* 6:229-234), 2  $\mu$ , pAG-1, Yep6, Yep13, pEMBLyE23, 5 pMFa (Kurjan and Herskowitz, (1982) *Cell* 30:933-943), pJRY88 (Schultz *et al.*, (1987) *Gene* 54:113-123), and pYES2 (Invitrogen Corporation, San Diego, CA). Vectors and methods for the construction of vectors appropriate for use in other fungi, such as the filamentous fungi, include those detailed in: van den Hondel, C.A.M.J.J. & Punt, P.J. 10 (1991) "Gene transfer systems and vector development for filamentous fungi, in: Applied Molecular Genetics of Fungi, J.F. Peberdy, *et al.*, eds., p. 1-28, Cambridge University Press: Cambridge, and Pouwels *et al.*, eds. (1985) *Cloning Vectors*. Elsevier: New York (IBSN 0 444 904018).

- Alternatively, the RRP proteins of the invention can be expressed in insect cells 15 using baculovirus expression vectors. Baculovirus vectors available for expression of proteins in cultured insect cells (*e.g.*, Sf9 cells) include the pAc series (Smith *et al.* (1983) *Mol. Cell Biol.* 3:2156-2165) and the pVL series (Lucklow and Summers (1989) *Virology* 170:31-39).

- In another embodiment, the RRP proteins of the invention may be expressed in 20 unicellular plant cells (such as algae) or in plant cells from higher plants (*e.g.*, the spermatophytes, such as crop plants). Examples of plant expression vectors include those detailed in: Becker, D., Kemper, E., Schell, J. and Masterson, R. (1992) "New plant binary vectors with selectable markers located proximal to the left border", *Plant Mol. Biol.* 20: 1195-1197; and Bevan, M.W. (1984) "Binary *Agrobacterium* vectors for 25 plant transformation", *Nucl. Acid. Res.* 12: 8711-8721, and include pLGV23, pGHIac+, pBIN19, pAK2004, and pDH51 (Pouwels *et al.*, eds. (1985) *Cloning Vectors*. Elsevier: New York IBSN 0 444 904018). In yet another embodiment, a nucleic acid of the invention is expressed in mammalian cells using a mammalian expression vector. Examples of mammalian expression vectors include pCDM8 (Seed, B. (1987) *Nature* 30: 329:840) and pMT2PC (Kaufman *et al.* (1987) *EMBO J.* 6:187-195). When used in 30 mammalian cells, the expression vector's control functions are often provided by viral regulatory elements. For example, commonly used promoters are derived from polyoma, Adenovirus 2, cytomegalovirus and Simian Virus 40. For other suitable expression systems for both prokaryotic and eukaryotic cells see chapters 16 and 17 of 35 Sambrook, J., Fritsh, E. F., and Maniatis, T. *Molecular Cloning: A Laboratory Manual*. 2nd, ed., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989.

In another embodiment, the recombinant mammalian expression vector is capable of directing expression of the nucleic acid preferentially in a particular cell type (e.g., tissue-specific regulatory elements are used to express the nucleic acid). Tissue-specific regulatory elements are known in the art. Non-limiting examples of suitable tissue-specific promoters include the albumin promoter (liver-specific; Pinkert *et al.* (1987) *Genes Dev.* 1:268-277), lymphoid-specific promoters (Calame and Eaton (1988) *Adv. Immunol.* 43:235-275), in particular promoters of T cell receptors (Winoto and Baltimore (1989) *EMBO J.* 8:729-733) and immunoglobulins (Banerji *et al.* (1983) *Cell* 33:729-740; Queen and Baltimore (1983) *Cell* 33:741-748), neuron-specific promoters (e.g., the neurofilament promoter; Byrne and Ruddle (1989) *PNAS* 86:5473-5477), pancreas-specific promoters (Edlund *et al.* (1985) *Science* 230:912-916), and mammary gland-specific promoters (e.g., milk whey promoter; U.S. Patent No. 4,873,316 and European Application Publication No. 264,166). Developmentally-regulated promoters are also encompassed, for example the murine hox promoters (Kessel and Gruss (1990) *Science* 249:374-379) and the  $\alpha$ -fetoprotein promoter (Campes and Tilghman (1989) *Genes Dev.* 3:537-546).

The invention further provides a recombinant expression vector comprising a DNA molecule of the invention cloned into the expression vector in an antisense orientation. That is, the DNA molecule is operatively linked to a regulatory sequence in a manner which allows for expression (by transcription of the DNA molecule) of an RNA molecule which is antisense to RRP mRNA. Regulatory sequences operatively linked to a nucleic acid cloned in the antisense orientation can be chosen which direct the continuous expression of the antisense RNA molecule in a variety of cell types, for instance viral promoters and/or enhancers, or regulatory sequences can be chosen which direct constitutive, tissue specific or cell type specific expression of antisense RNA. The antisense expression vector can be in the form of a recombinant plasmid, phagemid or attenuated virus in which antisense nucleic acids are produced under the control of a high efficiency regulatory region, the activity of which can be determined by the cell type into which the vector is introduced. For a discussion of the regulation of gene expression using antisense genes see Weintraub, H. *et al.*, Antisense RNA as a molecular tool for genetic analysis, *Reviews - Trends in Genetics*, Vol. 1(1) (1986).

Another aspect of the invention pertains to host cells into which a recombinant expression vector of the invention has been introduced. The terms "host cell" and "recombinant host cell" are used interchangeably herein. It is understood that such terms refer not only to the particular subject cell but to the progeny or potential progeny of such a cell. Because certain modifications may occur in succeeding generations due to either mutation or environmental influences, such progeny may not, in fact, be

identical to the parent cell, but are still included within the scope of the term as used herein.

A host cell can be any prokaryotic or eukaryotic cell. For example, an RRP protein can be expressed in bacterial cells such as *C. glutamicum*, insect cells, yeast or mammalian cells (such as Chinese hamster ovary cells (CHO) or COS cells). Other suitable host cells are known to one of ordinary skill in the art. Microorganisms related to *Corynebacterium glutamicum* which may be conveniently used as host cells for the nucleic acid and protein molecules of the invention are set forth in Table 3.

Vector DNA can be introduced into prokaryotic or eukaryotic cells via conventional transformation or transfection techniques. As used herein, the terms "transformation" and "transfection", "conjugation" and "transduction" are intended to refer to a variety of art-recognized techniques for introducing foreign nucleic acid (e.g., linear DNA or RNA (e.g., a linearized vector or a gene construct alone without a vector) or nucleic acid in the form of a vector (e.g., a plasmid, phage, phasmid, phagemid, transposon or other DNA) into a host cell, including calcium phosphate or calcium chloride co-precipitation, DEAE-dextran-mediated transfection, lipofection, natural competence, chemical-mediated transfer, or electroporation. Suitable methods for transforming or transfecting host cells can be found in Sambrook, *et al.* (*Molecular Cloning: A Laboratory Manual*. 2nd, ed., Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989), and other laboratory manuals.

For stable transfection of mammalian cells, it is known that, depending upon the expression vector and transfection technique used, only a small fraction of cells may integrate the foreign DNA into their genome. In order to identify and select these integrants, a gene that encodes a selectable marker (e.g., resistance to antibiotics) is generally introduced into the host cells along with the gene of interest. Preferred selectable markers include those which confer resistance to drugs, such as G418, hygromycin and methotrexate. Nucleic acid encoding a selectable marker can be introduced into a host cell on the same vector as that encoding an RRP protein or can be introduced on a separate vector. Cells stably transfected with the introduced nucleic acid can be identified by, for example, drug selection (e.g., cells that have incorporated the selectable marker gene will survive, while the other cells die).

To create a homologous recombinant microorganism, a vector is prepared which contains at least a portion of an RRP gene into which a deletion, addition or substitution has been introduced to thereby alter, e.g., functionally disrupt, the RRP gene.

Preferably, this RRP gene is a *Corynebacterium glutamicum* RRP gene, but it can be a homologue from a related bacterium or even from a mammalian, yeast, or insect source. In a preferred embodiment, the vector is designed such that, upon homologous

recombination, the endogenous RRP gene is functionally disrupted (*i.e.*, no longer encodes a functional protein; also referred to as a "knock out" vector). Alternatively, the vector can be designed such that, upon homologous recombination, the endogenous RRP gene is mutated or otherwise altered but still encodes functional protein (*e.g.*, the upstream regulatory region can be altered to thereby alter the expression of the endogenous RRP protein). In the homologous recombination vector, the altered portion of the RRP gene is flanked at its 5' and 3' ends by additional nucleic acid of the RRP gene to allow for homologous recombination to occur between the exogenous RRP gene carried by the vector and an endogenous RRP gene in a microorganism. The additional flanking RRP nucleic acid is of sufficient length for successful homologous recombination with the endogenous gene. Typically, several kilobases of flanking DNA (both at the 5' and 3' ends) are included in the vector (see *e.g.*, Thomas, K.R., and Capecchi, M.R. (1987) Cell 51: 503 for a description of homologous recombination vectors). The vector is introduced into a microorganism (*e.g.*, by electroporation) and cells in which the introduced RRP gene has homologously recombined with the endogenous RRP gene are selected, using art-known techniques.

In another embodiment, recombinant microorganisms can be produced which contain selected systems which allow for regulated expression of the introduced gene. For example, inclusion of an RRP gene on a vector placing it under control of the lac operon permits expression of the RRP gene only in the presence of IPTG. Such regulatory systems are well known in the art.

In another embodiment, an endogenous RRP gene in a host cell is disrupted (*e.g.*, by homologous recombination or other genetic means known in the art) such that expression of its protein product does not occur. In another embodiment, an endogenous or introduced RRP gene in a host cell has been altered by one or more point mutations, deletions, or inversions, but still encodes a functional RRP protein. In still another embodiment, one or more of the regulatory regions (*e.g.*, a promoter, repressor, or inducer) of an RRP gene in a microorganism has been altered (*e.g.*, by deletion, truncation, inversion, or point mutation) such that the expression of the RRP gene is modulated. One of ordinary skill in the art will appreciate that host cells containing more than one of the described RRP gene and protein modifications may be readily produced using the methods of the invention, and are meant to be included in the present invention.

A host cell of the invention, such as a prokaryotic or eukaryotic host cell in culture, can be used to produce (*i.e.*, express) an RRP protein. Accordingly, the invention further provides methods for producing RRP proteins using the host cells of the invention. In one embodiment, the method comprises culturing the host cell of

invention (into which a recombinant expression vector encoding an RRP protein has been introduced, or into which genome has been introduced a gene encoding a wild-type or altered RRP protein) in a suitable medium until RRP protein is produced. In another embodiment, the method further comprises isolating RRP proteins from the medium or

5 the host cell.

### C. Isolated RRP Proteins

Another aspect of the invention pertains to isolated RRP proteins, and biologically active portions thereof. An "isolated" or "purified" protein or biologically

10 active portion thereof is substantially free of cellular material when produced by recombinant DNA techniques, or chemical precursors or other chemicals when chemically synthesized. The language "substantially free of cellular material" includes preparations of RRP protein in which the protein is separated from cellular components of the cells in which it is naturally or recombinantly produced. In one embodiment, the

15 language "substantially free of cellular material" includes preparations of RRP protein having less than about 30% (by dry weight) of non-RRP protein (also referred to herein as a "contaminating protein"), more preferably less than about 20% of non-RRP protein, still more preferably less than about 10% of non-RRP protein, and most preferably less than about 5% non-RRP protein. When the RRP protein or biologically active portion

20 thereof is recombinantly produced, it is also preferably substantially free of culture medium, *i.e.*, culture medium represents less than about 20%, more preferably less than about 10%, and most preferably less than about 5% of the volume of the protein preparation. The language "substantially free of chemical precursors or other chemicals" includes preparations of RRP protein in which the protein is separated from

25 chemical precursors or other chemicals which are involved in the synthesis of the protein. In one embodiment, the language "substantially free of chemical precursors or other chemicals" includes preparations of RRP protein having less than about 30% (by dry weight) of chemical precursors or non-RRP chemicals, more preferably less than about 20% chemical precursors or non-RRP chemicals, still more preferably less than

30 about 10% chemical precursors or non-RRP chemicals, and most preferably less than about 5% chemical precursors or non-RRP chemicals. In preferred embodiments, isolated proteins or biologically active portions thereof lack contaminating proteins from the same organism from which the RRP protein is derived. Typically, such proteins are produced by recombinant expression of, for example, a *C. glutamicum* RRP protein in a

35 microorganism such as *C. glutamicum*.

An isolated RRP protein or a portion thereof of the invention can participate in the replication of *C. glutamicum* DNA, in *C. glutamicum* protein synthesis, or in the



pathogenicity of this microorganism, or has one or more of the activities set forth in Table 1. In preferred embodiments, the protein or portion thereof comprises an amino acid sequence which is sufficiently homologous to an amino acid sequence of Appendix B such that the protein or portion thereof maintains the ability to participate in the replication of *C. glutamicum* DNA, in *C. glutamicum* protein synthesis, or in the pathogenicity of this microorganism. The portion of the protein is preferably a biologically active portion as described herein. In another preferred embodiment, an RRP protein of the invention has an amino acid sequence shown in Appendix B. In yet another preferred embodiment, the RRP protein has an amino acid sequence which is encoded by a nucleotide sequence which hybridizes, e.g., hybridizes under stringent conditions, to a nucleotide sequence of Appendix A. In still another preferred embodiment, the RRP protein has an amino acid sequence which is encoded by a nucleotide sequence that is at least about 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, or 60%, preferably at least about 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, or 70%, more preferably at least about 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, or 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, or 90%, or 91%, 92%, 93%, 94%, and even more preferably at least about 95%, 96%, 97%, 98%, 99% or more homologous to one of the nucleic acid sequences of Appendix A, or a portion thereof. Ranges and identity values intermediate to the above-recited values, (e.g., 70-90% identical or 80-95% identical) are also intended to be encompassed by the present invention. For example, ranges of identity values using a combination of any of the above values recited as upper and/or lower limits are intended to be included. The preferred RRP proteins of the present invention also preferably possess at least one of the RRP activities described herein. For example, a preferred RRP protein of the present invention includes an amino acid sequence encoded by a nucleotide sequence which hybridizes, e.g., hybridizes under stringent conditions, to a nucleotide sequence of Appendix A, and which can participate in the replication of *C. glutamicum* DNA, in *C. glutamicum* protein synthesis, or in the pathogenicity of this microorganism, or which has one or more of the activities set forth in Table 1.

In other embodiments, the RRP protein is substantially homologous to an amino acid sequence of Appendix B and retains the functional activity of the protein of one of the sequences of Appendix B yet differs in amino acid sequence due to natural variation or mutagenesis, as described in detail in subsection I above. Accordingly, in another embodiment, the RRP protein is a protein which comprises an amino acid sequence which is at least about 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, or 60%, preferably at least about 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, or 70%, more preferably at least about 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%,

or 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, or 90%, or 91%, 92%, 93%, 94%, and even more preferably at least about 95%, 96%, 97%, 98%, 99% or more homologous to an entire amino acid sequence of Appendix B and which has at least one of the RRP activities described herein. Ranges and identity values intermediate to the above-recited values, (e.g., 70-90% identical or 80-95% identical) are also intended to be encompassed by the present invention. For example, ranges of identity values using a combination of any of the above values recited as upper and/or lower limits are intended to be included. In another embodiment, the invention pertains to a full length *C. glutamicum* protein which is substantially homologous to an entire amino acid sequence of Appendix B.

Biologically active portions of an RRP protein include peptides comprising amino acid sequences derived from the amino acid sequence of an RRP protein, e.g., an amino acid sequence shown in Appendix B or the amino acid sequence of a protein homologous to an RRP protein, which include fewer amino acids than a full length RRP protein or the full length protein which is homologous to an RRP protein, and exhibit at least one activity of an RRP protein. Typically, biologically active portions (peptides, e.g., peptides which are, for example, 5, 10, 15, 20, 30, 35, 36, 37, 38, 39, 40, 50, 100 or more amino acids in length) comprise a domain or motif with at least one activity of an RRP protein. Moreover, other biologically active portions, in which other regions of the protein are deleted, can be prepared by recombinant techniques and evaluated for one or more of the activities described herein. Preferably, the biologically active portions of an RRP protein include one or more selected domains/motifs or portions thereof having biological activity.

RRP proteins are preferably produced by recombinant DNA techniques. For example, a nucleic acid molecule encoding the protein is cloned into an expression vector (as described above), the expression vector is introduced into a host cell (as described above) and the RRP protein is expressed in the host cell. The RRP protein can then be isolated from the cells by an appropriate purification scheme using standard protein purification techniques. Alternative to recombinant expression, an RRP protein, polypeptide, or peptide can be synthesized chemically using standard peptide synthesis techniques. Moreover, native RRP protein can be isolated from cells (e.g., endothelial cells), for example using an anti-RRP antibody, which can be produced by standard techniques utilizing an RRP protein or fragment thereof of this invention.

The invention also provides RRP chimeric or fusion proteins. As used herein, an RRP "chimeric protein" or "fusion protein" comprises an RRP polypeptide operatively linked to a non-RRP polypeptide. An "RRP polypeptide" refers to a polypeptide having an amino acid sequence corresponding to an RRP protein, whereas a "non-RRP

polypeptide" refers to a polypeptide having an amino acid sequence corresponding to a protein which is not substantially homologous to the RRP protein, *e.g.*, a protein which is different from the RRP protein and which is derived from the same or a different organism. Within the fusion protein, the term "operatively linked" is intended to

- 5 indicate that the RRP polypeptide and the non-RRP polypeptide are fused in-frame to each other. The non-RRP polypeptide can be fused to the N-terminus or C-terminus of the RRP polypeptide. For example, in one embodiment the fusion protein is a GST-RRP fusion protein in which the RRP sequences are fused to the C-terminus of the GST sequences. Such fusion proteins can facilitate the purification of recombinant RRP  
10 proteins. In another embodiment, the fusion protein is an RRP protein containing a heterologous signal sequence at its N-terminus. In certain host cells (*e.g.*, mammalian host cells), expression and/or secretion of an RRP protein can be increased through use of a heterologous signal sequence.

- Preferably, an RRP chimeric or fusion protein of the invention is produced by  
15 standard recombinant DNA techniques. For example, DNA fragments coding for the different polypeptide sequences are ligated together in-frame in accordance with conventional techniques, for example by employing blunt-ended or stagger-ended termini for ligation, restriction enzyme digestion to provide for appropriate termini, filling-in of cohesive ends as appropriate, alkaline phosphatase treatment to avoid  
20 undesirable joining, and enzymatic ligation. In another embodiment, the fusion gene can be synthesized by conventional techniques including automated DNA synthesizers. Alternatively, PCR amplification of gene fragments can be carried out using anchor primers which give rise to complementary overhangs between two consecutive gene fragments which can subsequently be annealed and reamplified to generate a chimeric  
25 gene sequence (see, for example, *Current Protocols in Molecular Biology*, eds. Ausubel *et al.* John Wiley & Sons: 1992). Moreover, many expression vectors are commercially available that already encode a fusion moiety (*e.g.*, a GST polypeptide). An RRP-encoding nucleic acid can be cloned into such an expression vector such that the fusion moiety is linked in-frame to the RRP protein.

- 30 Homologues of the RRP protein can be generated by mutagenesis, *e.g.*, discrete point mutation or truncation of the RRP protein. As used herein, the term "homologue" refers to a variant form of the RRP protein which acts as an agonist or antagonist of the activity of the RRP protein. An agonist of the RRP protein can retain substantially the same, or a subset, of the biological activities of the RRP protein. An antagonist of the  
35 RRP protein can inhibit one or more of the activities of the naturally occurring form of the RRP protein, by, for example, competitively binding to a downstream or upstream member of a biochemical cascade which includes the RRP protein, by binding to a target

molecule with which the RRP protein interacts, such that no functional interaction is possible, or by binding directly to the RRP protein and inhibiting its normal activity.

In an alternative embodiment, homologues of the RRP protein can be identified by screening combinatorial libraries of mutants, *e.g.*, truncation mutants, of the RRP protein for RRP protein agonist or antagonist activity. In one embodiment, a variegated library of RRP variants is generated by combinatorial mutagenesis at the nucleic acid level and is encoded by a variegated gene library. A variegated library of RRP variants can be produced by, for example, enzymatically ligating a mixture of synthetic oligonucleotides into gene sequences such that a degenerate set of potential RRP sequences is expressible as individual polypeptides, or alternatively, as a set of larger fusion proteins (*e.g.*, for phage display) containing the set of RRP sequences therein. There are a variety of methods which can be used to produce libraries of potential RRP homologues from a degenerate oligonucleotide sequence. Chemical synthesis of a degenerate gene sequence can be performed in an automatic DNA synthesizer, and the synthetic gene then ligated into an appropriate expression vector. Use of a degenerate set of genes allows for the provision, in one mixture, of all of the sequences encoding the desired set of potential RRP sequences. Methods for synthesizing degenerate oligonucleotides are known in the art (see, *e.g.*, Narang, S.A. (1983) *Tetrahedron* 39:3; Itakura *et al.* (1984) *Annu. Rev. Biochem.* 53:323; Itakura *et al.* (1984) *Science* 198:1056; Ike *et al.* (1983) *Nucleic Acid Res.* 11:477).

In addition, libraries of fragments of the RRP protein coding can be used to generate a variegated population of RRP fragments for screening and subsequent selection of homologues of an RRP protein. In one embodiment, a library of coding sequence fragments can be generated by treating a double stranded PCR fragment of an RRP coding sequence with a nuclease under conditions wherein nicking occurs only about once per molecule, denaturing the double stranded DNA, renaturing the DNA to form double stranded DNA which can include sense/antisense pairs from different nicked products, removing single stranded portions from reformed duplexes by treatment with S1 nuclease, and ligating the resulting fragment library into an expression vector. By this method, an expression library can be derived which encodes N-terminal, C-terminal and internal fragments of various sizes of the RRP protein.

Several techniques are known in the art for screening gene products of combinatorial libraries made by point mutations or truncation, and for screening cDNA libraries for gene products having a selected property. Such techniques are adaptable for rapid screening of the gene libraries generated by the combinatorial mutagenesis of RRP homologues. The most widely used techniques, which are amenable to high through-put analysis, for screening large gene libraries typically include cloning the gene library into

replicable expression vectors, transforming appropriate cells with the resulting library of vectors, and expressing the combinatorial genes under conditions in which detection of a desired activity facilitates isolation of the vector encoding the gene whose product was detected. Recursive ensemble mutagenesis (REM), a new technique which enhances the frequency of functional mutants in the libraries, can be used in combination with the screening assays to identify RRP homologues (Arkin and Yourvan (1992) *PNAS* 89:7811-7815; Delgrave *et al.* (1993) *Protein Engineering* 6(3):327-331).

In another embodiment, cell based assays can be exploited to analyze a variegated RRP library, using methods well known in the art.

#### D. Uses and Methods of the Invention

The nucleic acid molecules, proteins, protein homologues, fusion proteins, primers, vectors, and host cells described herein can be used in one or more of the following methods: identification of *C. glutamicum* and related organisms; mapping of genomes of organisms related to *C. glutamicum*; identification and localization of *C. glutamicum* sequences of interest; evolutionary studies; determination of RRP protein regions required for function; modulation of an RRP protein activity; modulation of DNA synthesis; modulation of protein synthesis; modulation of *C. glutamicum* pathogenesis; and modulation of cellular production of a desired compound, such as a fine chemical.

The RRP nucleic acid molecules of the invention have a variety of uses. First, they may be used to identify an organism as being *Corynebacterium glutamicum* or a close relative thereof. Also, they may be used to identify the presence of *C. glutamicum* or a relative thereof in a mixed population of microorganisms. The invention provides the nucleic acid sequences of a number of *C. glutamicum* genes; by probing the extracted genomic DNA of a culture of a unique or mixed population of microorganisms under stringent conditions with a probe spanning a region of a *C. glutamicum* gene which is unique to this organism, one can ascertain whether this organism is present.

Although *Corynebacterium glutamicum* itself is not pathogenic in humans, it is related to species which are human pathogens, such as *Corynebacterium diphtheriae*. *Corynebacterium diphtheriae* is the causative agent of diphtheria, a rapidly developing, acute, febrile infection which involves both local and systemic pathology. In this disease, a local lesion develops in the upper respiratory tract and involves necrotic injury to epithelial cells; the bacilli secrete toxin which is disseminated through this lesion to distal susceptible tissues of the body. Degenerative changes brought about by the inhibition of protein synthesis in these tissues, which include heart, muscle, peripheral nerves, adrenals, kidneys, liver and spleen, result in the systemic pathology of the

disease. Diphtheria continues to have high incidence in many parts of the world, including Africa, Asia, Eastern Europe and the independent states of the former Soviet Union. An ongoing epidemic of diphtheria in the latter two regions has resulted in at least 5,000 deaths since 1990.

5 In one embodiment, the invention provides a method of identifying the presence or activity of *Corynebacterium diphtheriae* in a subject. This method includes detection of one or more of the nucleic acid or amino acid sequences of the invention (e.g., the sequences set forth in Appendix A or Appendix B) in a subject, thereby detecting the presence or activity of *Corynebacterium diphtheriae* in the subject. *C. glutamicum* and  
10 *C. diphtheriae* are related bacteria, and many of the nucleic acid and protein molecules in *C. glutamicum* are homologous to *C. diphtheriae* nucleic acid and protein molecules, and can therefore be used to detect *C. diphtheriae* in a subject.

The nucleic acid and protein molecules of the invention may also serve as markers for specific regions of the genome. This has utility not only in the mapping of  
15 the genome, but also for functional studies of *C. glutamicum* proteins. For example, to identify the region of the genome to which a particular *C. glutamicum* DNA-binding protein binds, the *C. glutamicum* genome could be digested, and the fragments incubated with the DNA-binding protein. Those which bind the protein may be additionally probed with the nucleic acid molecules of the invention, preferably with readily detectable  
20 labels; binding of such a nucleic acid molecule to the genome fragment enables the localization of the fragment to the genome map of *C. glutamicum*, and, when performed multiple times with different enzymes, facilitates a rapid determination of the nucleic acid sequence to which the protein binds. Further, the nucleic acid molecules of the invention may be sufficiently homologous to the sequences of related species such that  
25 these nucleic acid molecules may serve as markers for the construction of a genomic map in related bacteria, such as *Brevibacterium lactofermentum*.

The RRP nucleic acid molecules encoding proteins involved in the pathogenicity of *C. glutamicum* are also useful for purposes of genetic engineering of this microorganism. Frequently, the insertion of genetic information into the genome of an  
30 organism is a disruptive process, which may inadvertently impair the regulation or coding regions of multiple different genes. The RRP pathogenicity genes of the invention are not necessary for the continued survival of the organism in an artificial culture setting, and are not likely to add any benefit to the productivity of the organism for one or more fine chemicals. These genes, then, may serve as useful insertion points  
35 for the addition of genetic material to the genome of *C. glutamicum*, since their disruption should not affect the viability or the productivity of this microorganism.

The RRP nucleic acid molecules of the invention are also useful for evolutionary and protein structural studies. The processes involved in DNA replication, protein synthesis and pathogenesis in which the molecules of the invention participate are utilized by a wide variety of species; by comparing the sequences of the nucleic acid molecules of the present invention to those encoding similar enzymes from other organisms, the evolutionary relatedness of the organisms can be assessed. Similarly, such a comparison permits an assessment of which regions of the sequence are conserved and which are not, which may aid in determining those regions of the protein which are essential for the functioning of the enzyme. This type of determination is of value for protein engineering studies and may give an indication of what the protein can tolerate in terms of mutagenesis without losing function.

Manipulation of the RRP nucleic acid molecules of the invention may result in the production of RRP proteins having functional differences from the wild-type RRP proteins. These proteins may be improved in efficiency or activity, may be present in greater numbers in the cell than is usual, or may be decreased in efficiency or activity.

The invention provides methods for screening molecules which modulate the activity of an RRP protein, either by interacting with the protein itself or a substrate or binding partner of the RRP protein, or by modulating the transcription or translation of an RRP nucleic acid molecule of the invention. In such methods, a microorganism expressing one or more RRP proteins of the invention is contacted with one or more test compounds, and the effect of each test compound on the activity or level of expression of the RRP protein is assessed.

The alteration of activity or number of one or more of the RRP proteins of the invention involved in DNA replication may affect fine chemical production from a *C. glutamicum* (or related bacterial) cell containing such mutations. For example, by improving the rate at which a DNA polymerase of the invention synthesizes DNA, it may be possible to improve the overall replication rate of the genomic DNA. Similarly, by optimizing the activity of the topoisomerases or gyrases of the invention, it may be possible to more quickly unwind the DNA, thereby permitting increased progressivity of the polymerase complex along the bacterial chromosome. Further, it may be possible to engineer one or more of the proteins involved in DNA replication such that they are improved for function under conditions of high temperature and nonoptimal pH, such as those found in large-scale fermentor culture (e.g., amino acid replacements may be made such that the resulting structure of one of these proteins retains activity but is improved for stability at high temperature or acidic/basic pH). Improving the rate of DNA synthesis in *C. glutamicum* or related bacteria may permit more rapid rates of cell division, leading to increased numbers of cells present in large-scale cultures of the

bacterium. Relatively increased numbers of cells, each of which is producing one or more desired fine chemicals, should result in relatively increased yield, production, or efficiency of production of one or more fine chemicals from the culture.

- Also, by manipulating one or more of the RRP genes of the invention, it may be possible to increase the overall fidelity of replication in *C. glutamicum* or related bacterial cells. For example, the 3'-5' exonuclease activities of Pol III or Pol I (which are responsible for excising inappropriately incorporated bases from the growing DNA strand) may be optimized such that more incorrect bases are detected and removed. Similarly, the polymerization activity of the DNA polymerases of the invention may be improved such that the error rate in base incorporation is decreased. Both such modifications should result in improved fidelity in the replicated DNA, which in turn should decrease the rate of introduced mutations. Fewer introduced mutations not only helps to ensure that any other engineered genes will not be undesirably altered by random mutation, but also may permit increased viability of the cells in culture, since random mutations may impair the activity of genes necessary for cell survival. As before, increased numbers of viable cells in culture should result in increased yield, production, and/or efficiency of production of one or more fine chemicals produced by those cells.

- Mutations in genes and proteins involved in protein synthesis (e.g., ribosomal genes and proteins) may also have a significant effect on the production of one or more fine chemicals from *C. glutamicum* or related bacterial cultures. For example, by improving the rate of protein synthesis (e.g., by improving the rate of assembly of the ribosome, by improving the progressivity of the ribosome, or by increasing the rate at which the ribosome is able to productively bind to mRNA, all of which may be accomplished by altering the binding sites for the various ribosomal components such that binding and association of ribosomal proteins to each other or to tRNAs or to mRNAs are improved) it may be possible to increase the rate at which proteins involved in the synthesis of desired fine chemicals are produced, thereby potentially improving the production of one or more of these fine chemicals. This increased protein production may also permit increased growth and cell division of the cell, since increased cellular metabolism (which may occur due to the presence of increased numbers of metabolic proteins) may also result in more rapid cell division, thereby increasing the number of cells in a culture of the bacterium containing such mutation(s). Increased numbers of viable cells in large-scale fermentor culture, each of which is producing one or more desired fine chemicals, should result in an increase in yield, production, and/or efficiency of production of these fine chemicals.



Alteration of the number of the RRP proteins of the invention involved in the pathogenicity of *C. glutamicum* (e.g., hemolysin and invasins) may also increase the yield, production, and/or efficiency of production of one or more fine chemicals from *C. glutamicum* cells containing such mutations. These pathogenesis proteins may be of utility for the survival of *C. glutamicum* cells in their natural environments. However, in the artificial environment of fermentor culture, nutrients are typically supplied in excess, and there should be no other organisms with which these bacteria need to compete. Thus, the synthesis of these pathogenesis proteins represents the utilization of energy and biomaterials which could instead be shifted to the production of one or more desired fine chemicals. Thus, by decreasing the number of such pathogenesis genes in *C. glutamicum*, it may be possible to increase the available intermediate compounds (e.g., nucleotides, amino acids, or energy molecules such as ATP) such that metabolism in general, and fine chemical production in particular is increased.

These RRP proteins involved in pathogenesis may themselves also be considered desirable fine chemicals. These proteins may have significant pharmaceutical applications, as, for example, antimicrobial or antifungal agents. Further, although *C. glutamicum* is not a human pathogen, its pathogenesis proteins (e.g., hemolysins or adhesins) may be similar in structure and activity to those from bacterial species which are significant human pathogens (e.g., *E. coli* or *Pseudomonas* spp.) These *C. glutamicum* pathogenesis proteins may thus serve as useful targets for the development of vaccines or therapeutics against various human pathogens. By mutagenizing the genes encoding these proteins such that their synthesis and/or translation is no longer repressed by cellular regulatory mechanisms, or such their production is no longer subject to feedback inhibition (e.g., by mutagenizing regulatory regions upstream or downstream of the gene, or by mutagenizing regulatory regions on the protein itself) greater numbers of these proteins may be able to be expressed and harvested from culture.

The aforementioned mutagenesis strategies for RRP proteins to result in increased yields of a fine chemical from *C. glutamicum* are not meant to be limiting; variations on these strategies will be readily apparent to one of ordinary skill in the art. Using such strategies, and incorporating the mechanisms disclosed herein, the nucleic acid and protein molecules of the invention may be utilized to generate *C. glutamicum* or related strains of bacteria expressing mutated RRP nucleic acid and protein molecules such that the yield, production, and/or efficiency of production of a desired compound is improved. This desired compound may be any product produced by *C. glutamicum*, which includes the final products of biosynthesis pathways and intermediates of naturally-occurring metabolic pathways, as well as molecules which do not naturally

occur in the metabolism of *C. glutamicum*, but which are produced by a *C. glutamicum* strain of the invention.

This invention is further illustrated by the following examples which should not be construed as limiting. The contents of all references, patent applications, patents, published patent applications, Tables, Appendices, and the sequence listing cited throughout this application are hereby incorporated by reference.

### Exemplification

#### **Example 1: Preparation of total genomic DNA of *Corynebacterium glutamicum* ATCC 13032**

A culture of *Corynebacterium glutamicum* (ATCC 13032) was grown overnight at 30°C with vigorous shaking in BHI medium (Difco). The cells were harvested by centrifugation, the supernatant was discarded and the cells were resuspended in 5 ml buffer-I (5% of the original volume of the culture — all indicated volumes have been calculated for 100 ml of culture volume). Composition of buffer-I: 140.34 g/l sucrose, 2.46 g/l MgSO<sub>4</sub> x 7H<sub>2</sub>O, 10 ml/l KH<sub>2</sub>PO<sub>4</sub> solution (100 g/l, adjusted to pH 6.7 with KOH), 50 ml/l M12 concentrate (10 g/l (NH<sub>4</sub>)<sub>2</sub>SO<sub>4</sub>, 1 g/l NaCl, 2 g/l MgSO<sub>4</sub> x 7H<sub>2</sub>O, 0.2 g/l CaCl<sub>2</sub>, 0.5 g/l yeast extract (Difco), 10 ml/l trace-elements-mix (200 mg/l FeSO<sub>4</sub> x H<sub>2</sub>O, 10 mg/l ZnSO<sub>4</sub> x 7 H<sub>2</sub>O, 3 mg/l MnCl<sub>2</sub> x 4 H<sub>2</sub>O, 30 mg/l H<sub>3</sub>BO<sub>3</sub>, 20 mg/l CoCl<sub>2</sub> x 6 H<sub>2</sub>O, 1 mg/l NiCl<sub>2</sub> x 6 H<sub>2</sub>O, 3 mg/l Na<sub>2</sub>MoO<sub>4</sub> x 2 H<sub>2</sub>O, 500 mg/l complexing agent (EDTA or citric acid), 100 ml/l vitamins-mix (0.2 mg/l biotin, 0.2 mg/l folic acid, 20 mg/l p-amino benzoic acid, 20 mg/l riboflavin, 40 mg/l ca-pantothenate, 140 mg/l nicotinic acid, 40 mg/l pyridoxole hydrochloride, 200 mg/l myo-inositol). Lysozyme was added to the suspension to a final concentration of 2.5 mg/ml. After an approximately 4 h incubation at 37°C, the cell wall was degraded and the resulting protoplasts are harvested by centrifugation. The pellet was washed once with 5 ml buffer-I and once with 5 ml TE-buffer (10 mM Tris-HCl, 1 mM EDTA, pH 8). The pellet was resuspended in 4 ml TE-buffer and 0.5 ml SDS solution (10%) and 0.5 ml NaCl solution (5 M) are added. After adding of proteinase K to a final concentration of 200 µg/ml, the suspension is incubated for ca.18 h at 37°C. The DNA was purified by extraction with phenol, phenol-chloroform-isoamylalcohol and chloroform-isoamylalcohol using standard procedures. Then, the DNA was precipitated by adding 1/50 volume of 3 M sodium acetate and 2 volumes of ethanol, followed by a 30 min incubation at -20°C and a 30 min centrifugation at 12,000 rpm in a high speed centrifuge using a SS34 rotor (Sorvall). The DNA was dissolved in 1 ml TE-buffer containing 20

µg/ml RNaseA and dialysed at 4°C against 1000 ml TE-buffer for at least 3 hours. During this time, the buffer was exchanged 3 times. To aliquots of 0.4 ml of the dialysed DNA solution, 0.4 ml of 2 M LiCl and 0.8 ml of ethanol are added. After a 30 min incubation at -20°C, the DNA was collected by centrifugation (13,000 rpm, Biofuge  
5 Fresco, Heraeus, Hanau, Germany). The DNA pellet was dissolved in TE-buffer. DNA prepared by this procedure could be used for all purposes, including southern blotting or construction of genomic libraries.

10 **Example 2: Construction of genomic libraries in *Escherichia coli* of *Corynebacterium glutamicum* ATCC13032.**

Using DNA prepared as described in Example 1, cosmid and plasmid libraries were constructed according to known and well established methods (see e.g., Sambrook, J. et al. (1989) "Molecular Cloning : A Laboratory Manual", Cold Spring Harbor Laboratory Press, or Ausubel, F.M. et al. (1994) "Current Protocols in Molecular Biology", John Wiley &  
15 Sons.)

Any plasmid or cosmid could be used. Of particular use were the plasmids pBR322 (Sutcliffe, J.G. (1979) *Proc. Natl. Acad. Sci. USA*, 75:3737-3741); pACYC177 (Change & Cohen (1978) *J. Bacteriol* 134:1141-1156), plasmids of the pBS series (pBSSK+, pBSSK- and others; Stratagene, LaJolla, USA), or cosmids as SuperCos1 (Stratagene, LaJolla, USA) or  
20 Lorist6 (Gibson, T.J., Rosenthal A. and Waterson, R.H. (1987) *Gene* 53:283-286. Gene libraries specifically for use in *C. glutamicum* may be constructed using plasmid pSL109 (Lee, H.-S. and A. J. Sinskey (1994) *J. Microbiol. Biotechnol.* 4: 256-263).

**Example 3: DNA Sequencing and Computational Functional Analysis**

25 Genomic libraries as described in Example 2 were used for DNA sequencing according to standard methods, in particular by the chain termination method using ABI377 sequencing machines (see e.g., Fleischman, R.D. et al. (1995) "Whole-genome Random Sequencing and Assembly of Haemophilus Influenzae Rd., Science, 269:496-512). Sequencing primers with the following nucleotide sequences were used: 5'-  
30 GGAAACAGTATGACCATG-3' or 5'-GTAAACGACGCCAGT-3'.

**Example 4: *In vivo* Mutagenesis**

*In vivo* mutagenesis of *Corynebacterium glutamicum* can be performed by passage of plasmid (or other vector) DNA through *E. coli* or other microorganisms (e.g. *Bacillus* spp. or  
35 yeasts such as *Saccharomyces cerevisiae*) which are impaired in their capabilities to maintain the integrity of their genetic information. Typical mutator strains have mutations in the genes for the DNA repair system (e.g., mutHLS, mutD, mutT, etc.; for reference, see Rupp, W.D.

(1996) DNA repair mechanisms, in: *Escherichia coli* and *Salmonella*, p. 2277-2294, ASM: Washington.) Such strains are well known to one of ordinary skill in the art. The use of such strains is illustrated, for example, in Greener, A. and Callahan, M. (1994) Strategies 7: 32-34.

**5 Example 5: DNA Transfer Between *Escherichia coli* and *Corynebacterium glutamicum***

Several *Corynebacterium* and *Brevibacterium* species contain endogenous plasmids (as e.g., pHM1519 or pBL1) which replicate autonomously (for review see, e.g., Martin, J.F. et al. (1987) Biotechnology, 5:137-146). Shuttle vectors for *Escherichia coli* and *Corynebacterium glutamicum* can be readily constructed by using standard vectors for *E. coli* (Sambrook, J. et al. (1989), "Molecular Cloning: A Laboratory Manual", Cold Spring Harbor Laboratory Press or Ausubel, F.M. et al. (1994) "Current Protocols in Molecular Biology", John Wiley & Sons) to which a origin or replication for and a suitable marker from *Corynebacterium glutamicum* is added. Such origins of replication are preferably taken from endogenous plasmids isolated from *Corynebacterium* and *Brevibacterium* species. Of particular use as transformation markers for these species are genes for kanamycin resistance (such as those derived from the Tn5 or Tn903 transposons) or chloramphenicol (Winnacker, E.L. (1987) "From Genes to Clones — Introduction to Gene Technology, VCH, Weinheim). There are numerous examples in the literature of the construction of a wide variety of shuttle vectors which replicate in both *E. coli* and *C. glutamicum*, and which can be used for several purposes, including gene over-expression (for reference, see e.g., Yoshihama, M. et al. (1985) J. Bacteriol. 162:591-597, Martin J.F. et al. (1987) Biotechnology, 5:137-146 and Eikmanns, B.J. et al. (1991) Gene, 102:93-98).

Using standard methods, it is possible to clone a gene of interest into one of the shuttle vectors described above and to introduce such a hybrid vectors into strains of *Corynebacterium glutamicum*. Transformation of *C. glutamicum* can be achieved by protoplast transformation (Kastumata, R. et al. (1984) J. Bacteriol. 159:306-311), electroporation (Liebl, E. et al. (1989) FEMS Microbiol. Letters, 53:399-303) and in cases where special vectors are used, also by conjugation (as described e.g. in Schäfer, A et al. (1990) J. Bacteriol. 172:1663-1666). It is also possible to transfer the shuttle vectors for *C. glutamicum* to *E. coli* by preparing plasmid DNA from *C. glutamicum* (using standard methods well-known in the art) and transforming it into *E. coli*. This transformation step can be performed using standard methods, but it is advantageous to use an Mer-deficient *E. coli* strain, such as NM522 (Gough & Murray (1983) J. Mol. Biol. 166:1-19).

Genes may be overexpressed in *C. glutamicum* strains using plasmids which comprise pCG1 (U.S. Patent No. 4,617,267) or fragments thereof, and optionally the

gene for kanamycin resistance from TN903 (Grindley, N.D. and Joyce, C.M. (1980) *Proc. Natl. Acad. Sci. USA* 77(12): 7176-7180). In addition, genes may be overexpressed in *C. glutamicum* strains using plasmid pSL109 (Lee, H.-S. and A. J. Sinskey (1994) *J. Microbiol. Biotechnol.* 4: 256-263).

5        Aside from the use of replicative plasmids, gene overexpression can also be achieved by integration into the genome. Genomic integration in *C. glutamicum* or other *Corynebacterium* or *Brevibacterium* species may be accomplished by well-known methods, such as homologous recombination with genomic region(s), restriction endonuclease mediated integration (REMI) (see, e.g., DE Patent 19823834), or through  
10      the use of transposons. It is also possible to modulate the activity of a gene of interest by modifying the regulatory regions (e.g., a promoter, a repressor, and/or an enhancer) by sequence modification, insertion, or deletion using site-directed methods (such as homologous recombination) or methods based on random events (such as transposon mutagenesis or REMI). Nucleic acid sequences which function as transcriptional  
15      terminators may also be inserted 3' to the coding region of one or more genes of the invention; such terminators are well-known in the art and are described, for example, in Winnacker, E.L. (1987) *From Genes to Clones - Introduction to Gene Technology*. VCH: Weinheim.

#### 20      **Example 6: Assessment of the Expression of the Mutant Protein**

Observations of the activity of a mutated protein in a transformed host cell rely on the fact that the mutant protein is expressed in a similar fashion and in a similar quantity to that of the wild-type protein. A useful method to ascertain the level of transcription of the mutant gene (an indicator of the amount of mRNA available for translation to the gene  
25      product) is to perform a Northern blot (for reference see, for example, Ausubel *et al.* (1988) *Current Protocols in Molecular Biology*, Wiley: New York), in which a primer designed to bind to the gene of interest is labeled with a detectable tag (usually radioactive or chemiluminescent), such that when the total RNA of a culture of the organism is extracted, run on gel, transferred to a stable matrix and incubated with this probe, the  
30      binding and quantity of binding of the probe indicates the presence and also the quantity of mRNA for this gene. This information is evidence of the degree of transcription of the mutant gene. Total cellular RNA can be prepared from *Corynebacterium glutamicum* by several methods, all well-known in the art, such as that described in Bormann, E.R. *et al.* (1992) *Mol. Microbiol.* 6: 317-326.

35      To assess the presence or relative quantity of protein translated from this mRNA, standard techniques, such as a Western blot, may be employed (see, for example, Ausubel *et al.* (1988) *Current Protocols in Molecular Biology*, Wiley: New York). In this process,

total cellular proteins are extracted, separated by gel electrophoresis, transferred to a matrix such as nitrocellulose, and incubated with a probe, such as an antibody, which specifically binds to the desired protein. This probe is generally tagged with a chemiluminescent or colorimetric label which may be readily detected. The presence and quantity of label observed indicates the presence and quantity of the desired mutant protein present in the cell.

#### **Example 7: Growth of Genetically Modified *Corynebacterium glutamicum* — Media and Culture Conditions**

- Genetically modified *Corynebacteria* are cultured in synthetic or natural growth media. A number of different growth media for *Corynebacteria* are both well-known and readily available (Lieb *et al.* (1989) Appl. Microbiol. Biotechnol., 32:205-210; von der Osten *et al.* (1998) Biotechnology Letters, 11:11-16; Patent DE 4,120,867; Liebl (1992) "The Genus *Corynebacterium*, in: The Prokaryotes, Volume II, Balows, A. *et al.*, eds. Springer-Verlag). These media consist of one or more carbon sources, nitrogen sources, inorganic salts, vitamins and trace elements. Preferred carbon sources are sugars, such as mono-, di-, or polysaccharides. For example, glucose, fructose, mannose, galactose, ribose, sorbose, ribulose, lactose, maltose, sucrose, raffinose, starch or cellulose serve as very good carbon sources. It is also possible to supply sugar to the media via complex compounds such as molasses or other by-products from sugar refinement. It can also be advantageous to supply mixtures of different carbon sources. Other possible carbon sources are alcohols and organic acids, such as methanol, ethanol, acetic acid or lactic acid. Nitrogen sources are usually organic or inorganic nitrogen compounds, or materials which contain these compounds. Exemplary nitrogen sources include ammonia gas or ammonia salts, such as  $\text{NH}_4\text{Cl}$  or  $(\text{NH}_4)_2\text{SO}_4$ ,  $\text{NH}_4\text{OH}$ , nitrates, urea, amino acids or complex nitrogen sources like corn steep liquor, soy bean flour, soy bean protein, yeast extract, meat extract and others.

- Inorganic salt compounds which may be included in the media include the chloride-, phosphorous- or sulfate- salts of calcium, magnesium, sodium, cobalt, molybdenum, potassium, manganese, zinc, copper and iron. Chelating compounds can be added to the medium to keep the metal ions in solution. Particularly useful chelating compounds include dihydroxyphenols, like catechol or protocatechuate, or organic acids, such as citric acid. It is typical for the media to also contain other growth factors, such as vitamins or growth promoters, examples of which include biotin, riboflavin, thiamin, folic acid, nicotinic acid, pantothenate and pyridoxin. Growth factors and salts frequently originate from complex media components such as yeast extract, molasses, corn steep liquor and others. The exact composition of the media compounds depends strongly on

the immediate experiment and is individually decided for each specific case. Information about media optimization is available in the textbook "Applied Microbiol. Physiology, A Practical Approach" (eds. P.M. Rhodes, P.F. Stanbury, IRL Press (1997) pp. 53-73, ISBN 0 19 963577 3). It is also possible to select growth media from commercial suppliers, like  
5 standard 1 (Merck) or BHI (grain heart infusion, DIFCO) or others.

All medium components are sterilized, either by heat (20 minutes at 1.5 bar and 121°C) or by sterile filtration. The components can either be sterilized together or, if necessary, separately. All media components can be present at the beginning of growth, or they can optionally be added continuously or batchwise.

10 Culture conditions are defined separately for each experiment. The temperature should be in a range between 15°C and 45°C. The temperature can be kept constant or can be altered during the experiment. The pH of the medium should be in the range of 5 to 8.5, preferably around 7.0, and can be maintained by the addition of buffers to the media. An exemplary buffer for this purpose is a potassium phosphate buffer. Synthetic buffers  
15 such as MOPS, HEPES, ACES and others can alternatively or simultaneously be used. It is also possible to maintain a constant culture pH through the addition of NaOH or NH<sub>4</sub>OH during growth. If complex medium components such as yeast extract are utilized, the necessity for additional buffers may be reduced, due to the fact that many complex compounds have high buffer capacities. If a fermentor is utilized for culturing the micro-  
20 organisms, the pH can also be controlled using gaseous ammonia.

The incubation time is usually in a range from several hours to several days. This time is selected in order to permit the maximal amount of product to accumulate in the broth. The disclosed growth experiments can be carried out in a variety of vessels, such as microtiter plates, glass tubes, glass flasks or glass or metal fermentors of different sizes.  
25 For screening a large number of clones, the microorganisms should be cultured in microtiter plates, glass tubes or shake flasks, either with or without baffles. Preferably 100 ml shake flasks are used, filled with 10% (by volume) of the required growth medium. The flasks should be shaken on a rotary shaker (amplitude 25 mm) using a speed-range of 100 – 300 rpm. Evaporation losses can be diminished by the maintenance  
30 of a humid atmosphere; alternatively, a mathematical correction for evaporation losses should be performed.

If genetically modified clones are tested, an unmodified control clone or a control clone containing the basic plasmid without any insert should also be tested. The medium is inoculated to an OD<sub>600</sub> of 0.5 – 1.5 using cells grown on agar plates, such as CM plates  
35 (10 g/l glucose, 2.5 g/l NaCl, 2 g/l urea, 10 g/l polypeptone, 5 g/l yeast extract, 5 g/l meat extract, 22 g/l NaCl, 2 g/l urea, 10 g/l polypeptone, 5 g/l yeast extract, 5 g/l meat extract, 22 g/l agar, pH 6.8 with 2M NaOH) that had been incubated at 30°C. Inoculation of the

media is accomplished by either introduction of a saline suspension of *C. glutamicum* cells from CM plates or addition of a liquid preculture of this bacterium.

**Example 8 – In vitro Analysis of the Function of Mutant Proteins**

- 5       The determination of activities and kinetic parameters of enzymes is well established in the art. Experiments to determine the activity of any given altered enzyme must be tailored to the specific activity of the wild-type enzyme, which is well within the ability of one of ordinary skill in the art. Overviews about enzymes in general, as well as specific details concerning structure, kinetics, principles, methods, applications and examples for the determination of many enzyme activities may be found, for example, in the following references: Dixon, M., and Webb, E.C., (1979) *Enzymes*. Longmans: London; Fersht, (1985) *Enzyme Structure and Mechanism*. Freeman: New York; Walsh, (1979) *Enzymatic Reaction Mechanisms*. Freeman: San Francisco; Price, N.C., Stevens, L. (1982) *Fundamentals of Enzymology*. Oxford Univ. Press: Oxford; Boyer, P.D., ed. (1983) *The Enzymes*, 3<sup>rd</sup> ed. Academic Press: New York; Bisswanger, H., (1994) *Enzymkinetik*, 2<sup>nd</sup> ed. VCH: Weinheim (ISBN 3527300325); Bergmeyer, H.U., Bergmeyer, J., Graßl, M., eds. (1983-1986) *Methods of Enzymatic Analysis*, 3<sup>rd</sup> ed., vol. I-XII, Verlag Chemie: Weinheim; and Ullmann's Encyclopedia of Industrial Chemistry (1987) vol. A9, "Enzymes". VCH: Weinheim, p. 20 352-363.

- The activity of proteins which bind to DNA can be measured by several well-established methods, such as DNA band-shift assays (also called gel retardation assays). The effect of such proteins on the expression of other molecules can be measured using reporter gene assays (such as that described in Kolmar, H. *et al.* (1995) *EMBO J.* 14: 25 3895-3904 and references cited therein). Reporter gene test systems are well known and established for applications in both pro- and eukaryotic cells, using enzymes such as beta-galactosidase, green fluorescent protein, and several others.

- The determination of activity of membrane-transport proteins can be performed according to techniques such as those described in Gennis, R.B. (1989) "Pores, Channels and Transporters", in *Biomembranes, Molecular Structure and Function*, Springer: Heidelberg, p. 85-137; 199-234; and 270-322.

**Example 9: Analysis of Impact of Mutant Protein on the Production of the Desired Product**

- 35       The effect of the genetic modification in *C. glutamicum* on production of a desired compound (such as an amino acid) can be assessed by growing the modified microorganism under suitable conditions (such as those described above) and analyzing



- the medium and/or the cellular component for increased production of the desired product (*i.e.*, an amino acid). Such analysis techniques are well known to one of ordinary skill in the art, and include spectroscopy, thin layer chromatography, staining methods of various kinds, enzymatic and microbiological methods, and analytical chromatography such as high performance liquid chromatography (see, for example,
- 5 Ullman, Encyclopedia of Industrial Chemistry, vol. A2, p. 89-90 and p. 443-613, VCH: Weinheim (1985); Fallon, A. *et al.*, (1987) "Applications of HPLC in Biochemistry" in: Laboratory Techniques in Biochemistry and Molecular Biology, vol. 17; Rehm *et al.* (1993) Biotechnology, vol. 3, Chapter III: "Product recovery and purification", page
- 10 469-714, VCH: Weinheim; Belter, P.A. *et al.* (1988) Bioseparations: downstream processing for biotechnology, John Wiley and Sons; Kennedy, J.F. and Cabral, J.M.S. (1992) Recovery processes for biological materials, John Wiley and Sons; Shaeiwitz, J.A. and Henry, J.D. (1988) Biochemical separations, in: Ulmann's Encyclopedia of Industrial Chemistry, vol. B3, Chapter 11, page 1-27, VCH: Weinheim; and Dechow,
- 15 F.J. (1989) Separation and purification techniques in biotechnology, Noyes Publications.)

- In addition to the measurement of the final product of fermentation, it is also possible to analyze other components of the metabolic pathways utilized for the production of the desired compound, such as intermediates and side-products, to
- 20 determine the overall efficiency of production of the compound. Analysis methods include measurements of nutrient levels in the medium (*e.g.*, sugars, hydrocarbons, nitrogen sources, phosphate, and other ions), measurements of biomass composition and growth, analysis of the production of common metabolites of biosynthetic pathways, and measurement of gasses produced during fermentation. Standard methods for these
- 25 measurements are outlined in Applied Microbial Physiology, A Practical Approach, P.M. Rhodes and P.F. Stanbury, eds., IRL Press, p. 103-129; 131-163; and 165-192 (ISBN: 0199635773) and references cited therein.

#### **Example 10: Purification of the Desired Product from *C. glutamicum* Culture**

- 30 Recovery of the desired product from the *C. glutamicum* cells or supernatant of the above-described culture can be performed by various methods well known in the art. If the desired product is not secreted from the cells, the cells can be harvested from the culture by low-speed centrifugation, the cells can be lysed by standard techniques, such as mechanical force or sonication. The cellular debris is removed by centrifugation, and
- 35 the supernatant fraction containing the soluble proteins is retained for further purification of the desired compound. If the product is secreted from the *C. glutamicum*

cells, then the cells are removed from the culture by low-speed centrifugation, and the supernate fraction is retained for further purification.

The supernatant fraction from either purification method is subjected to chromatography with a suitable resin, in which the desired molecule is either retained on  
5 a chromatography resin while many of the impurities in the sample are not, or where the impurities are retained by the resin while the sample is not. Such chromatography steps may be repeated as necessary, using the same or different chromatography resins. One of ordinary skill in the art would be well-versed in the selection of appropriate chromatography resins and in their most efficacious application for a particular molecule  
10 to be purified. The purified product may be concentrated by filtration or ultrafiltration, and stored at a temperature at which the stability of the product is maximized.

There are a wide array of purification methods known to the art and the preceding method of purification is not meant to be limiting. Such purification techniques are described, for example, in Bailey, J.E. & Ollis, D.F. *Biochemical Engineering Fundamentals*, McGraw-Hill: New York (1986).  
15

The identity and purity of the isolated compounds may be assessed by techniques standard in the art. These include high-performance liquid chromatography (HPLC), spectroscopic methods, staining methods, thin layer chromatography, NIRS, enzymatic assay, or microbiologically. Such analysis methods are reviewed in: Patek *et al.* (1994)  
20 *Appl. Environ. Microbiol.* 60: 133-140; Malakhova *et al.* (1996) *Biotechnologiya* 11: 27-32; and Schmidt *et al.* (1998) *Bioprocess Engineer.* 19: 67-70. *Ulmann's Encyclopedia of Industrial Chemistry*, (1996) vol. A27, VCH: Weinheim, p. 89-90, p. 521-540, p. 540-547, p. 559-566, 575-581 and p. 581-587; Michal, G. (1999) *Biochemical Pathways: An Atlas of Biochemistry and Molecular Biology*, John Wiley and Sons; Fallon, A. *et al.*  
25 (1987) *Applications of HPLC in Biochemistry in: Laboratory Techniques in Biochemistry and Molecular Biology*, vol. 17.

#### **Example 11: Analysis of the Gene Sequences of the Invention**

The comparison of sequences and determination of percent homology between  
30 two sequences are art-known techniques, and can be accomplished using a mathematical algorithm, such as the algorithm of Karlin and Altschul (1990) *Proc. Natl. Acad. Sci. USA* 87:2264-68, modified as in Karlin and Altschul (1993) *Proc. Natl. Acad. Sci. USA* 90:5873-77. Such an algorithm is incorporated into the NBLAST and XBLAST programs (version 2.0) of Altschul, *et al.* (1990) *J. Mol. Biol.* 215:403-10. BLAST  
35 nucleotide searches can be performed with the NBLAST program, score = 100, wordlength = 12 to obtain nucleotide sequences homologous to RRP nucleic acid molecules of the invention. BLAST protein searches can be performed with the

XBLAST program, score = 50, wordlength = 3 to obtain amino acid sequences homologous to RRP protein molecules of the invention. To obtain gapped alignments for comparison purposes, Gapped BLAST can be utilized as described in Altschul *et al.*, (1997) *Nucleic Acids Res.* 25(17):3389-3402. When utilizing BLAST and Gapped

5 BLAST programs, one of ordinary skill in the art will know how to optimize the parameters of the program (*e.g.*, XBLAST and NBLAST) for the specific sequence being analyzed.

Another example of a mathematical algorithm utilized for the comparison of sequences is the algorithm of Meyers and Miller ((1988) *Comput. Appl. Biosci.* 4: 11-17). Such an algorithm is incorporated into the ALIGN program (version 2.0) which is

10 part of the GCG sequence alignment software package. When utilizing the ALIGN program for comparing amino acid sequences, a PAM120 weight residue table, a gap length penalty of 12, and a gap penalty of 4 can be used. Additional algorithms for sequence analysis are known in the art, and include ADVANCE and ADAM, described

15 in Torelli and Robotti (1994) *Comput. Appl. Biosci.* 10:3-5; and FASTA, described in Pearson and Lipman (1988) *P.N.A.S.* 85:2444-8.

The percent homology between two amino acid sequences can also be accomplished using the GAP program in the GCG software package (available at <http://www.gcg.com>), using either a Blosum 62 matrix or a PAM250 matrix, and a gap

20 weight of 12, 10, 8, 6, or 4 and a length weight of 2, 3, or 4. The percent homology between two nucleic acid sequences can be accomplished using the GAP program in the GCG software package, using standard parameters, such as a gap weight of 50 and a length weight of 3.

A comparative analysis of the gene sequences of the invention with those present

25 in Genbank has been performed using techniques known in the art (see, *e.g.*, Bexevanis and Ouellette, eds. (1998) *Bioinformatics: A Practical Guide to the Analysis of Genes and Proteins*. John Wiley and Sons: New York). The gene sequences of the invention were compared to genes present in Genbank in a three-step process. In a first step, a BLASTN analysis (*e.g.*, a local alignment analysis) was performed for each of the

30 sequences of the invention against the nucleotide sequences present in Genbank, and the top 500 hits were retained for further analysis. A subsequent FASTA search (*e.g.*, a combined local and global alignment analysis, in which limited regions of the sequences are aligned) was performed on these 500 hits. Each gene sequence of the invention was subsequently globally aligned to each of the top three FASTA hits, using the GAP

35 program in the GCG software package (using standard parameters). In order to obtain correct results, the length of the sequences extracted from Genbank were adjusted to the length of the query sequences by methods well-known in the art. The results of this

analysis are set forth in Table 4. The resulting data is identical to that which would have been obtained had a GAP (global) analysis alone been performed on each of the genes of the invention in comparison with each of the references in Genbank, but required significantly reduced computational time as compared to such a database-wide GAP (global) analysis. Sequences of the invention for which no alignments above the cutoff values were obtained are indicated on Table 4 by the absence of alignment information. It will further be understood by one of ordinary skill in the art that the GAP alignment homology percentages set forth in Table 4 under the heading "% homology (GAP)" are listed in the European numerical format, wherein a ',' represents a decimal point. For example, a value of "40,345" in this column represents "40.345%".

#### Example 12: Construction and Operation of DNA Microarrays

The sequences of the invention may additionally be used in the construction and application of DNA microarrays (the design, methodology, and uses of DNA arrays are well known in the art, and are described, for example, in Schena, M. *et al.* (1995) *Science* 270: 467-470; Wodicka, L. *et al.* (1997) *Nature Biotechnology* 15: 1359-1367; DeSaizieu, A. *et al.* (1998) *Nature Biotechnology* 16: 45-48; and DeRisi, J.L. *et al.* (1997) *Science* 278: 680-686).

DNA microarrays are solid or flexible supports consisting of nitrocellulose, nylon, glass, silicone, or other materials. Nucleic acid molecules may be attached to the surface in an ordered manner. After appropriate labeling, other nucleic acids or nucleic acid mixtures can be hybridized to the immobilized nucleic acid molecules, and the label may be used to monitor and measure the individual signal intensities of the hybridized molecules at defined regions. This methodology allows the simultaneous quantification of the relative or absolute amount of all or selected nucleic acids in the applied nucleic acid sample or mixture. DNA microarrays, therefore, permit an analysis of the expression of multiple (as many as 6800 or more) nucleic acids in parallel (see, e.g., Schena, M. (1996) *BioEssays* 18(5): 427-431).

The sequences of the invention may be used to design oligonucleotide primers which are able to amplify defined regions of one or more *C. glutamicum* genes by a nucleic acid amplification reaction such as the polymerase chain reaction. The choice and design of the 5' or 3' oligonucleotide primers or of appropriate linkers allows the covalent attachment of the resulting PCR products to the surface of a support medium described above (and also described, for example, Schena, M. *et al.* (1995) *Science* 270: 467-470).

Nucleic acid microarrays may also be constructed by *in situ* oligonucleotide synthesis as described by Wodicka, L. *et al.* (1997) *Nature Biotechnology* 15: 1359-

1367. By photolithographic methods, precisely defined regions of the matrix are exposed to light. Protective groups which are photolabile are thereby activated and undergo nucleotide addition, whereas regions that are masked from light do not undergo any modification. Subsequent cycles of protection and light activation permit the synthesis of different oligonucleotides at defined positions. Small, defined regions of the genes of the invention may be synthesized on microarrays by solid phase oligonucleotide synthesis.

- The nucleic acid molecules of the invention present in a sample or mixture of nucleotides may be hybridized to the microarrays. These nucleic acid molecules can be labeled according to standard methods. In brief, nucleic acid molecules (e.g., mRNA molecules or DNA molecules) are labeled by the incorporation of isotopically or fluorescently labeled nucleotides, e.g., during reverse transcription or DNA synthesis. Hybridization of labeled nucleic acids to microarrays is described (e.g., in Schena, M. *et al.* (1995) *supra*; Wodicka, L. *et al.* (1997), *supra*; and DeSaizieu A. *et al.* (1998), *supra*). The detection and quantification of the hybridized molecule are tailored to the specific incorporated label. Radioactive labels can be detected, for example, as described in Schena, M. *et al.* (1995) *supra* and fluorescent labels may be detected, for example, by the method of Shalon *et al.* (1996) *Genome Research* 6: 639-645).

- The application of the sequences of the invention to DNA microarray technology, as described above, permits comparative analyses of different strains of *C. glutamicum* or other *Corynebacteria*. For example, studies of inter-strain variations based on individual transcript profiles and the identification of genes that are important for specific and/or desired strain properties such as pathogenicity, productivity and stress tolerance are facilitated by nucleic acid array methodologies. Also, comparisons of the profile of expression of genes of the invention during the course of a fermentation reaction are possible using nucleic acid array technology.

### **Example 13: Analysis of the Dynamics of Cellular Protein Populations (Proteomics)**

- The genes, compositions, and methods of the invention may be applied to study the interactions and dynamics of populations of proteins, termed 'proteomics'. Protein populations of interest include, but are not limited to, the total protein population of *C. glutamicum* (e.g., in comparison with the protein populations of other organisms), those proteins which are active under specific environmental or metabolic conditions (e.g., during fermentation, at high or low temperature, or at high or low pH), or those proteins which are active during specific phases of growth and development.

Protein populations can be analyzed by various well-known techniques, such as gel electrophoresis. Cellular proteins may be obtained, for example, by lysis or extraction, and may be separated from one another using a variety of electrophoretic techniques. Sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PAGE) separates proteins largely on the basis of their molecular weight. Isoelectric focusing polyacrylamide gel electrophoresis (IEF-PAGE) separates proteins by their isoelectric point (which reflects not only the amino acid sequence but also posttranslational modifications of the protein). Another, more preferred method of protein analysis is the consecutive combination of both IEF-PAGE and SDS-PAGE, known as 2-D-gel electrophoresis (described, for example, in Hermann *et al.* (1998) *Electrophoresis* 19: 3217-3221; Fountoulakis *et al.* (1998) *Electrophoresis* 19: 1193-1202; Langen *et al.* (1997) *Electrophoresis* 18: 1184-1192; Antelmann *et al.* (1997) *Electrophoresis* 18: 1451-1463). Other separation techniques may also be utilized for protein separation, such as capillary gel electrophoresis; such techniques are well known in the art.

Proteins separated by these methodologies can be visualized by standard techniques, such as by staining or labeling. Suitable stains are known in the art, and include Coomassie Brilliant Blue, silver stain, or fluorescent dyes such as Sypro Ruby (Molecular Probes). The inclusion of radioactively labeled amino acids or other protein precursors (*e.g.*,  $^{35}\text{S}$ -methionine,  $^{35}\text{S}$ -cysteine,  $^{14}\text{C}$ -labelled amino acids,  $^{15}\text{N}$ -amino acids,  $^{15}\text{NO}_3$  or  $^{15}\text{NH}_4^+$  or  $^{13}\text{C}$ -labelled amino acids) in the medium of *C. glutamicum* permits the labeling of proteins from these cells prior to their separation. Similarly, fluorescent labels may be employed. These labeled proteins can be extracted, isolated and separated according to the previously described techniques.

Proteins visualized by these techniques can be further analyzed by measuring the amount of dye or label used. The amount of a given protein can be determined quantitatively using, for example, optical methods and can be compared to the amount of other proteins in the same gel or in other gels. Comparisons of proteins on gels can be made, for example, by optical comparison, by spectroscopy, by image scanning and analysis of gels, or through the use of photographic films and screens. Such techniques are well-known in the art.

To determine the identity of any given protein, direct sequencing or other standard techniques may be employed. For example, N- and/or C-terminal amino acid sequencing (such as Edman degradation) may be used, as may mass spectrometry (in particular MALDI or ESI techniques (*see, e.g.,* Langen *et al.* (1997) *Electrophoresis* 18: 1184-1192)). The protein sequences provided herein can be used for the identification of *C. glutamicum* proteins by these techniques.

The information obtained by these methods can be used to compare patterns of protein presence, activity, or modification between different samples from various biological conditions (*e.g.*, different organisms, time points of fermentation, media conditions, or different biotopes, among others). Data obtained from such experiments alone, or in combination with other techniques, can be used for various applications, such as to compare the behavior of various organisms in a given (*e.g.*, metabolic) situation, to increase the productivity of strains which produce fine chemicals or to increase the efficiency of the production of fine chemicals.

10 **Equivalents**

Those skilled of ordinary skill in the art will recognize, or will be able to ascertain using no more than routine experimentation, many equivalents to the specific embodiments of the invention described herein. Such equivalents are intended to be encompassed by the following claims.

What is claimed:

1. An isolated nucleic acid molecule from *Corynebacterium glutamicum* encoding an RRP protein, or a portion thereof, provided that the nucleic acid molecule does not consist of any of the F-designated genes set forth in Table 1.
2. The isolated nucleic acid molecule of claim 1, wherein said nucleic acid molecule encodes an RRP protein involved in the production of a fine chemical.
3. An isolated *Corynebacterium glutamicum* nucleic acid molecule selected from the group consisting of those sequences set forth in Appendix A, or a portion thereof, provided that the nucleic acid molecule does not consist of any of the F-designated genes set forth in Table 1.
4. An isolated nucleic acid molecule which encodes a polypeptide sequence selected from the group consisting of those sequences set forth in Appendix B, provided that the nucleic acid molecule does not consist of any of the F-designated genes set forth in Table 1.
5. An isolated nucleic acid molecule which encodes a naturally occurring allelic variant of a polypeptide selected from the group of amino acid sequences consisting of those sequences set forth in Appendix B, provided that the nucleic acid molecule does not consist of any of the F-designated genes set forth in Table 1.
6. An isolated nucleic acid molecule comprising a nucleotide sequence which is at least 50% homologous to a nucleotide sequence selected from the group consisting of those sequences set forth in Appendix A, or a portion thereof, provided that the nucleic acid molecule does not consist of any of the F-designated genes set forth in Table 1.
7. An isolated nucleic acid molecule comprising a fragment of at least 15 nucleotides of a nucleic acid comprising a nucleotide sequence selected from the group consisting of those sequences set forth in Appendix A, provided that the nucleic acid molecule does not consist of any of the F-designated genes set forth in Table 1.



8. An isolated nucleic acid molecule which hybridizes to the nucleic acid molecule of any one of claims 1-7 under stringent conditions.
9. An isolated nucleic acid molecule comprising the nucleic acid molecule of claim 1 or a portion thereof and a nucleotide sequence encoding a heterologous polypeptide.
10. A vector comprising the nucleic acid molecule of claim 1.
11. The vector of claim 10, which is an expression vector.
12. A host cell transfected with the expression vector of claim 11.
13. The host cell of claim 12, wherein said cell is a microorganism.
14. The host cell of claim 13, wherein said cell belongs to the genus *Corynebacterium* or *Brevibacterium*.
15. The host cell of claim 12, wherein the expression of said nucleic acid molecule results in the modulation in production of a fine chemical from said cell.
16. The host cell of claim 15, wherein said fine chemical is selected from the group consisting of: organic acids, proteinogenic and nonproteinogenic amino acids, purine and pyrimidine bases, nucleosides, nucleotides, lipids, saturated and unsaturated fatty acids, diols, carbohydrates, aromatic compounds, vitamins, cofactors, polyketides, and enzymes.
17. A method of producing a polypeptide comprising culturing the host cell of claim 12 in an appropriate culture medium to, thereby, produce the polypeptide.
18. An isolated RRP polypeptide from *Corynebacterium glutamicum*, or a portion thereof.
19. The polypeptide of claim 18, wherein said polypeptide is involved in the production of a fine chemical production.

20. An isolated polypeptide comprising an amino acid sequence selected from the group consisting of those sequences set forth in Appendix B, provided that the amino acid sequence is not encoded by any of the F-designated genes set forth in Table 1.
- 5 21. An isolated polypeptide comprising a naturally occurring allelic variant of a polypeptide comprising an amino acid sequence selected from the group consisting of those sequences set forth in Appendix B, or a portion thereof, provided that the amino acid sequence is not encoded by any of the F-designated genes set forth in Table 1.
- 10 22. The isolated polypeptide of claim 18, further comprising heterologous amino acid sequences.
- 15 23. An isolated polypeptide which is encoded by a nucleic acid molecule comprising a nucleotide sequence which is at least 50% homologous to a nucleic acid selected from the group consisting of those sequences set forth in Appendix A, provided that the nucleic acid molecule does not consist of any of the F-designated nucleic acid molecules set forth in Table 1.
- 20 24. An isolated polypeptide comprising an amino acid sequence which is at least 50% homologous to an amino acid sequence selected from the group consisting of those sequences set forth in Appendix B, provided that the amino acid sequence is not encoded by any of the F-designated genes set forth in Table 1.
- 25 25. A method for producing a fine chemical, comprising culturing a cell containing a vector of claim 12 such that the fine chemical is produced.
26. The method of claim 25, wherein said method further comprises the step of recovering the fine chemical from said culture.
- 30 27. The method of claim 25, wherein said method further comprises the step of transfecting said cell with the vector of claim 11 to result in a cell containing said vector.
- 35 28. The method of claim 25, wherein said cell belongs to the genus *Corynebacterium* or *Brevibacterium*.

29. The method of claim 25, wherein said cell is selected from the group consisting of:  
*Corynebacterium glutamicum*, *Corynebacterium herculis*, *Corynebacterium lilium*,  
*Corynebacterium acetoacidophilum*, *Corynebacterium acetoglutamicum*,  
5 *Corynebacterium acetophilum*, *Corynebacterium ammoniagenes*, *Corynebacterium*  
*fujioense*, *Corynebacterium nitrilophilus*, *Brevibacterium ammoniagenes*,  
*Brevibacterium butanicum*, *Brevibacterium divaricatum*, *Brevibacterium flavum*,  
*Brevibacterium healii*, *Brevibacterium ketoglutamicum*, *Brevibacterium*  
*ketosoreductum*, *Brevibacterium lactofermentum*, *Brevibacterium linens*,  
*Brevibacterium paraffinolyticum*, and those strains set forth in Table 3.
- 10 30. The method of claim 25, wherein expression of the nucleic acid molecule from said  
vector results in modulation of production of said fine chemical.
- 15 31. The method of claim 25, wherein said fine chemical is selected from the group  
consisting of: organic acids, proteinogenic and nonproteinogenic amino acids, purine  
and pyrimidine bases, nucleosides, nucleotides, lipids, saturated and unsaturated  
fatty acids, diols, carbohydrates, aromatic compounds, vitamins, cofactors,  
polyketides, and enzymes.
- 20 32. The method of claim 25, wherein said fine chemical is an amino acid.
33. The method of claim 32, wherein said amino acid is drawn from the group consisting  
of: lysine, glutamate, glutamine, alanine, aspartate, glycine, serine, threonine,  
methionine, cysteine, valine, leucine, isoleucine, arginine, proline, histidine,  
25 tyrosine, phenylalanine, and tryptophan.
34. A method for producing a fine chemical, comprising culturing a cell whose genomic  
DNA has been altered by the inclusion of a nucleic acid molecule of any one of  
claims 1-9.
- 30 35. A method for diagnosing the presence or activity of *Corynebacterium diphtheriae* in  
a subject, comprising detecting the presence of one or more of the sequences set forth in  
Appendix A or Appendix B in the subject, provided that the sequences are not or are not  
encoded by any of the F-designated sequences set forth in Table 1, thereby diagnosing  
35 the presence or activity of *Corynebacterium diphtheriae* in the subject.

36. A host cell comprising a nucleic acid molecule selected from the group consisting of the nucleic acid molecules set forth in Appendix A, wherein the nucleic acid molecule is disrupted.

5 37. A host cell comprising a nucleic acid molecule selected from the group consisting of the nucleic acid molecules set forth in Appendix A, wherein the nucleic acid molecule comprises one or more nucleic acid modifications from the sequence set forth in Appendix A.

10 38. A host cell comprising a nucleic acid molecule selected from the group consisting of the nucleic acid molecules set forth in Appendix A, wherein the regulatory region of the nucleic acid molecule is modified relative to the wild-type regulatory region of the molecule.

**CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS  
INVOLVED IN DNA REPLICATION, PROTEIN SYNTHESIS, AND  
PATHOGENESIS**

5

**Abstract of the Disclosure**

Isolated nucleic acid molecules, designated RRP nucleic acid molecules, which encode novel RRP proteins from *Corynebacterium glutamicum* are described. The invention also provides antisense nucleic acid molecules, recombinant expression  
10 vectors containing RRP nucleic acid molecules, and host cells into which the expression vectors have been introduced. The invention still further provides isolated RRP proteins, mutated RRP proteins, fusion proteins, antigenic peptides and methods for the improvement of production of a desired compound from *C. glutamicum* based on genetic engineering of RRP genes in this organism.

15

TABLE 1: Genes in the Application

Nucleic Acid Seq ID NO	Amino Acid Seq ID NO	Identification Code	Contig	NT Start	NT Stop	Function
1	2	FXAD00625	VW0135	5	946	(093902) extracellular nuclease [Synchrotytis sp.]
3	4	FXAD00625	GR00165	3920	8862	(093902) extracellular nuclease [Synchrotytis sp.]
5	6	FXAD00625	VW0103	1271	4	(093902) extracellular nuclease [Synchrotytis sp.]
7	8	FXAD00625	GR00221	3656	4345	ENDONUCLEASE III (EC 4.2.99.18)
9	10	FXAD00625	GR00039	12248	13864	ENDONUCLEASE III (EC 4.2.99.18)
11	12	FXAD00625	GR00297	637	1572	THROMBIN-DEPENDENT PRECURSOR (EC 3.1.31.1)
13	14	FXAD00625	VW0229	12195	11377	HEMOLYSIN
15	16	FXAD00625	GR00447	2580	3323	HEMOLYSIN
17	18	FXAD00625	GR00488	540	55	HEMOLYSIN
19	20	FXAD00625	VW0146	626	891	HEMOLYSIN
21	22	FXAD00625	VW0103	5761	6483	HEMOLYSIN III
23	24	FXAD00625	GR00150	405	1034	HEMOLYSIN III
25	26	FXAD00625	VW0099	18771	20069	HEMOLYSIN
27	28	FXAD00625	GR00242	15953	17227	HEMOLYSIN
29	30	FXAD00625	GR00242	15953	17227	HEMOLYSIN
Nucleic Acid Seq ID NO	Amino Acid Seq ID NO	Identification Code	Contig	NT Start	NT Stop	Function
31	32	FXAD00772	VW0050	2864	3361	KU1 Superfamily II DNA and RNA helicase
33	34	FXAD00772	GR00502	4774	2381	KU1 Superfamily II DNA and RNA helicase
35	36	FXAD00772	GR00506	10755	15564	KU1 Superfamily II DNA and RNA helicase
37	38	FXAD00772	VW0137	5576	2901	Hypothetical ATP-Dependent RNA Helicase
39	40	FXAD00772	GR00068	1249	542	Hypothetical ATP-Dependent RNA Helicase
41	42	FXAD00772	VW0015	32429	33604	I. Superfamily II DNA and RNA(7) helicases (SNF2 family)
43	44	FXAD00772	GR00296	2007	3182	Hypothetical ATP-Dependent RNA Helicase
45	46	FXAD00772	GR00489	4702	5296	I. Superfamily II DNA and RNA(7) helicases (SNF2 family)
47	48	FXAD00772	GR00065	1666	3534	Superfamily I DNA and RNA helicase
49	50	FXAD00772	VW0317	2787	4	Superfamily I DNA and RNA helicase
51	52	FXAD00772	GR00769	2787	2870	(ALD2186) putative ATP-dependent DNA helicase [Mycobacterium tuberculosis]
53	54	FXAD00772	GR00014	4677	5116	ATP-DEPENDENT DNA HELICASE
55	56	FXAD00772	VW0068	6162	4	ATP-DEPENDENT DNA HELICASE
57	58	FXAD00772	GR00000	615	4	ATP-DEPENDENT DNA HELICASE
59	60	FXAD00772	GR00038	1610	6	ATP-DEPENDENT DNA HELICASE REP (EC 3.6.1.-)
61	62	FXAD00772	VW0145	188	2038	ATP-DEPENDENT DNA HELICASE REP (EC 3.6.1.-)
63	64	FXAD00772	GR00536	2765	1324	ATP-DEPENDENT DNA HELICASE REP (EC 3.6.1.-)
65	66	FXAD00772	GR00536	2765	1324	ATP-DEPENDENT DNA HELICASE REP (EC 3.6.1.-)

# Genes involved in DNA replication, topology, and packaging

Nucleic Acid Seq ID NO	Amino Acid Seq ID NO	Identification Code	Contig	NT Start	NT Stop	Function
67	68	RYA00544	GR00140	1269	3168	REPLICATIVE DNA HELICASE (EC 3.6.1.-)
69	70	RYA001866	GR00533	6	6	ATP-DEPENDENT HELICASE HHPA
71	72	RYA001867	GR00533	853	382	ATP-DEPENDENT HELICASE HHPA
73	74	RYA003166	VV0322	2933	699	ATP-DEPENDENT HELICASE HHPA
75	76	RYA000361	GR00072	1833	6	ATP-DEPENDENT HELICASE HHPA
77	78	RYA002293	VV0127	19879	22366	ATP-DEPENDENT HELICASE HHPB
79	80	RYA002293	GR00662	2819	5206	ATP-DEPENDENT HELICASE
81	82	RYA002755	GR00766	951	2945	ATP-DEPENDENT HELICASE
83	84	RYA001374	VV00991	7624	8865	HYPOXANTHINE-DEPENDENT RNA HELICASE
85	86	RYA001374	GR00400	885	33366	PROBABLE ATP-DEPENDENT HELICASE HEPA
87	88	RYA000817	VV0054	35739	5	PROBABLE ATP-DEPENDENT HELICASE LHR (EC 3.6.1.-)
89	90	RYA000819	GR00218	61388	4679	PROBABLE ATP-DEPENDENT HELICASE LHR (EC 3.6.1.-)
91	92	RYA000817	VV0129	11188	15747	PROBABLE ATP-DEPENDENT HELICASE LHR (EC 3.6.1.-)
93	94	RYA00103	GR00014	19360	11301	PROBABLE ATP-DEPENDENT HELICASE LHR (EC 3.6.1.-)
95	96	RYA002357	VV0051	23376	1707	PROBABLE ATP-DEPENDENT HELICASE LHR (EC 3.6.1.-)
97	98	RYA001363	GR00365	1408	2106	PROBABLE ATP-DEPENDENT HELICASE LHR (EC 3.6.1.-)
99	100	RYA002357	GR00365	1408	2106	PROBABLE ATP-DEPENDENT HELICASE LHR (EC 3.6.1.-)
101	102	RYA002357	GR00365	1408	2106	PROBABLE ATP-DEPENDENT HELICASE LHR (EC 3.6.1.-)
103	104	RYA002785	GR00776	2	3856	PUTATIVE ATP-DEPENDENT HELICASE LHR (EC 3.6.1.-)
105	106	RYA001740	GR00483	5314	6735	PUTATIVE DNA HELICASE (EC 5.99.1.2)
107	108	RYA001683	VV0179	5275	7242	DNA GRASSY SUBUNIT A (EC 5.99.1.3)
109	110	RYA001682	GR00468	1	234	DNA GRASSY SUBUNIT A (EC 5.99.1.3)
111	112	RYA001683	GR00468	146	385	DNA GRASSY SUBUNIT A (EC 5.99.1.3)
113	114	RYA001684	GR00469	3	930	DNA GRASSY SUBUNIT A (EC 5.99.1.3)
115	116	RYA001688	VV0179	1	564	DNA GRASSY SUBUNIT B (EC 5.99.1.3)
117	118	RYA001688	VV0221	1920	3035	DNA GRASSY SUBUNIT B (EC 5.99.1.3)
119	120	RYA001688	GR00472	3	778	DNA GRASSY SUBUNIT B (EC 5.99.1.3)
121	122	RYA001735	GR00482	1213	1494	DNA GRASSY SUBUNIT B (EC 5.99.1.3)
123	124	RYA00093	VV0054	36970	38808	DNA GRASSY SUBUNIT B (EC 5.99.1.3)
125	126	RYA000798	GR00213	2525	171	DNA TOPOISOMERASE I (EC 5.99.1.2)
129	130	RYA000990	VV0210	4462	4468	DNA TOPOISOMERASE I (EC 5.99.1.2)
131	132	RYA000990	GR00261	2	448	ATP-DEPENDENT RNA HELICASE DEAD
133	134	RYA000994	VV0106	356	6	ATP-DEPENDENT RNA HELICASE DEAD
135	136	RYA000994	GR00232	787	1138	ATP-DEPENDENT RNA HELICASE DEAD
137	138	RYA002468	VV0211	760	1983	ATP-DEPENDENT RNA HELICASE DEAD
139	140	RYA002463	GR00713	141	254	ATP-DEPENDENT RNA HELICASE DEAD
141	142	RYA002468	GR00714	760	1290	ATP-DEPENDENT RNA HELICASE DEAD
143	144	RYA000050	GR00008	5451	3256	ATP-DEPENDENT RNA HELICASE DEAD
145	146	RYA002682	GR00754	6902	6576	DNA-BINDING PROTEIN
147	148	RYA000542	VV0079	36158	38832	SINGLE-STRAND BINDING PROTEIN
149	150	RYA000542	GR00140	519	41	SINGLE-STRAND BINDING PROTEIN
151	152	RYA002833	VV0050	823	49	CHROMOSOMAL REPLICATION INITIATOR PROTEIN DNAA
153	154	RYA002833	GR00822	627	12658	CHROMOSOMAL REPLICATION INITIATOR PROTEIN DNAA
155	156	RYA001480	GR00422	14550	6010	DNA PRIMASE (EC 2.7.7.-)
157	158	RYA002141	VV0204	4514	10743	PRIMOSOMAL PROTEIN N' (replication factor V)
159	160	RYA002241	GR00654	846		PRIMOSOMAL PROTEIN N' (replication factor V)

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig	NT Start	NT Stop	Function
161	162	RXN00081	VW0044	4256	1590	DNA POLYMERASE II (EC 2.7.7.7)
163	164	RXN00080	GR00009	9582	11643	DNA POLYMERASE I (EC 2.7.7.7)
165	166	RXN00091	GR00009	11643	11852	DNA POLYMERASE I (EC 2.7.7.7)
167	168	RXN00091	GR00032	11053	14614	DNA POLYMERASE III, ALPHA CHAIN (EC 2.7.7.7)
169	170	RXN00128	GR00038	29655	4365	DNA POLYMERASE III, ALPHA CHAIN (EC 2.7.7.7)
171	172	RXN00007	VW0086	55677	58340	DNA POLYMERASE III, ALPHA CHAIN (EC 2.7.7.7)
173	174	RXN00040	GR00091	3	578	DNA POLYMERASE III, ALPHA CHAIN (EC 2.7.7.7)
175	176	RXN00045	VW0086	4519	6480	DNA POLYMERASE III, ALPHA CHAIN (EC 2.7.7.7)
177	178	RXN00044	GR00092	4172	55684	DNA POLYMERASE III, ALPHA CHAIN (EC 2.7.7.7)
179	180	RXN00044	VW0089	63067	61856	DNA POLYMERASE III, DELTA SUBUNIT (EC 2.7.7.7)
181	182	RXN00807	GR00216	423	1541	DNA POLYMERASE III, DELTA SUBUNIT (EC 2.7.7.7)
183	184	RXN00807	GR00032	13046	13756	DNA POLYMERASE III, EPSILON CHAIN (EC 2.7.7.7)
185	186	RXN00214	GR00035	4919	3840	DNA POLYMERASE III, EPSILON CHAIN (EC 2.7.7.7)
188	189	RXN00255	VW0012	816	4	DNA POLYMERASE III, SUBUNIT GAMMA AND TAU (EC 2.7.7.7)
189	190	RXN00066	VW0010	466	5306	DNA POLYMERASE III, SUBUNIT GAMMA AND TAU (EC 2.7.7.7)
191	192	RXN00637	VW0156	666	4	DNA POLYMERASE III, SUBUNIT GAMMA AND TAU (EC 2.7.7.7)
193	194	RXN00637	GR00455	312	4	DNA POLYMERASE III, SUBUNIT GAMMA AND TAU (EC 2.7.7.7)
195	196	RXN00637	GR00455	312	4	DNA POLYMERASE III, SUBUNIT GAMMA AND TAU (EC 2.7.7.7)
197	198	RXN00212	GR00032	12407	10948	DNA LIGASE (EC 6.5.1.2)
199	200	RXN00213	GR00032	12888	12316	DNA LIGASE (EC 6.5.1.2)
201	202	RXN00789	GR00209	1268	1024	EXODEOXYRIBONUCLEASE SMALL SUBUNIT (EC 3.1.11.6)
203	204	RXN00789	VW0321	1983	3044	EXODEOXYRIBONUCLEASE LARGE SUBUNIT (EC 3.1.11.6)
205	206	RXN00789	GR00209	1268	1024	EXODEOXYRIBONUCLEASE LARGE SUBUNIT (EC 3.1.11.6)
207	208	RXN00898	GR00245	1246	1345	EXODEOXYRIBONUCLEASE III (EC 3.1.11.2)
209	210	RXN00898	GR00245	1246	1345	EXODEOXYRIBONUCLEASE III (EC 3.1.11.2)
211	212	RXN00898	GR00059	3384	4990	EXODEOXYRIBONUCLEASE III (EC 3.1.11.2)
213	214	RXN00898	GR00059	3384	4990	EXODEOXYRIBONUCLEASE III (EC 3.1.11.2)
215	216	RXN00898	GR00059	3384	4990	EXODEOXYRIBONUCLEASE III (EC 3.1.11.2)
217	218	RXN00898	GR00059	3384	4990	EXODEOXYRIBONUCLEASE III (EC 3.1.11.2)
219	220	RXN00898	GR00059	3384	4990	EXODEOXYRIBONUCLEASE III (EC 3.1.11.2)
221	222	RXN00898	GR00059	3384	4990	EXODEOXYRIBONUCLEASE III (EC 3.1.11.2)
223	224	RXN00898	GR00059	3384	4990	EXODEOXYRIBONUCLEASE III (EC 3.1.11.2)
225	226	RXN00898	GR00059	3384	4990	EXODEOXYRIBONUCLEASE III (EC 3.1.11.2)
227	228	RXN00898	GR00059	3384	4990	EXODEOXYRIBONUCLEASE III (EC 3.1.11.2)
229	230	RXN00898	GR00059	3384	4990	EXODEOXYRIBONUCLEASE III (EC 3.1.11.2)
231	232	RXN00898	GR00059	3384	4990	EXODEOXYRIBONUCLEASE III (EC 3.1.11.2)
233	234	RXN00898	GR00059	3384	4990	EXODEOXYRIBONUCLEASE III (EC 3.1.11.2)
235	236	RXN00898	GR00059	3384	4990	EXODEOXYRIBONUCLEASE III (EC 3.1.11.2)
237	238	RXN00898	GR00059	3384	4990	EXODEOXYRIBONUCLEASE III (EC 3.1.11.2)
239	240	RXN00898	GR00059	3384	4990	EXODEOXYRIBONUCLEASE III (EC 3.1.11.2)
241	242	RXN00898	GR00059	3384	4990	EXODEOXYRIBONUCLEASE III (EC 3.1.11.2)
243	244	RXN00898	GR00059	3384	4990	EXODEOXYRIBONUCLEASE III (EC 3.1.11.2)
245	246	RXN00898	GR00059	3384	4990	EXODEOXYRIBONUCLEASE III (EC 3.1.11.2)
247	248	RXN00898	GR00059	3384	4990	EXODEOXYRIBONUCLEASE III (EC 3.1.11.2)
249	250	RXN00898	GR00059	3384	4990	EXODEOXYRIBONUCLEASE III (EC 3.1.11.2)
251	252	RXN00898	GR00059	3384	4990	EXODEOXYRIBONUCLEASE III (EC 3.1.11.2)
253	254	RXN00898	GR00059	3384	4990	EXODEOXYRIBONUCLEASE III (EC 3.1.11.2)

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Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig	NT Start	NT Stop	Function
255	266	RXN01389	VW0276	1350	667	DNA-DIRECTED RNA POLYMERASE BETA CHAIN (EC 2.7.6)
257	268	RXN02100	VW0222	6319	7198	MRP PROTEIN HOMOLOG
259	260	RXN02062	VW0318	21225	24134	CHROMOSOME SEGREGATION PROTEIN SMC2

## Ribosomal genes

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig	NT Start	NT Stop	Function
261	262	RXAU1495	GR00423	8970	8524	RIBOSOME-BINDING FACTOR A
263	264	RXAU1883	GR00542	8767	1425	Ribosome Recycling Factor (RRF)
265	266	RXAU1958	GR00437	2164	2330	RIBOSOMAL-PROTEIN-ALANINE ACETYLTRANSFERASE (EC 2.3.1.128)
267	268	RXAU1661	GR00440	1737	1787	RNA METHYLTRANSFERASE (EC 2.1.1.3)
269	270	RXAU1581	GR00063	3992	1689	RNA METHYLTRANSFERASE (EC 2.1.1.3)
271	272	RXAU0340	VW0066	64448	3954	RNA METHYLTRANSFERASE (EC 2.1.1.3)
273	274	RXAU0460	GR00116	382	5	RNA METHYLTRANSFERASE (EC 2.1.1.3)
275	276	RXAU02178	GR00641	15333	14526	23S RNA METHYLTRANSFERASE (EC 2.1.1.3)
277	278	RXAU02522	GR00725	311	853	16S RNA PROCESSING PROTEIN RIMM
279	280	RXAU02177	GR00188	3617	4576	RIBOSOMAL LARGE SUBUNIT PSEUDOURIDINE SYNTHASE B (EC 4.2.1.70)
281	282	RXAU0615	GR00744	973	338	RIBOSOMAL-PROTEIN-ALANINE ACETYLTRANSFERASE (EC 2.3.1.128)
283	284	RXN01343	VW0025	33585	34302	LSU ribosomal protein L1p
285	286	F RXAU1343	GR00389	13513	12863	LSU ribosomal protein L2p
287	288	RXN01951	GR00561	1218	1778	LSU ribosomal protein L2p
289	290	F RXAU1950	GR00561	938	1321	LSU ribosomal protein L2p
291	292	RXAU1266	GR00372	730	77	LSU ribosomal protein L2p
293	294	RXAU1948	GR00561	3	605	LSU ribosomal protein L2p (= L4p)
295	296	RXN00706	VW0065	2208	2780	LSU ribosomal protein L2p
297	298	F RXAU0711	GR00166	650	815	LSU ribosomal protein L2p
299	300	RXAU00706	GR00166	1	267	LSU ribosomal protein L2p
301	302	RXAU00695	GR00166	5118	5651	LSU ribosomal protein L2p
303	304	RXAU00643	GR00140	679	11034	LSU ribosomal protein L2p
305	306	RXAU1335	GR00589	2736	2224	LSU ribosomal protein L10p
307	308	RXN02826	VW0023	33031	33465	LSU ribosomal protein L11p
309	310	RXAU02826	GR00589	67	465	LSU ribosomal protein L11p
311	312	RXAU1334	GR00589	2143	1760	LSU ribosomal protein L12p (L7/L12)
313	314	RXAU02826	GR00589	1	330	LSU ribosomal protein L12p
315	316	RXAU02826	GR00181	6934	7377	LSU ribosomal protein L13p
317	318	RXAU02826	GR00181	720	1133	LSU ribosomal protein L16p
319	320	RXAU00870	GR00176	2420	1932	LSU ribosomal protein L16p
321	322	RXAU00896	GR00181	5558	6059	LSU ribosomal protein L18p
323	324	RXAU1335	GR00393	972	1310	LSU ribosomal protein L18p
325	326	RXAU02420	GR00705	5564	6334	LSU ribosomal protein L20p
327	328	RXAU02371	VW0102	318	4	LSU ribosomal protein L21p
329	330	F RXAU02371	GR00687	6483	6752	LSU ribosomal protein L21p
331	332	RXAU1949	GR00561	608	910	LSU ribosomal protein L23p

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig	NT Start	NT Stop	Function
335	336	RXN00709	VO0005	1523	1888	LSU ribosomal protein L24P
337	338	F RXA00709	GR00186	2	340	LSU ribosomal protein L24P
339	340	RXA00710	GR00186	346	507	LSU ribosomal protein L24P
341	342	RXA00835	GR00186	7946	8079	LSU ribosomal protein L28P
342	343	RXA00835	GR00022	1136	1276	LSU ribosomal protein L28P
343	344	RXA00835	GR00181	6742	6824	LSU ribosomal protein L30P
344	345	RXA00835	GR00048	5506	5243	LSU ribosomal protein L31P
345	346	RXA00835	GR00048	8085	8246	LSU ribosomal protein L33P
346	347	RXA00835	GR00047	715	855	LSU ribosomal protein L34P
347	348	RXA01423	GR00075	5699	5890	LSU ribosomal protein L35P
348	349	RXA02419	GR00042	1277	2734	SSU ribosomal protein S1P
349	350	RXN01912	VO0150	876	1613	SSU ribosomal protein S2P
350	351	RXN01912	GR00547	876	1646	SSU ribosomal protein S2P
351	352	RXN02041	GR00622	1	714	SSU ribosomal protein S3P
352	353	RXN02041	GR00176	4215	3613	SSU ribosomal protein S4P
353	354	RXN00697	GR00181	6103	6735	SSU ribosomal protein S5P
354	355	RXN00697	VO0079	35852	36118	SSU ribosomal protein S6P
355	356	F RXA00545	GR00141	562	816	SSU ribosomal protein S7P
356	357	RXN02129	GR00369	3240	2776	SSU ribosomal protein S8P
357	358	RXN02129	GR00181	4700	5095	SSU ribosomal protein S9P
358	359	RXN02038	VO0118	333	701	SSU ribosomal protein S9P
359	360	RXN02038	GR00620	1068	768	SSU ribosomal protein S9P
360	361	RXN02038	GR00372	1068	1442	SSU ribosomal protein S11P
361	362	RXN02038	GR00176	4531	3450	SSU ribosomal protein S11P
362	363	RXN02038	GR00048	8243	8553	SSU ribosomal protein S14P
363	364	RXN02038	GR00042	1172	906	SSU ribosomal protein S14P
364	365	RXN02038	GR00064	6709	7203	SSU ribosomal protein S16P
365	366	RXN02038	GR00065	504	764	SSU ribosomal protein S20P
366	367	RXN02038	VO0005	3462	2479	DNA-DIRECTED RNA POL. YMERASE ALPHA CHAIN (EC 2.7.6)
367	368	RXN02038	VO0005	35599	35964	SSU ribosomal protein S1P
368	369	RXN02038	VO0129	35552	35304	SSU ribosomal protein S1P
369	370	RXN02038	VO0005	35970	36371	SSU ribosomal protein S1P
370	371	RXN02038	VO0232	10755	11315	RIBOSOMAL-PROTEIN-ALANINE ACETYLTRANSFERASE (EC 2.3.1.128)
371	372	RXN02038	VO0140	1725	4755	RIBOSOMAL-PROTEIN-ALANINE ACETYLTRANSFERASE (EC 2.3.1.128)
372	373	RXN02038	VO0224	15361	17559	TEX PROTEIN

## Genes Involved in Pathogenesis

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig	NT Start	NT Stop	Function
407	408	RXN00157	GR00023	11848	10586	IMASIN 1
409	410	RXN00208	GR00032	7467	7039	WUUBINACTIN UTILIZATION PROTEIN WUUB
411	412	RXN00208	GR00097	989	989	WUUBINACTIN ASSOCIATED PROTEIN 1
413	414	RXN01149	GR00023	2501	2758	WUUBINACTIN ASSOCIATED PROTEIN 1

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Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig	NT Start	NT Stop	Function
415	416	RXA01305	GR00376	4435	2570	SEROTYPE-SPECIFIC ANTIGEN 1 (EC 3.4.21.-)
417	418	RXA01463	GR00419	2865	2951	VIRULENCE-ASSOCIATED PROTEIN A
419	420	RXA01824	GR00516	1367	2188	VIRULENCE-ASSOCIATED PROTEIN A
421	422	RXA01832	GR00516	11787	10894	VIRULENCE-ASSOCIATED PROTEIN A
423	424	RXA02533	GR00726	3775	3208	ANNEXIN VII
425	426	RXA02727	VV0017	6287	5376	(D90768) Immunity repressor protein [Escherichia coli]
						ANTIGEN 84

## Nucleases

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig	NT Start	NT Stop	Function
427	428	RXN01575	VV0009	50041	48022	RIBONUCLEASE H (EC 3.1.26.4)
429	430	RXN01986	VV0156	5673	5017	OLIGORIBONUCLEASE (EC 3.1.-.-)

TABLE 2: GENES IDENTIFIED FROM GENBANK

GenBank™ Accession No.	Gene Name	Gene Function	Reference
A09073	pyg	Phosphoenol pyruvate carboxylase	Bachmann, B. et al. "DNA fragment coding for phosphoenolpyruvate carboxylase, recombinant DNA carrying said fragment, strains carrying the recombinant DNA and method for producing L- amino acids using said strains." Patent: EP 0358940-A 3 03/21/90
A45579, A45581, A45583, A45585 A45587		Threonine dehydratase	Moeckel, B. et al. "Production of L-isoleucine by means of recombinant micro-organisms with deregulated threonine dehydratase." Patent: WO 95/19442-A 5 07/20/95
AB003132	murC, ftsQ, ftsZ		Kobayashi, M. et al. "Cloning, sequencing, and characterization of the ftsZ gene from corynebacterium bacteria." <i>Biochem. Biophys. Res. Commun.</i> , 236(2):383-388 (1997)
AB015023	murC, ftsQ		Wachi, M. et al. "A murC gene from Corynebacterium bacteria." <i>Biochem. Biophys. Res. Commun.</i> , 51(2):223-228 (1999)
AB018530	disR		Kimura, E. et al. "Molecular cloning of a novel gene, disR, which rescues the detergent sensitivity of a mutant derived from <i>Brevibacterium lactofermentum</i> ." <i>Biosci. Biotechnol. Biochem.</i> , 60(10):1565-1570 (1996)
AB018531	disk1, disk2		
AB020624	murI	D- glutamate racemase	
AB023377	tki	transketolase	
AB024708	glbB, glbD	Glutamate 2-oxoglutarate aminotransferase large and small subunits	
AB025424	acn	aconitase	
AB027714	rep	Replication protein	
AB027715	rep, and	Replication protein; aminoglycoside adenylyltransferase	
AF005242	argC	N- acetylglutamate-5-semialdehyde dehydrogenase	
AF005635	gluA	Glutamate synthetase	
AF030405	hisF	Cyclase	
AF030520	argG	Argininosuccinate synthetase	
AF031518	argF	Ornithine carbamoyltransferase	
AF036932	aroD	3-dehydroquinate dehydratase	

GenBank™ Accession No.	Gene Name	Gene Function	Reference
AF038548	pyc	Pyruvate carboxylase	
AF038651	deiA/E; apt; rel	Dipeptide-binding protein; adenine phosphoribosyltransferase; GTP pyrophosphokinase	Wehner, L. et al. "The role of the <i>Corynebacterium glutamicum</i> rel gene in (p)ppCpP metabolism," <i>Microbiology</i> , 144:1853-1862 (1998)
AF041436	argR	Arginine repressor	
AF043998	impA	Inositol monophosphate phosphatase	
AF048764	argH	Argininosuccinate lyase	
AF049897	argC; argJ; argB; argD; argT; argR; argG; argH	N-acetylglutarylphosphate reductase; ornithine acetyltransferase; N-acetylglutamate kinase; acetylornithine transaminase; ornithine carbamoyltransferase; arginine repressor; argininosuccinate synthase; argininosuccinate lyase	
AF050109	inhA	Enoyl-acyl carrier protein reductase	
AF050166	hscG	ATP phosphoribosyltransferase	
AF051846	hscA	Phosphoribosylformimino-5-amino-1-phosphoribosyl-4-imidazolecarboxamide isomerase	
AF052652	metA	Homoserine O-acetyltransferase	Park, S. et al. "Isolation and analysis of metA, a methionine biosynthetic gene encoding homoserine acetyltransferase in <i>Corynebacterium glutamicum</i> ," <i>Mol. Cell.</i> , 8(3):286-294 (1998)
AF053071	arob	Dehydroquininate synthetase	
AF060558	hscH	Glutamine amidotransferase	
AF086704	hscE	Phosphoribosyl-ATP. Pyrophosphohydrolyase	
AF114253	aroA	5-enolpyruvylshikimate 3-phosphate synthase	
AF116184	pand	L-aspartate-alpha-decarboxylase precursor	Dusch, N. et al. "Expression of the <i>Corynebacterium glutamicum</i> pand gene encoding L-aspartate-alpha-decarboxylase leads to pantoic acid overproduction in <i>Escherichia coli</i> ," <i>Appl. Environ. Microbiol.</i> , 65(4):1530-1539 (1999)

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GenBank™ Accession No.	Gene Name	Gene Function	Reference
AF124518	aroD; aroE	3-dehydroquinate; shikimate dehydrogenase	
AF124600	aroC; aroK; aroB; pepQ	Chorismate synthase; shikimate kinase; 3-dehydroquinate synthase; putative cytoplasmic peptidase	
AF145897	inhA		
AF145898	inhA		
AI001436	ectP	Transport of ectoine, glycine betaine, proline	Peter, H. et al. "Corynebacterium glutamicum is equipped with four secondary carriers for compatible solutes: Identification, sequencing, and characterization of the proline/ectoine uptake system, ProP, and the ectoine/proline/glycine betaine carrier, EctP." <i>J. Bacteriol.</i> , 180(22):6005-6012 (1998)
AI004934	dapD	Tetrahydrodipicolinate succinylase (incomplete)	Wehrmann, A. et al. "Different modes of diaminopimelate synthesis and their role in cell wall integrity: A study with <i>Corynebacterium glutamicum</i> ," <i>J. Bacteriol.</i> , 180(12):3159-3165 (1998)
AI007732	ppc; secG; amt; ocd; soxA	Phosphoenolpyruvate-carboxylase; $\gamma$ -high affinity ammonium uptake protein; ornithine-cyclodextranase; succinate oxidase	Jakoby, M. et al. "Nitrogen regulation in <i>Corynebacterium glutamicum</i> ; Isolation of genes involved in biochemical characterization of corresponding proteins," <i>FEMS Microbiol.</i> , 173(2):303-310 (1999)
AI010319	ftsY; glnB; glnD; srf; amtP	Involved in cell division; PI protein; uridylyltransferase (uridylyl-removing enzyme); signal recognition particle; low affinity ammonium uptake protein	
AI132968	cat	Chloramphenicol acetyl transferase	
AD224946	mgo	L-malate: quinone oxidoreductase	Moldenauer, D. et al. "Biochemical and genetic characterization of the membrane-associated malate dehydrogenase (aceppor) from <i>Corynebacterium glutamicum</i> ," <i>Eur. J. Biochem.</i> , 234(2):395-403 (1996)
AI238250	nhd	NADH dehydrogenase	
AD238703	porA	Porin	Lichtinger, T. et al. "Biochemical and biophysical characterization of the cell wall porin of <i>Corynebacterium glutamicum</i> . The channel is formed by a low molecular mass polypeptide," <i>Biochemistry</i> , 37(43):15024-15032 (1998)
D17429		Transposable element IS31831	Veres, A.A. et al. "Isolation and characterization of IS31831, a transposable element from <i>Corynebacterium glutamicum</i> ," <i>Mol. Microbiol.</i> , 11(4):739-746 (1994)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
D84102	odhA	2-oxoglutarate dehydrogenase	Usuda, Y. et al., "Molecular cloning of the Corynebacterium glutamicum (Brevibacterium lactofermentum AJ12056) <i>odhA</i> gene encoding a novel type of 2-oxoglutarate dehydrogenase," <i>Microbiology</i> , 142:3347-3354 (1996)
E01358	hch, hK	Homoserine dehydrogenase; homoserine kinase	Kasumata, R. et al., "Production of L-threonine and L-isoleucine," Patent: JP 1987232392-A 1 10/12/87
E01359		Upstream of the start codon of homoserine kinase gene	Kasumata, R. et al., "Production of L-threonine and L-isoleucine," Patent: JP 1987232392-A 2 10/12/87
E01375		Tryptophan operon	
E01376	trpL, trpE	Leader peptide; anthranilate synthase	Matsui, K. et al., "Tryptophan operon, peptide and protein coded thereby, utilization of tryptophan operon gene expression and production of tryptophan," Patent: JP 1987244382-A 1 10/24/87
E01377		Promoter and operator regions of tryptophan operon	Matsui, K. et al., "Tryptophan operon, peptide and protein coded thereby, utilization of tryptophan operon gene expression and production of tryptophan," Patent: JP 1987244382-A 1 10/24/87
E03937		Biotin-synthase	Harakeyama, K. et al., "DNA fragment containing gene capable of coding biotin synthase and its utilization," Patent: JP 1992278088-A 1 10/02/92
E04040		Diamino pelargonic acid aminotransferase	Kohama, K. et al., "Gene coding diamino pelargonic acid aminotransferase and deshiobiotin synthase and its utilization," Patent: JP 1992330284-A 1 11/18/92
E04041		Deshiobiotin synthase	Kohama, K. et al., "Gene coding diamino pelargonic acid aminotransferase and deshiobiotin synthase and its utilization," Patent: JP 1992330284-A 1 11/18/92
E04307		Flavum aspartase	Kurusu, Y. et al., "Gene DNA coding aspartase and utilization thereof," Patent: JP 1993030977-A 1 02/09/93
E04376		Isocitric acid lyase	Kasumata, R. et al., "Gene manifestation controlling DNA," Patent: JP 1993056782-A 3 03/09/93
E04377		Isocitric acid lyase N-terminal fragment	Kasumata, R. et al., "Gene manifestation controlling DNA," Patent: JP 1993056782-A 3 03/09/93
E04484		Prephenate dehydratase	Soenuchi, N. et al., "Production of L-phenylalanine by fermentation," Patent: JP 1993076352-A 2 03/30/93
E05108		Aspartokinase	Fugeno, N. et al., "Gene DNA coding Aspartokinase and its use," Patent: JP 1993184366-A 1 07/27/93
E05112		Dihydro-dipicolinate synthetase	Harakeyama, K. et al., "Gene DNA coding dihydrodipicolinate acid synthetase and its use," Patent: JP 1993184371-A 1 07/27/93

GenBank™ Accession No.	Gene Name	Gene Function	Reference
E05776		Diaminopimelic acid dehydrogenase	Kobayashi, M. et al. "Gene DNA coding Diaminopimelic acid dehydrogenase and its use," Patent: JP 1993284970-A 1 11/02/93
E05779		Threonine synthase	Kohama, K. et al. "Gene DNA coding threonine synthase and its use," Patent: JP 1993284972-A 1 11/02/93
E06110		Prephenate dehydratase	Kikuchi, T. et al. "Production of L-phenylalanine by fermentation method," Patent: JP 1993344881-A 1 12/27/93
E06111		Mutated Prephenate dehydratase	Kikuchi, T. et al. "Production of L-phenylalanine by fermentation method," Patent: JP 1993344881-A 1 12/27/93
E06146		Acetohydroxy acid synthetase	Imi, M. et al. "Gene capable of coding Acetohydroxy acid synthetase and its use," Patent: JP 1993344893-A 1 12/27/93
E06825		Aspartokinase	Sugimoto, M. et al. "Mutant aspartokinase gene," patent: JP 1994062866-A 1 03/08/94
E06826		Mutated aspartokinase alpha subunit	Sugimoto, M. et al. "Mutant aspartokinase gene," patent: JP 1994062866-A 1 03/08/94
E06827		Mutated aspartokinase alpha subunit	Sugimoto, M. et al. "Mutant aspartokinase gene," patent: JP 1994062866-A 1 03/08/94
E07701	secY		Homo, N. et al. "Gene DNA participating in integration of membranous protein to membrane," Patent: JP 1994169780-A 1 06/21/94
E08177		Aspartokinase	Sato, Y. et al. "Genetic DNA capable of coding Aspartokinase released from feedback inhibition and its utilization," Patent: JP 1994261766-A 1 09/20/94
E08178, E08179, E08180, E08181, E08182		Feedback inhibition-released Aspartokinase	Sato, Y. et al. "Genetic DNA capable of coding Aspartokinase released from feedback inhibition and its utilization," Patent: JP 1994261766-A 1 09/20/94
E08232		Acetohydroxy-acid isomerase	Imi, M. et al. "Gene DNA coding acetohydroxy acid isomerase," Patent: JP 1994277067-A 1 10/04/94
E08234	secE		Asai, Y. et al. "Gene DNA coding for translocation machinery of protein," Patent: JP 1994277073-A 1 10/04/94
E08643		FT aminotransferase and deshydrobiotin synthase promoter region	Hatakeyama, K. et al. "DNA fragment having promoter function in Corynebacterium," Patent: JP 1995031476-A 1 02/03/95
E08646		Biotin synthase	Hatakeyama, K. et al. "DNA fragment having promoter function in Corynebacterium," Patent: JP 1995031476-A 1 02/03/95

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GenBank™ Accession No.	Gene Name	Gene Function	Reference
F08649		Asparaginase	Kohama, K. et al. "DNA fragment having promoter function in corynebacterium." Patent: JP 199501478-A 1 02/03/95
E08900		Dihydrodipicolinate reductase	Madori, M. et al. "cDNA fragment containing gene coding Dihydrodipicolinate acid reductase and utilization thereof." Patent: JP 1995075578-A 1 03/20/95
E08901		Diaminopimelic acid decarboxylase	Madori, M. et al. "cDNA fragment containing gene coding Diaminopimelic acid decarboxylase and utilization thereof." Patent: JP 1995075579-A 1 03/20/95
E12594		Serine hydroxymethyltransferase	Hatakeyama, K. et al. "Production of L-tryptophan." Patent: JP 1997028391-A 1 02/04/97
E12760, E12759, E12758		transposase	Moriya, M. et al. "Amplification of gene using artificial transposon." Patent: JP 1997070291-A 03/18/97
E12764		Arginyl-tRNA synthetase; diaminopimelic acid decarboxylase	Moriya, M. et al. "Amplification of gene using artificial transposon." Patent: JP 1997070291-A 03/18/97
E12767		Dihydrodipicolinic acid synthetase	Moriya, M. et al. "Amplification of gene using artificial transposon." Patent: JP 1997070291-A 03/18/97
E12770		aspartokinase	Moriya, M. et al. "Amplification of gene using artificial transposon." Patent: JP 1997070291-A 03/18/97
E12773		Dihydrodipicolinic acid reductase	Moriya, M. et al. "Amplification of gene using artificial transposon." Patent: JP 1997070291-A 03/18/97
E13655		Glucose-6-phosphate dehydrogenase	Hatakeyama, K. et al. "Glucose-6-phosphate dehydrogenase and DNA capable of coding the same." Patent: JP 1997224661-A 1 09/02/97
L01508	IlvA	Threonine dehydratase	Moeckel, B. et al. "Functional and structural analysis of the threonine dehydratase of <i>Corynebacterium glutamicum</i> ." <i>J. Bacteriol.</i> , 174:8065-8072 (1992)
L07603	EC 4.2.1.15	3-deoxy-D-arabinosephosphonate-7-phosphate synthase	Chen, C. et al. "The cloning and nucleotide sequence of <i>Corynebacterium glutamicum</i> 3-deoxy-D-arabinosephosphonate-7-phosphate synthase gene." <i>FEMS Microbiol. Lett.</i> , 107:223-230 (1993)
L09232	IlvB; IlvN; IlvC	Acetylhydroxy acid synthase large subunit; Acetylhydroxy acid synthase small subunit; Acetylhydroxy acid isomerase	Kellauer, C. et al. "Solvent synthesis in <i>Corynebacterium glutamicum</i> : molecular analysis of the IlvB-IlvN-IlvC operon." <i>J. Bacteriol.</i> , 175(17):5595-5603 (1993)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
L18874	psmI	Phosphoenolpyruvate sugar phosphotransferase	Foerster, A. et al. "Bacillus subtilis sucrose-specific enzyme II of the phosphotransferase system: expression in <i>Escherichia coli</i> and homology to enzymes II from enteric bacteria," <i>PNAS USA</i> , 84(24):8773-8777 (1987); Lee, J.K. et al. "Nucleotide sequence of the gene encoding the Corynebacterium glutamicum mannose enzyme II and analyses of the deduced protein sequence," <i>FEMS Microbiol. Lett.</i> , 119(1-2):137-145 (1994)
L27123	acdB	Malate synthase	Lee, H.S. et al. "Molecular characterization of acdB, a gene encoding malate synthase in <i>Corynebacterium glutamicum</i> ," <i>J. Microbiol. Biotechnol.</i> , 4(4):256-263 (1994)
L27126		Pyruvate kinase	Jetten, M. S. et al. "Structural and functional analysis of pyruvate kinase from <i>Corynebacterium glutamicum</i> ," <i>Appl. Environ. Microbiol.</i> , 60(7):2501-2507 (1994)
L28760	aceA	Isocitrate lyase	Onizuka, J.A. et al. "Molecular cloning, DNA sequence analysis, and characterization of the <i>Corynebacterium diptheriae</i> dtxR from <i>Brevibacterium lactofermentum</i> ," <i>J. Bacteriol.</i> , 177(2):465-467 (1995)
L35906	dtxR	Diphtheria toxin repressor	Follisette, M.T. et al. "Molecular cloning and nucleotide sequence of the <i>Corynebacterium glutamicum</i> pldA gene," <i>J. Bacteriol.</i> , 167(6):705-702 (1986)
M13774		Prephenate dehydratase	Park, Y.-H. et al. "Phylogenetic analysis of the coryneform bacteria by 5S rRNA sequences," <i>J. Bacteriol.</i> , 169:1801-1806 (1987)
M16175	5S rRNA		Sano, K. et al. "Structure and function of the up operon control regions of <i>Brevibacterium lactofermentum</i> , a glutamic-acid-producing bacterium," <i>Gene</i> , 52:191-200 (1987)
M16663	trpE	Anthraniolate synthase, 5' end	Sano, K. et al. "Structure and function of the trp operon control regions of <i>Brevibacterium lactofermentum</i> , a glutamic-acid-producing bacterium," <i>Gene</i> , 52:191-200 (1987)
M16664	trpA	Tryptophan synthase, 3' end	O'Regan, M. et al. "Cloning and nucleotide sequence of the Phosphoenolpyruvate carboxylase-coding gene of <i>Corynebacterium glutamicum</i> ATCC13032," <i>Gene</i> , 77(2):237-251 (1989)
M25819		Phosphoenolpyruvate carboxylase	Roller, C. et al. "Gran-positive bacteria with a high DNA G+C content are characterized by a common insertion within their 23S rRNA genes," <i>J. Gen. Microbiol.</i> , 138:1167-1175 (1992)
M85106		23S rRNA gene insertion sequence	

GenBank™ Accession No.	Gene Name	Gene Function	Reference
M83107, M83108		23S rRNA gene insertion sequence	Roller, C. et al., "Gram-positive bacteria with a high DNA G+C content are characterized by a common insertion within their 23S rRNA genes," <i>J. Gen. Microbiol.</i> , 138:1161-1175 (1992)
M89231	acdD, bmrQ, ybhW	Beta C-S lyase; branched-chain amino acid uptake carrier; hypothetical protein ybhW	Rossol, L. et al., "The Corynebacterium glutamicum acdD gene encodes a C-S lyase with alpha, beta-elimination activity that degrades aminohydroxyisoleucine," <i>J. Bacteriol.</i> , 174(9):2968-2977 (1992); Taneh, A. et al., "Isoleucine uptake in Corynebacterium glutamicum ATCC 13032 is directed by the bmrQ gene product," <i>Arch. Microbiol.</i> , 169(4):303-312 (1996)
S59299	trp	Leader gene (promoter)	Henry, D.M. et al., "Cloning of the trp gene cluster from a tryptophan-hyperproducing strain of Corynebacterium glutamicum: identification of a mutation in the trp leader sequence," <i>Appl. Environ. Microbiol.</i> , 59(3):791-799 (1993)
U11545	trpD	Anthranilate phosphoribosyltransferase	O'Garra, J.P. and Duncan, L.K. (1994) Complete nucleotide sequence of the Corynebacterium glutamicum ATCC 21850 ptd gene." Thesis, Microbiology Department, University College Galway, Ireland.
U13922	cgIIIM, cgIIIR, cgIIIR	Putative type II 5-cytosine methyltransferase; putative type II restriction endonuclease; putative type I or type III restriction endonuclease	Schafer, A. et al., "Cloning and characterization of a DNA region encoding a stress-sensitive restriction system from Corynebacterium glutamicum ATCC 13032 and analysis of its role in intergeneric conjugation with Escherichia coli," <i>J. Bacteriol.</i> , 176(23):7309-7319 (1994); Schafer, A. et al., "The Corynebacterium glutamicum cgIIIM gene encoding a 5-cytosine in an MsrBC-deficient Escherichia coli strain," <i>Gene</i> , 203(2):95-101 (1997)
U14965	recA		Aarki, S. et al., "Mutations in the Corynebacterium glutamicumproline biosynthetic pathway: A natural bypass of the proA step," <i>J. Bacteriol.</i> , 178(15):4412-4419 (1996)
U31224	ppx		Aarki, S. et al., "Mutations in the Corynebacterium glutamicumproline biosynthetic pathway: A natural bypass of the proA step," <i>J. Bacteriol.</i> , 178(15):4412-4419 (1996)
U31225	proC	L-proline: NADP+ 5-oxidoreductase	Aarki, S. et al., "Mutations in the Corynebacterium glutamicumproline biosynthetic pathway: A natural bypass of the proA step," <i>J. Bacteriol.</i> , 178(15):4412-4419 (1996)
U31230	ohg, proB, unkch	?gamma glutamyl kinase; similar to D-isomer specific 2-hydroxyacid dehydrogenases	Aarki, S. et al., "Mutations in the Corynebacterium glutamicumproline biosynthetic pathway: A natural bypass of the proA step," <i>J. Bacteriol.</i> , 178(15):4412-4419 (1996)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
U31281	bioB	Biotin synthase	Serebriiski, I.G., "Two new members of the bio B superfamily: Cloning, sequencing and expression of bio B genes of <i>Methylobacillus flagellatum</i> and <i>Corynebacterium glutamicum</i> ," <i>Gene</i> , 173:15-22 (1996)
U35023	thrR, accBC	Thiosulfate sulfurtransferase, acyl CoA carboxylase	Jager, W. et al., "A <i>Corynebacterium glutamicum</i> gene encoding a two-domain protein similar to biotin carboxylases and biotin-carboxyl-carrier proteins," <i>Arch. Microbiol.</i> , 166(2):76-82 (1996)
U43535	cmr	Multidrug resistance protein	Jager, W. et al., "A <i>Corynebacterium glutamicum</i> gene conferring multidrug resistance in the heterologous host <i>Escherichia coli</i> ," <i>J. Bacteriol.</i> , 179(7):2449-2451 (1997)
U43536	clpB	Heat shock ATP-binding protein	
U3587	aphA-3	3'-5'-aminoglycoside phosphotransferase	
U89648		<i>Corynebacterium glutamicum</i> unidentified sequence involved in histidine biosynthesis, partial sequence	
X04960	trpA, trpB, trpC, trpD, trpE, trpG, trpL	Tryptophan operon	Mansui, K. et al., "Complete nucleotide and deduced amino acid sequences of the <i>Brevibacterium lactofermentum</i> tryptophan operon," <i>Nucleic Acids Res.</i> , 14(25):10113-10114 (1986)
X07563	lys A	DAP decarboxylase (meso-diaminopimelate decarboxylase, EC 4.1.1.20)	Yeh, P. et al., "Nucleic sequence of the <i>lysA</i> gene of <i>Corynebacterium glutamicum</i> and possible mechanisms for modulation of its expression," <i>Mol. Gen. Genet.</i> , 212(1):112-119 (1988)
X14234	EC 4.1.1.31	Phosphoenolpyruvate carboxylase	Elknam, B.J. et al., "The Phosphoenolpyruvate carboxylase gene of <i>Corynebacterium glutamicum</i> : Molecular cloning, nucleotide sequence, and expression," <i>Mol. Gen. Genet.</i> , 218(2):330-339 (1989); Legnante, L. et al., "Sorbum Phosphoenolpyruvate carboxylase gene family: structure, function and molecular evolution," <i>Plant Mol. Biol.</i> , 21 (3):487-502 (1993)
X17113	fda	Fructose-bisphosphate aldolase	Von der Osten, C.H. et al., "Molecular cloning, nucleotide sequence and fine-structural analysis of the <i>Corynebacterium glutamicum</i> fda gene: structural comparison of C. glutamicum fructose-1, 6-bisphosphate aldolase to class I and class II aldolases," <i>Mol. Microbiol.</i>
X53993	dapA	L-2, 3-dihydrodipicolinate synthetase (EC 4.2.1.32)	Bomastie, S. et al., "Nucleic sequence of the dapA gene from <i>Corynebacterium glutamicum</i> ," <i>Nucleic Acids Res.</i> , 18(21):6421 (1990)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
X54223		ATB-related site	Ciancioffo, N. et al. "DNA sequence homology between atB-related sites of <i>Corynebacterium diptheriae</i> , <i>Corynebacterium ulcerans</i> , <i>Corynebacterium glutamicum</i> , and the atp site of <i>lamidacorynephage</i> ," <i>FEMS. Microbiol. Lett.</i> , 66:299-302 (1990).
X54740	argS, lysA	Arginyl-tRNA synthetase; Diaminopimelate decarboxylase	Marcel, T. et al. "Nucleotide sequence and organization of the upstream region of the <i>Corynebacterium glutamicum</i> lysA gene," <i>Mol. Microbiol.</i> , 4(11):1819-1830 (1990).
X55994	trpL, trpE	Putative leader peptide; anthranilate synthase component 1	Heery, D.M. et al. "Nucleotide sequence of the <i>Corynebacterium glutamicum</i> trpE gene," <i>Nucleic Acids Res.</i> , 18(23):7138 (1990).
X56037	thrC	Threonine synthase	Han, K.S. et al. "The molecular structure of the <i>Corynebacterium glutamicum</i> threonine synthase gene," <i>Mol. Microbiol.</i> , 4(10):1693-1702 (1990).
X56075	atbB-related site	Attachment site	Ciancioffo, N. et al. "DNA sequence homology between atB-related sites of <i>Corynebacterium diptheriae</i> , <i>Corynebacterium ulcerans</i> , <i>Corynebacterium glutamicum</i> , and the atp site of <i>lamidacorynephage</i> ," <i>FEMS. Microbiol. Lett.</i> , 66:299-302 (1990).
X57226	lysC-alpha, lysC-beta; asd	Aspartokinase-alpha subunit; Aspartokinase-beta subunit; aspartate beta semialdehyde dehydrogenase	Kalinoski, J. et al. "Genetic and biochemical analysis of the Aspartokinase from <i>Corynebacterium glutamicum</i> ," <i>Mol. Microbiol.</i> , 5(5):1197-1204 (1991); Kalinoski, J. et al. "Aspartokinase genes lysC alpha and lysC beta overlap and are adjacent to the aspartate beta-semialdehyde dehydrogenase gene asd in <i>Corynebacterium glutamicum</i> ," <i>Mol. Gen. Genet.</i> , 224(3):317-324 (1990).
X59403	gap,pgk, tpi	Glyceralddehyde-3-phosphate; phosphoglycerate kinase; triosephosphate isomerase	Elkann, B.J. "Identification, sequence analysis, and expression of a <i>Corynebacterium glutamicum</i> gene cluster encoding the three glycolytic enzymes glyceraldehyde-3-phosphate dehydrogenase, 3-phosphoglycerate kinase, and triosephosphate isomerase," <i>J. Bacteriol.</i> , 174(19):6076-6086 (1992).
X59404	gdh	Glutamate dehydrogenase	Borrmann, E.R. et al. "Molecular analysis of the <i>Corynebacterium glutamicum</i> gdh gene encoding glutamate dehydrogenase," <i>Mol. Microbiol.</i> , 6(3):317-326 (1992).
X60312	lysI	L-lysine permease	Seep-Feldhaus, A.H. et al. "Molecular analysis of the <i>Corynebacterium glutamicum</i> lysI gene involved in lysine uptake," <i>Mol. Microbiol.</i> , 5(12):2995-3005 (1991).

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GenBank™ Accession No.	Gene Name	Gene Function	Reference
X66078	copI	Psl protein	Jollif, G. et al. "Cloning and nucleotide sequence of the copI gene encoding Psl, one of the two major secreted proteins of <i>Corynebacterium glutamicum</i> . The deduced N-terminal region of Psl is similar to the Mycobacterium antigen 85 complex." <i>Mol. Microbiol.</i> 6(16):2349-2362 (1992)
X66112	glt	Citrate synthase	Eikmanns, B.J. et al. "Cloning sequence, expression and transcriptional analysis of the <i>Corynebacterium glutamicum</i> gltA gene encoding citrate synthase." <i>Microbiol.</i> 140:1817-1828 (1994)
X67737	dnbB	Dihydrodipicolinate reductase	Peyret, J.L. et al. "Characterization of the csbB gene encoding PS2, an ordered surface-layer protein in <i>Corynebacterium glutamicum</i> ." <i>Mol. Microbiol.</i> 9(1):97-109 (1993)
X69103	esp2	Surface layer protein PS2	Bonamy, C. et al. "Identification of ISI206, a <i>Corynebacterium glutamicum</i> IS3-related insertion sequence and phylogenetic analysis." <i>Mol. Microbiol.</i> 14(3):571-581 (1994)
X69104		IS3 related insertion element	Paek, M. et al. "Leucine synthesis in <i>Corynebacterium glutamicum</i> : enzyme activities, structure of leuA, and effect of leuA inactivation on lysine synthesis." <i>Appl. Environ. Microbiol.</i> 60(1):133-140 (1994)
X70959	leuA	Isopropylmalate synthase	Eikmanns, B.J. et al. "Cloning sequence analysis, expression, and inactivation of the <i>Corynebacterium glutamicum</i> icd gene encoding isocitrate dehydrogenase and biochemical characterization of the enzyme." <i>J. Bacteriol.</i> 177(3):774-782 (1995)
X71489	icd	Isocitrate dehydrogenase (NADP+)	
X72855	GDHA	Glutamate dehydrogenase (NADP+)	Heery, D.M. et al. "A sequence from a tryptophan-hydroproducing strain of <i>Corynebacterium glutamicum</i> encoding resistance to 5-methyltryptophan." <i>Biochem. Biophys. Res. Commun.</i> 201(3):1255-1262 (1994)
X75083, X70584	mtfA	5-methyltryptophan resistance	Fitzpatrick, R. et al. "Construction and characterization of recA mutant strains of <i>Corynebacterium glutamicum</i> and <i>Brevibacterium lactofermentum</i> ." <i>Appl. Microbiol. Biotechnol.</i> 42(4):575-580 (1994)
X75085	recA		Reinisch, D.J. et al. "Characterization of the isocitrate lyase gene from <i>Corynebacterium glutamicum</i> and biochemical analysis of the enzyme." <i>J. Bacteriol.</i> 176(12):3474-3483 (1994)
X75504	aceA, thtX	Partial Isocitrate lyase; ?	Ludwig, W. et al. "Phylogenetic relationships of bacteria based on comparative sequence analysis of elongation factor Tu and ATP-synthase beta-subunit genes." <i>Antonie Van Leeuwenhoek</i> 64:285-305 (1993)
X76875		ATPase beta-subunit	

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GenBank™ Accession No.	Gene Name	Gene Function	Reference
X77034	urf	Elongation factor Tu	Ludwig, W. et al. "Phylogenetic relationships of bacteria based on comparative sequence analysis of elongation factor Tu and ATP-synthase beta-subunit genes." <i>Annuale Van Leeuwenhoek</i> , 64:285-305 (1995)
X77384	recA		Billman-Jacobe, H. "Nucleotide sequence of a recA gene from <i>Corynebacterium glutamicum</i> ." <i>DNA Seq.</i> , 4(6):403-404 (1994)
X78491	acbB	Malate synthase	Reinscheid, D.J. et al. "Malate synthase from <i>Corynebacterium glutamicum</i> pta-ack operon encoding phosphotransacetylase: sequence analysis." <i>Microbiology</i> , 140:3099-3108 (1994)
X80629	16S rDNA	16S ribosomal RNA	Railey, F.A. et al. "Phylogenetic analysis of the genera <i>Rhodococcus</i> and <i>Nocardia</i> and evidence for the evolutionary origin of the genus <i>Nocardia</i> from within the radiation of <i>Rhodococcus</i> species." <i>Microbiol.</i> , 141:523-528 (1995)
X81191	gluA; glub; gluC; gluD	Glutamate uptake system	Kronmeyer, W. et al. "Structure of the gluABCD cluster encoding the glutamate uptake system of <i>Corynebacterium glutamicum</i> ." <i>J. Bacteriol.</i> , 177(5):1152-1158 (1995)
X81379	dapE	Succinyldiaminopimelate desuccinylase	Wehrmann, A. et al. "Analysis of different DNA fragments of <i>Corynebacterium glutamicum</i> complementing dapE of <i>Escherichia coli</i> ." <i>Microbiology</i> , 40:3349-36 (1994)
X82061	16S rDNA	16S ribosomal RNA	Raun, R. et al. "Phylogeny of the genus <i>Corynebacterium</i> deduced from analyses of small-subunit ribosomal DNA sequences." <i>Int. J. Syst. Bacteriol.</i> , 45(4):740-746 (1995)
X82928	asd; lysC	Aspartate-semialdehyde dehydrogenase; ?	Serebrjiski, I. et al. "Multicopy suppression by asd gene and osmotic stress-dependent complementation by heterologous proA in proA mutants." <i>J. Bacteriol.</i> , 177(24):7255-7260 (1995)
X82929	proA	Gamma-glutamyl phosphate reductase	Serebrjiski, I. et al. "Multicopy suppression by asd gene and osmotic stress-dependent complementation by heterologous proA in proA mutants." <i>J. Bacteriol.</i> , 177(24):7255-7260 (1995)
X84257	16S rDNA	16S ribosomal RNA	Pascual, C. et al. "Phylogenetic analysis of the genus <i>Corynebacterium</i> based on 16S rRNA gene sequences." <i>Int. J. Syst. Bacteriol.</i> , 45(4):724-728 (1995)
X85965	arop; dapE	Aromatic amino acid permease; ?	Wehrmann, A. et al. "Functional analysis of sequences adjacent to dapE of <i>Corynebacterium glutamicum</i> reveals the presence of arp, which encodes the aromatic amino acid transporter." <i>J. Bacteriol.</i> , 177(20):5991-5993 (1995)

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GenBank™ Accession No.	Gene Name	Gene Function	Reference
X86157	argB; argC; argD; argH; argJ	Acetylglutamate kinase; N-acetyl-γ-glutamyl-phosphate reductase; acetylornithine aminotransferase; ornithine carbamoyltransferase; glutamate N-acetyltransferase	Sakanyan, V. et al. "Genes and enzymes of the acetyl cycle of arginine biosynthesis in <i>Corynebacterium glutamicum</i> : enzyme evolution in the early steps of the arginine pathway." <i>Microbiology</i> , 142:99-108 (1996)
X89084	pta; ackA	Phosphatase acetyltransferase; acetate kinase	Reinscheld, D.J. et al. "Cloning, sequence analysis, expression and inactivation of the <i>Corynebacterium glutamicum</i> pta-ack operon encoding phosphotransacetylase and acetate kinase." <i>Microbiology</i> , 145:503-513 (1999)
X89850	attB	Attachment site	Le Marrec, C. et al. "Genetic characterization of site-specific integration functions of phi AAV2 infecting "Arthrobacter aureus CT0." <i>J. Bacteriol.</i> , 178(7):1996-2004 (1996)
X90356		Promoter fragment F1	Patel, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif." <i>Microbiology</i> , 142:1297-1309 (1996)
X90357		Promoter fragment F2	Patel, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif." <i>Microbiology</i> , 142:1297-1309 (1996)
X90358		Promoter fragment F10	Patel, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif." <i>Microbiology</i> , 142:1297-1309 (1996)
X90359		Promoter fragment F13	Patel, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif." <i>Microbiology</i> , 142:1297-1309 (1996)
X90360		Promoter fragment F22	Patel, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif." <i>Microbiology</i> , 142:1297-1309 (1996)
X90361		Promoter fragment F34	Patel, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif." <i>Microbiology</i> , 142:1297-1309 (1996)
X90362		Promoter fragment F37	Patel, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif." <i>Microbiology</i> , 142:1297-1309 (1996)

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GenBank™ Accession No.	Gene Name	Gene Function	Reference
X90363		Promoter fragment F45	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif." <i>Microbiology</i> , 142:1297-1309 (1996)
X90364		Promoter fragment F64	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif." <i>Microbiology</i> , 142:1297-1309 (1996)
X90365		Promoter fragment F75	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif." <i>Microbiology</i> , 142:1297-1309 (1996)
X90366		Promoter fragment PF101	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif." <i>Microbiology</i> , 142:1297-1309 (1996)
X90367		Promoter fragment PF104	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif." <i>Microbiology</i> , 142:1297-1309 (1996)
X90368		Promoter fragment PF109	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif." <i>Microbiology</i> , 142:1297-1309 (1996)
X90313	amt	Ammonium transport system	Sieve, R.M. et al. "Functional and genetic characterization of the (methyl) ammonium uptake carrier of <i>Corynebacterium glutamicum</i> ." <i>J. Biol. Chem.</i> , 271(10):5398-5403 (1996)
X93514	betP	Glycine betaine transport system	Peter, H. et al. "Isolation, characterization, and expression of the <i>Corynebacterium glutamicum</i> betP gene, encoding the transport system for the compatible solute glycine betaine." <i>J. Bacteriol.</i> , 178(17):5229-5234 (1996)
X95649	orf4		Patek, M. et al. "Identification and transcriptional analysis of the dapB-ORF2-dapA-ORF4 operon of <i>Corynebacterium glutamicum</i> , encoding two enzymes involved in L-lysine synthesis." <i>Biotechnol. Lett.</i> , 19:1115-1117 (1997)
X96471	lysE; lysG	Lysine exporter protein; Lysine export regulation protein	Vrjlig, M. et al. "A new type of transporter with a new type of cellular function: L-lysine export from <i>Corynebacterium glutamicum</i> ." <i>Mol. Microbiol.</i> , 22(5):815-826 (1996)

00001573-000700

GenBank™ Accession No.	Gene Name	Gene Function	Reference
X96580	panB, panC, yvJB	3-methyl-2-oxobutanoate hydroxymethyltransferase; pantoate-beta-alanine ligase; xylokinase	Sahn, H. et al. "D-pantoic acid synthesis in <i>Corynebacterium glutamicum</i> and use of panB and genes encoding L-valine synthase for D-pantoic acid overproduction," <i>Appl. Environ. Microbiol.</i> , 65(5):1973-1979 (1999)
X96962		Insertion sequence IS1207 and transposase	
X99289		Elongation factor P	Ramos, A. et al. "Cloning, sequencing and expression of the gene encoding elongation factor P in the amino acid producer <i>Brevibacterium lactofermentum</i> ( <i>Corynebacterium glutamicum</i> ATCC 13869)," <i>Gene</i> , 198:217-222 (1997)
Y00140	thrB	Homoserine kinase	Mateos, L.M. et al. "Nucleotide sequence of the homoserine kinase (thrB) gene of the <i>Brevibacterium lactofermentum</i> ," <i>Nucleic Acids Res.</i> , 15(9):3922 (1987)
Y00151	dth	Meso-diaminopimelate D-dehydrogenase (EC 1.4.1.16)	Ishino, S. et al. "Nucleotide sequence of the meso-diaminopimelate D-dehydrogenase gene from <i>Corynebacterium glutamicum</i> ," <i>Nucleic Acids Res.</i> , 15(9):3917 (1987)
Y00476	thrA	Homoserine dehydrogenase	Mateos, L.M. et al. "Nucleotide sequence of the homoserine dehydrogenase (thrA) gene of the <i>Brevibacterium lactofermentum</i> ," <i>Nucleic Acids Res.</i> , 15(24):10598 (1987)
Y00546	hom, thrB	Homoserine dehydrogenase; homoserine kinase	Peoples, O.P. et al. "Nucleotide sequence and fine structural analysis of the <i>Corynebacterium glutamicum</i> hom-thrB operon," <i>Mol. Microbiol.</i> , 21(1):63-72 (1988)
Y08964	murC, ftsQ/ftsZ, ftsZ	UDP-N-acetylmuramate-alanine ligase; division initiation protein or cell division protein; cell division protein	Horrobin, M.P. et al. "Identification, characterization, and chromosomal organization of the ftsZ gene from <i>Brevibacterium lactofermentum</i> ," <i>Mol. Gen. Genet.</i> , 259(1):97-104 (1998)
Y09163	putP	High affinity proline transport system	Peter, H. et al. "Isolation of the putP gene of <i>Corynebacterium glutamicum</i> and characterization of a low-affinity uptake system for compatible solutes," <i>Arch. Microbiol.</i> , 168(2):143-151 (1997)
Y09548	pyc	Pyruvate carboxylase	Peters-Wendisch, P.G. et al. "Pyruvate carboxylase from <i>Corynebacterium glutamicum</i> : characterization, expression and inactivation of the pyc gene," <i>Microbiol.</i> , 144:915-927 (1998)
Y09578	leuB	3-isopropylmalate dehydrogenase	Paek, M. et al. "Analysis of the leuB gene from <i>Corynebacterium glutamicum</i> ," <i>Appl. Microbiol. Biotechnol.</i> , 50(1):42-47 (1998)
Y12472		Attachment site bacteriophage Phi-16	Morreau, S. et al. "Site-specific integration of coryneophage Phi-16: The construction of an integration vector," <i>Microbiol.</i> , 145:539-548 (1999)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
Y12537	proP	Proline/ectoine uptake system protein	Peter, H. et al. "Corynebacterium glutamicum is equipped with four secondary carriers for compatible solutes: Identification, sequencing, and characterization of the proline/ectoine uptake system, ProP, and the ectoine/proline/glycine betaine carrier, EcP." <i>J. Bacteriol.</i> , 180(22):6005-6012 (1998)
Y13221	glmA	Glutamine synthetase I	Jakoby, M. et al. "Isolation of <i>Corynebacterium glutamicum</i> glmA gene encoding glutamine synthetase I." <i>FEBS Microbiol. Lett.</i> , 154(1):81-88 (1997)
Y16642	lpl	Dihydrolipoamide dehydrogenase	Moreau, S. et al. "Analysis of the integration functions of $\delta$ phl:304L, an integrase module among corynephages." <i>Virology</i> , 255(1):150-159 (1999)
Y18059		Attachment site Corynephage 304L	Oguzta, J.A. et al. "A gene encoding arginyl-tRNA synthetase is located in the upstream region of the lysA gene in <i>Brevibacterium lactofermentum</i> : Regulation of argS-lysA cluster expression by arginine." <i>J. Bacteriol.</i> , 175(22):7356-7362 (1993)
Z21501	argS; lysA	Arginyl-tRNA synthetase; diaminopimelate decarboxylase (partial)	Pisabarro, A. et al. "A cluster of three genes (dapA, orf2, and dapB) of <i>Brevibacterium lactofermentum</i> encodes dihydrolipoic acid reductase, and a third polypeptide of unknown function." <i>J. Bacteriol.</i> , 175(9):2743-2749 (1993)
Z21502	dapA; dapB	Dihydrolipoic acid synthetase; dihydrolipoic acid reductase	Malumbres, M. et al. "Analysis and expression of the thrC gene of the encoded threonine synthase." <i>Appl. Environ. Microbiol.</i> , 60(7):2209-2219 (1994)
Z29563	thrC	Threonine synthase	
Z46753	16S rDNA	Gene for 16S ribosomal RNA	Oguzta, J.A. et al. "Multiple sigma factor genes in <i>Brevibacterium lactofermentum</i> : Characterization of sigA and sigB." <i>J. Bacteriol.</i> , 178(2):550-553 (1996)
Z49822	sigA	SigA sigma factor	Oguzta, J.A. et al. "The galE gene encoding the UDP-galactose 4-epimerase of <i>Brevibacterium lactofermentum</i> is coupled transcriptionally to the dmhR gene." <i>Gene</i> , 177:103-107 (1996)
Z49823	galE; dmhR	Catalytic activity UDP-galactose 4-epimerase; dihydrotoxin regulatory protein	Oguzta, J.A. et al. "Multiple sigma factor genes in <i>Brevibacterium lactofermentum</i> : Characterization of sigA and sigB." <i>J. Bacteriol.</i> , 178(2):550-553 (1996)
Z49824	orf1; sigB	?, SigB sigma factor	Correa, A. et al. "Cloning and characterization of an IS-like element present in the genome of <i>Brevibacterium lactofermentum</i> ATCC 13869." <i>Gene</i> , 170(1):91-94 (1996)
Z66534		Transposase	

A sequence for this gene was published in the indicated reference. However, the sequence obtained by the inventors of the present application is significantly longer than the published version. It is believed that the published version relied on an incorrect start codon, and thus represents only a fragment of the actual coding region.

TABLE 3: Corynebacterium and Brevibacterium Strains Which May be Used in the Practice of the Invention

Genus	Species	ATCC	DSMZ	NRRL	CECT	NCIMB	CBS	NCIC	DSMZ
Brevibacterium	ammoniaenes	21054							
Brevibacterium	ammoniaenes	19350							
Brevibacterium	ammoniaenes	19351							
Brevibacterium	ammoniaenes	19352							
Brevibacterium	ammoniaenes	19353							
Brevibacterium	ammoniaenes	19354							
Brevibacterium	ammoniaenes	19355							
Brevibacterium	ammoniaenes	19356							
Brevibacterium	ammoniaenes	21055							
Brevibacterium	ammoniaenes	21077							
Brevibacterium	ammoniaenes	21553							
Brevibacterium	ammoniaenes	21580							
Brevibacterium	ammoniaenes	39101							
Brevibacterium	bulanicum	21196							
Brevibacterium	divaricatum	21792	p928						
Brevibacterium	flavum	21474							
Brevibacterium	flavum	21129							
Brevibacterium	flavum	21518							
Brevibacterium	flavum			B11474					
Brevibacterium	flavum			B11472					
Brevibacterium	flavum	21127							
Brevibacterium	flavum	21128							
Brevibacterium	flavum	21427							
Brevibacterium	flavum	21475							
Brevibacterium	flavum	21517							
Brevibacterium	flavum	21528							
Brevibacterium	flavum	21529							

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Brevibacterium	flavum		B11477						
Brevibacterium	flavum		B11478						
Brevibacterium	flavum	21127							
Brevibacterium	flavum		B11474						
Brevibacterium	heali	15527							
Brevibacterium	keoglucanicum	21004							
Brevibacterium	keoglucanicum	21089							
Brevibacterium	ketoreductum	21914				70			
Brevibacterium	lactofermentum				74				
Brevibacterium	lactofermentum				77				
Brevibacterium	lactofermentum	21798							
Brevibacterium	lactofermentum	21799							
Brevibacterium	lactofermentum	21800							
Brevibacterium	lactofermentum	21801							
Brevibacterium	lactofermentum		B11470						
Brevibacterium	lactofermentum		B11471						
Brevibacterium	lactofermentum	21086							
Brevibacterium	lactofermentum	21420							
Brevibacterium	lactofermentum	21086							
Brevibacterium	lactofermentum	31269							
Brevibacterium	lactofermentum	9174							
Brevibacterium	linens	19391							
Brevibacterium	linens	8377							
Brevibacterium	paraffinilyticum				11160				
Brevibacterium	spec.				717.73				
Brevibacterium	spec.	14604			717.73				
Brevibacterium	spec.	21860							
Brevibacterium	spec.	21864							
Brevibacterium	spec.	21865							

[illegible]

Corynebacterium	glutamicum	21514																	
Corynebacterium	glutamicum	21516																	
Corynebacterium	glutamicum	21299																	
Corynebacterium	glutamicum	21300																	
Corynebacterium	glutamicum	39684																	
Corynebacterium	glutamicum	21488																	
Corynebacterium	glutamicum	21649																	
Corynebacterium	glutamicum	21650																	
Corynebacterium	glutamicum	19723																	
Corynebacterium	glutamicum	13869																	
Corynebacterium	glutamicum	21157																	
Corynebacterium	glutamicum	21158																	
Corynebacterium	glutamicum	21159																	
Corynebacterium	glutamicum	21355																	
Corynebacterium	glutamicum	31808																	
Corynebacterium	glutamicum	21674																	
Corynebacterium	glutamicum	21562																	
Corynebacterium	glutamicum	21563																	
Corynebacterium	glutamicum	21564																	
Corynebacterium	glutamicum	21565																	
Corynebacterium	glutamicum	21566																	
Corynebacterium	glutamicum	21567																	
Corynebacterium	glutamicum	21568																	
Corynebacterium	glutamicum	21569																	
Corynebacterium	glutamicum	21570																	
Corynebacterium	glutamicum	21571																	
Corynebacterium	glutamicum	21572																	
Corynebacterium	glutamicum	21573																	
Corynebacterium	glutamicum	21579																	
Corynebacterium	glutamicum	19049																	
Corynebacterium	glutamicum	19050																	





ATCC, American Type Culture Collection, Rockville, MD, USA

NRRL: ARS Culture Collection, Northern Regional Research Laboratory, Peoria, IL, USA

NCIMB: National Collection of Industrial and Marine Bacteria Ltd., Aberdeen, UK

NCTC: National Collection of Type Cultures, London, UK

DSMZ: Deutsche Sammlung von Mikroorganismen und Zellkulturen, Braunschweig, Germany

DSMZ: Deutsche Sammlung von Mikroorganismen und Zellkulturen, 37071 Braunschweig, Germany.  
For reference see Sugawara, H. et al. (1993) World directory of collections of cultures of microorganisms: Bacteria, fungi and yeasts (4th edn), World Federation for Culture Collections, world data center on microorganisms, Saitama, Japan.

TABLE 4: ALIGNMENT RESULTS

ID #	length (nt)	Genbank Hit	Accession	Name of Genbank Hit	Source of Genbank Hit	(GAP)	Deposit
ra00060 2319		GB_BA1.MTCY50	36030 Z77157	Mycobacterium tuberculosis H37RV complete genome; segment 55/162.	Mycobacterium tuberculosis	56,005	17-Jun-88
		GB_BAZ.EKOUW67.0	U18997	Escherichia coli K-12 chromosome region from 67.4 to 76.0 minutes.	Escherichia coli	37,165	23-Jan-86
		GB_BAZ.EKOUW67.0	A0000397	Escherichia coli K-12 MG1655 section 287 of 400 of the complete genome.	Escherichia coli	37,165	12-Nov-96
ra00061 2790		GB_BA1.SC7H2	AI109732	Streptomyces coelicolor cosmid 712.	Streptomyces coelicolor A3(2)	38,650	2-Aug-99
		GB_BA1.MT0052	35935 Z95554	Mycobacterium tuberculosis H37RV complete genome; segment 72/162.	Mycobacterium tuberculosis	57,626	17-Jun-88
		GB_BA1.MS6P04	3157 L11920	Mycobacterium tuberculosis DNA polymerase I (polI), complete cts.	Mycobacterium tuberculosis	64,841	16-MAY-1996
ra00066 913		GB_BA1.ML.CB0407	35615 A1023366	Mycobacterium leprae cosmid B240.	Mycobacterium leprae	38,765	27-Aug-98
		GB_BA1.MT0025	121155 A1022121	Mycobacterium tuberculosis H37RV complete genome; segment 155/162.	Mycobacterium tuberculosis	60,241	21-Sep-99
		GB_BA2.SC025	41822 AL118514	Streptomyces coelicolor cosmid J25.	Streptomyces coelicolor A3(2)	60,260	17-Jun-88
		GB_BA1.MTCY1007	39800 M77490	E. coli genomic sequence of the region from 64.2 to 86.5 minutes.	Escherichia coli	50,438	29-MAY-1995
ra00095 2412		GB_BA1.ECOLW65	91414 AF028736	Serratia marcescens at specific recombinase (recA) and DNA helicase II (uvrD) genes, complete cts.	Serratia marcescens	52,153	20-Apr-98
		GB_BA1.ECOLW65	4113 AF028736	Serratia marcescens at specific recombinase (recA) and DNA helicase II (uvrD) genes, complete cts.	Serratia marcescens	52,153	20-Apr-98
ra00103 4683		GB_BA1.SCTC7	31635 AU010131	Streptomyces coelicolor cosmid TC7.	Streptomyces coelicolor	38,447	6-Jul-98
		GB_BA1.BDB089	19451 D90693	E. coli genomic DNA, Kohara clone #3181(C) 2,37.6 min).	Escherichia coli	52,004	29-MAR-1997
		GB_BAZ.AE000260	10877 AE000056	Escherichia coli K-12 MG1655 section 150 of 400 of the complete genome.	Escherichia coli	52,004	12-Nov-96
ra00157 1286		GB_IN2.AC004295	84551 AC004295	Drosophila melanogaster DNA sequence [F1 DS18374 (D180)]. complete sequence.	Drosophila melanogaster	33,359	29-Jul-98
		GB_IN2.AC004295	84551 AC004295	Drosophila melanogaster DNA sequence [F1 DS18374 (D180)]. complete sequence.	Drosophila melanogaster	33,359	29-Jul-98
		GB_IN2.AC004295	84551 AC004295	Drosophila melanogaster DNA sequence [F1 DS18374 (D180)]. complete sequence.	Drosophila melanogaster	36,150	29-Jul-98
		GB_BA1.MTCV71	42729 Z92771	Mycobacterium tuberculosis H37RV complete genome; segment 141/162.	Mycobacterium tuberculosis	42,051	10-Feb-99
		GB_HT02.AC008199	124050 AC008199	Drosophila melanogaster chromosome 3 clone BACR01.K01 (D756) RFCl-86	Drosophila melanogaster	35,510	2-Aug-99
ra00163 741		GB_HT02.AC008199	124050 AC008199	O1 K 3 map g4D-g4D strain y. cw bp. *** SEQUENCING IN PROGRESS *** *** 83 unordered pieces.	Drosophila melanogaster	35,510	2-Aug-99
		GB_HT02.AC008199	124050 AC008199	Drosophila melanogaster chromosome 3 clone BACR01.K08 (D756) RFCl-98	Drosophila melanogaster	35,510	2-Aug-99
		GB_HT02.AC008199	124050 AC008199	O1 K 8 map g4D-g4D strain y. cw bp. *** SEQUENCING IN PROGRESS *** *** 63 unordered pieces.	Drosophila melanogaster	35,510	2-Aug-99
		GB_BA1.BL.NARK	1421 V16671	Bacillus licheniformis nark, fir and wvic genes.	Bacillus licheniformis	41,975	30-Jun-88
		GB_BA1.OIGLO	3595 X71489	C-glutaminase cod gene for monomeric isoproteic dehydrogenase.	Corynebacterium glutamicum	47,097	17-Feb-95
ra00208 972		GB_BA1.OIGLO	190753 AC005234	Homo sapiens BAC clone NT04934122 from 2, complete sequence.	Homo sapiens	39,343	4-Feb-99
		GB_OVAF.I16539	1063 AF118539	Danio rerio intranuclear ribonucleo protein 2 (lbp-2), mRNA, complete cds.	Danio rerio	39,437	08-Oct-1989
		GB_OVAF.I16539	1063 AF118539	Danio rerio intranuclear ribonucleo protein 2 (lbp-2), mRNA, complete cds.	Danio rerio	39,437	23-Jun-99
ra00212 1683		GB_BA1.MT0102	70287 AL021787	Mycobacterium tuberculosis H37RV complete genome; segment 132/162.	Mycobacterium tuberculosis	60,464	17-Sep-97
		GB_BA1.ML.CB837	44882 Z89263	Mycobacterium leprae cosmid B307.	Mycobacterium leprae	60,902	17-Sep-97
		GB_BA1.SC0D89	36881 AF055669	Streptomyces coelicolor cosmid 805.	Streptomyces coelicolor	40,500	26-Feb-98
		GB_GSS1.F05655024	397 AC065024	Shedder DNA-21O17, genomic survey sequences.	Typhimysoma brucei	40,500	22-Jun-98
ra00213 696		GB-HTG1.HSA.C0003801	64266 AC000380	Homo sapiens chromosome 3 clone pJ01111, *** SEQUENCING IN PROGRESS *** 2 unordered pieces.	Homo sapiens	38,466	26-MAR-1997
		GB-HTG1.HSA.C0003801	64266 AC000380	Homo sapiens chromosome 3 clone pJ01111, *** SEQUENCING IN PROGRESS *** 2 unordered pieces.	Homo sapiens	38,466	26-MAR-1997
		GB-HTG1.HSA.C0003801	64266 AC000380	Homo sapiens chromosome 3 clone pJ01111, *** SEQUENCING IN PROGRESS *** 2 unordered pieces.	Homo sapiens	38,466	26-MAR-1997
		GB-HTG1.HSA.C0003801	64266 AC000380	Homo sapiens chromosome 5 clone Crl-HSPIC_236F.12, *** SEQUENCING IN PROGRESS *** 64 unordered pieces.	Homo sapiens	34,836	3-Aug-99
ra00214 834		GB-HTG1.HSA.C000391	40119 AC008391	Homo sapiens chromosome 5 clone Crl-HSPIC_236F.12, *** SEQUENCING IN PROGRESS *** 64 unordered pieces.	Homo sapiens	34,836	3-Aug-99

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ra00331	1652	GB_HTTG2.HSMM1_4	110000	AJ011929	Homo sapiens chromosome 21 clone Ceantids 44C5.Q16H18.14C10.25D2.B7D5 map 21q22.2.D2.IS349-MX1. *** SEQUENCING IN PROGRESS ***	Homo sapiens	34,836	3-Aug-99
ra00331	1653	GB_HTTG3.ACO08391	40119	AC008391	Homo sapiens chromosome 5 clone C17-15PC_239F12. *** SEQUENCING IN PROGRESS *** 64 uncloned pieces.	Homo sapiens	34,836	3-Aug-99
ra00331	1654	GB_EST17.AM46451	427	AM46451	w7212.11 Stragene mouse strain #607313) Mus musculus cDNA clone IMAGE1151855 5 similar to gp267868 TRANSLOC PLASE (HUMAN). gpU09569 Mus musculus LAP1 translocase mRNA, complete cds. (MOLSE). mRNA sequence.	Mus musculus	40,376	26-Oct-1997
ra00331	1655	GB_HTTG3.HSMM1_4	110000	AJ011929	Homo sapiens chromosome 21 clone Ceantids 44C5.Q16H18.14C10.25D2.B7D5 map 21q22.2.D2.IS349-MX1. *** SEQUENCING IN PROGRESS ***	Homo sapiens	38,462	15-Sep-99
ra00331	1656	GB_HTTG3.HSMM1_4	110000	AJ011929	Homo sapiens chromosome 21 clone Ceantids 44C5.Q16H18.14C10.25D2.B7D5 map 21q22.2.D2.IS349-MX1. *** SEQUENCING IN PROGRESS ***	Homo sapiens	38,462	15-Sep-99
ra00331	1657	GB_HTTG3.HSMM1_4	110000	AJ011929	Homo sapiens chromosome 21 clone Ceantids 44C5.Q16H18.14C10.25D2.B7D5 map 21q22.2.D2.IS349-MX1. *** SEQUENCING IN PROGRESS ***	Homo sapiens	38,462	15-Sep-99
ra00331	1658	GB_HTTG3.HSMM1_4	110000	AJ011929	Homo sapiens chromosome 21 clone Ceantids 44C5.Q16H18.14C10.25D2.B7D5 map 21q22.2.D2.IS349-MX1. *** SEQUENCING IN PROGRESS ***	Homo sapiens	38,462	15-Sep-99
ra00331	1659	GB_HTTG3.HSMM1_4	110000	AJ011929	Homo sapiens chromosome 21 clone Ceantids 44C5.Q16H18.14C10.25D2.B7D5 map 21q22.2.D2.IS349-MX1. *** SEQUENCING IN PROGRESS ***	Homo sapiens	38,462	15-Sep-99
ra00331	1660	GB_HTTG3.HSMM1_4	110000	AJ011929	Homo sapiens chromosome 21 clone Ceantids 44C5.Q16H18.14C10.25D2.B7D5 map 21q22.2.D2.IS349-MX1. *** SEQUENCING IN PROGRESS ***	Homo sapiens	38,462	15-Sep-99
ra00331	1661	GB_HTTG3.HSMM1_4	110000	AJ011929	Homo sapiens chromosome 21 clone Ceantids 44C5.Q16H18.14C10.25D2.B7D5 map 21q22.2.D2.IS349-MX1. *** SEQUENCING IN PROGRESS ***	Homo sapiens	38,462	15-Sep-99
ra00331	1662	GB_HTTG3.HSMM1_4	110000	AJ011929	Homo sapiens chromosome 21 clone Ceantids 44C5.Q16H18.14C10.25D2.B7D5 map 21q22.2.D2.IS349-MX1. *** SEQUENCING IN PROGRESS ***	Homo sapiens	38,462	15-Sep-99
ra00331	1663	GB_HTTG3.HSMM1_4	110000	AJ011929	Homo sapiens chromosome 21 clone Ceantids 44C5.Q16H18.14C10.25D2.B7D5 map 21q22.2.D2.IS349-MX1. *** SEQUENCING IN PROGRESS ***	Homo sapiens	38,462	15-Sep-99
ra00331	1664	GB_HTTG3.HSMM1_4	110000	AJ011929	Homo sapiens chromosome 21 clone Ceantids 44C5.Q16H18.14C10.25D2.B7D5 map 21q22.2.D2.IS349-MX1. *** SEQUENCING IN PROGRESS ***	Homo sapiens	38,462	15-Sep-99
ra00331	1665	GB_HTTG3.HSMM1_4	110000	AJ011929	Homo sapiens chromosome 21 clone Ceantids 44C5.Q16H18.14C10.25D2.B7D5 map 21q22.2.D2.IS349-MX1. *** SEQUENCING IN PROGRESS ***	Homo sapiens	38,462	15-Sep-99
ra00331	1666	GB_HTTG3.HSMM1_4	110000	AJ011929	Homo sapiens chromosome 21 clone Ceantids 44C5.Q16H18.14C10.25D2.B7D5 map 21q22.2.D2.IS349-MX1. *** SEQUENCING IN PROGRESS ***	Homo sapiens	38,462	15-Sep-99
ra00331	1667	GB_HTTG3.HSMM1_4	110000	AJ011929	Homo sapiens chromosome 21 clone Ceantids 44C5.Q16H18.14C10.25D2.B7D5 map 21q22.2.D2.IS349-MX1. *** SEQUENCING IN PROGRESS ***	Homo sapiens	38,462	15-Sep-99
ra00331	1668	GB_HTTG3.HSMM1_4	110000	AJ011929	Homo sapiens chromosome 21 clone Ceantids 44C5.Q16H18.14C10.25D2.B7D5 map 21q22.2.D2.IS349-MX1. *** SEQUENCING IN PROGRESS ***	Homo sapiens	38,462	15-Sep-99
ra00331	1669	GB_HTTG3.HSMM1_4	110000	AJ011929	Homo sapiens chromosome 21 clone Ceantids 44C5.Q16H18.14C10.25D2.B7D5 map 21q22.2.D2.IS349-MX1. *** SEQUENCING IN PROGRESS ***	Homo sapiens	38,462	15-Sep-99
ra00331	1670	GB_HTTG3.HSMM1_4	110000	AJ011929	Homo sapiens chromosome 21 clone Ceantids 44C5.Q16H18.14C10.25D2.B7D5 map 21q22.2.D2.IS349-MX1. *** SEQUENCING IN PROGRESS ***	Homo sapiens	38,462	15-Sep-99
ra00331	1671	GB_HTTG3.HSMM1_4	110000	AJ011929	Homo sapiens chromosome 21 clone Ceantids 44C5.Q16H18.14C10.25D2.B7D5 map 21q22.2.D2.IS349-MX1. *** SEQUENCING IN PROGRESS ***	Homo sapiens	38,462	15-Sep-99
ra00331	1672	GB_HTTG3.HSMM1_4	110000	AJ011929	Homo sapiens chromosome 21 clone Ceantids 44C5.Q16H18.14C10.25D2.B7D5 map 21q22.2.D2.IS349-MX1. *** SEQUENCING IN PROGRESS ***	Homo sapiens	38,462	15-Sep-99
ra00331	1673	GB_HTTG3.HSMM1_4	110000	AJ011929	Homo sapiens chromosome 21 clone Ceantids 44C5.Q16H18.14C10.25D2.B7D5 map 21q22.2.D2.IS349-MX1. *** SEQUENCING IN PROGRESS ***	Homo sapiens	38,462	15-Sep-99
ra00331	1674	GB_HTTG3.HSMM1_4	110000	AJ011929	Homo sapiens chromosome 21 clone Ceantids 44C5.Q16H18.14C10.25D2.B7D5 map 21q22.2.D2.IS349-MX1. *** SEQUENCING IN PROGRESS ***	Homo sapiens	38,462	15-Sep-99
ra00331	1675	GB_HTTG3.HSMM1_4	110000	AJ011929	Homo sapiens chromosome 21 clone Ceantids 44C5.Q16H18.14C10.25D2.B7D5 map 21q22.2.D2.IS349-MX1. *** SEQUENCING IN PROGRESS ***	Homo sapiens	38,462	15-Sep-99
ra00331	1676	GB_HTTG3.HSMM1_4	110000	AJ011929	Homo sapiens chromosome 21 clone Ceantids 44C5.Q16H18.14C10.25D2.B7D5 map 21q22.2.D2.IS349-MX1. *** SEQUENCING IN PROGRESS ***	Homo sapiens	38,4	

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[illegible]

[illegible]

# TABLE 4: ALIGNMENT RESULTS

GB_EACV032716	1618	U32716	Hemophilus influenzae Rd section 31 of 161 of the complete genome	Hemophilus influenzae Rd	39,588	29-MAY-1998
GB_HJTGZ.ACO06842	299015	AC006842	Caenorhabditis elegans clone Y104H12X. *** SEQUENCING IN PROGRESS *** 13 unordered pieces	Caenorhabditis elegans	36,003	24-Feb-99
ra00888 912	42741	AD000014	Myobacterium tuberculosis sequences from clone y423	Myobacterium tuberculosis	54,945	10-DEC-1996
GB_BA1.MS0423	35420	284724	Myobacterium tuberculosis H37Rv complete genome; segment 21/162	Myobacterium tuberculosis	39,522	17-Jun-98
GB_JNI.CTC123	23674	281467	Caenorhabditis elegans cosmid C12C2, complete sequence	Caenorhabditis elegans	36,170	23-Nov-98
ra00867 411	92073	AC006244	Drosophila melanogaster chromosome 2, clone D50012 (D463) map 60F1-60F2 strain Y, on bw sp. *** SEQUENCING IN PROGRESS *** 3 unordered pieces	Drosophila melanogaster	36,165	30-Jul-99
GB_GSS1.CNS0080E0	1101	AL056856	Drosophila melanogaster genome survey sequence T7 and of BAC # BACR23K12 of RP04 library from Drosophila melanogaster (fruit fly).	Drosophila melanogaster	34,772	4-Jun-99
GB_HJTGZ.ACO06244	92079	AC006244	genomic survey sequence. Drosophila melanogaster chromosome 2, clone D50012 (D463) map 60F1-60F2 strain Y, on bw sp. *** SEQUENCING IN PROGRESS *** 3 unordered pieces	Drosophila melanogaster	38,765	30-Jul-99
ra00990 488	565	AC078675	CIT-HSP-2298L22 TF CIT-HSP Homo sapiens genomic clone 2386L22.	Homo sapiens	39,200	20-Aug-98
GB_GSS8.ACO04280	323	AC004280	genomic survey sequence. Arabidopsis thaliana DNA chromosome 4, BAC clone F1613 (ESSA project)	Homo sapiens	38,434	11-Jul-98
GB_PL1.ATF16.13	107800	AL049638	genomic survey sequence. Arabidopsis thaliana DNA chromosome 4, BAC clone F1613 (ESSA project)	Arabidopsis thaliana	43,220	14-Apr-99
ra00994 451	301	C74578	C74578 Rice particle shorter than 3cm Oryza sativa cDNA clone E3180L1A. Oryza sativa	Oryza sativa	51,174	29-Sep-97
GB_EST1T.C74578	827	AF155027	mRNA sequence. AF155027 Zebrafish kidney cDNA random primed, RZPD library no. 576	Danio rerio	35,268	22-Jul-99
GB_EST36.AF155027	457	AA023112	Danio rerio cDNA clone C1H0P57B0062323 T7 primer, mRNA sequence. mbsc12.1 Soares mouse placenta ANM17.5 14.5 Mus musculus cDNA clone IMAGE455926 5 similar to PRC510960 ST0960 myofibrillar protein-bovine. mRNA sequence.	Mus musculus	41,859	21-Jan-97
GB_EST8.AA023112	127964	AC011344	Homo sapiens chromosome 5, clone CIT-HSPC_287014. *** SEQUENCING IN PROGRESS *** 36 unordered pieces.	Homo sapiens	37,718	06-OCT-1999
ra01030 1299	127964	AC011344	Homo sapiens chromosome 5, clone CIT-HSPC_287014. *** SEQUENCING IN PROGRESS *** 36 unordered pieces.	Homo sapiens	37,718	06-OCT-1999
GB_HTG3.ACO11344	127964	AC011344	Homo sapiens chromosome 5, clone CIT-HSPC_287014. *** SEQUENCING IN PROGRESS *** 36 unordered pieces.	Homo sapiens	34,752	11-Nov-98
GB_HTG3.ACO11344	23973	AJ235273	Rickettsia prowazekii strain Madrid E, complete genome; segment 4/4	Rickettsia prowazekii	39,059	8-Sep-97
GB_BA11.PRX004	456614	AA56614	nc08911.1 NC_CGAP_Phe1 Homo sapiens cDNA clone IMAGE1100132	Homo sapiens	38,859	3-Jun-99
ra01064 759	150070	AC007720	3. mRNA sequence. Homo sapiens clone 31_B_4. *** SEQUENCING IN PROGRESS *** 7 unordered pieces.	Homo sapiens	38,859	3-Jun-99
GB_HTG2.ACO07720	150070	AC007720	Homo sapiens clone 31_B_4. *** SEQUENCING IN PROGRESS *** 7 unordered pieces.	Homo sapiens	38,859	3-Jun-99
GB_HTG2.ACO07720	150070	AC007720	Homo sapiens clone 31_B_4. *** SEQUENCING IN PROGRESS *** 7 unordered pieces.	Homo sapiens	37,401	08-MAY-1999
ra01149 381	115661	AC006871	Homo sapiens P4C clone DU0791C19 from 7p11.2-q11.21, complete	Homo sapiens	36,364	31-OCT-1989
GB_PPR4.ACO06871	167025	AC007347	Homo sapiens chromosome 16, clone RP04-11_488J11. *** SEQUENCING IN PROGRESS *** 2 ordered pieces.	Homo sapiens	36,364	31-OCT-1989
GB_HTG4.ACO07347	167025	AC007347	Homo sapiens chromosome 16, clone RP04-11_488J11. *** SEQUENCING IN PROGRESS *** 2 ordered pieces.	Homo sapiens	39,879	24-Jun-99
ra01157 1705	39430	Z73966	Myobacterium tuberculosis H37Rv complete genome; segment 93/162	Myobacterium tuberculosis		

rs601235	1203	GB_EST37.A044834	388	A194834	bioRxiv03.1 Drosophila melanogaster rRNA testis library	Drosophila melanogaster	40.310	17-Aug-99
		GB_EST11.16608	235	T16608	meigenan cDNA clone isoB6303.5, adult testis	Homo sapiens	41.277	25-Jul-96
		GB_EST10.AA141530	515	AA141530	mRNA sequence.	Drosophila melanogaster	38.477	29-Nov-98
rs601279	588	GB_BA1.MLB1790G	37617	Z14314	CKR313 spRme CK Drosophila melanogaster embryo BlueScript Drosophila melanogaster cDNA clone CKR313 spRme, rRNA sequence.	Mycobacterium leprae	17.088	11-Feb-93
		GB_BA1.MLB1790G	37617	Z14314	Melepie genes rplL, rplB, rplC, end, rpsL, rpsG, 69g, ttr, rpsL, rplC for ribosomal protein L7, RNA polymerase beta subunit, RNA polymerase beta subunit, endonuclease, ribosomal protein S7, ribosomal protein S12, elongation factor G, elongation factor Tu, ribosomal protein S10, ribosomal protein L3 and nrl gene.	Mycobacterium leprae	65.654	23-Feb-95
		GB_BA1.MSGRSLG	1199	L34681	Mycobacterium smegmatis ribosomal protein S12 (rpsL) gene, complete cds.	Mycobacterium smegmatis	76.408	23-Feb-95
		GB_BA1.MLUSTROA	5291	M17788	ribosomal protein S7 (rpsS) gene, complete cds.	Micrococcus luteus	71.599	26-Apr-93
rs601230	489	GB_BA1.MLB1790G	37617	Z14314	M.luteus str optero encoding ribosomal protein S12 (69t or rpsL) ribosomal protein S7 (rpsG) EF-G (fus) and EF-Tu (tuf).	Mycobacterium leprae	65.654	11-Feb-93
		GB_BA1.MLB1790G	37617	Z14314	Melepie genes rplL, rplB, rplC, end, rpsL, rpsG, 69g, ttr, rpsL, rplC for ribosomal protein L7, RNA polymerase beta subunit, RNA polymerase beta subunit, endonuclease, ribosomal protein S7, ribosomal protein S12, elongation factor G, elongation factor Tu, ribosomal protein S10, ribosomal protein L3 and nrl gene.	Mycobacterium leprae	65.654	11-Feb-93
		GB_BA2.ECOLW67_2	110000	U18997	Escherichia coli K-12 chromosome region from 67.4 to 76.0 minutes.	Escherichia coli	37.037	23-Jan-98
		GB_BA1.MATY040	15100	A1021943	Mycobacterium tuberculosis H37Rv complete genome, segment 33/162.	Mycobacterium tuberculosis	65.649	17-Jun-96
rs601268	777	GB_BA1.PR2.HSU2742	37144	X19830	P. rosea ttr, ttr, rpsL and rplC genes.	Planobspora rosea	67.525	19-Nov-90
		GB_BA1.MLDC292	37144	Z28355	Mycobacterium leprae cosmid B2492.	Mycobacterium leprae	67.1211	28-Aug-97
		GB_BA1.MTCT210	38904	Z28355	Mycobacterium tuberculosis H37Rv complete genome, segment 34/162.	Mycobacterium tuberculosis	67.0041	17-Jun-96
rs601287	426	GB_BA1.MTCT210	38904	Z28355	Mycobacterium tuberculosis H37Rv complete genome, segment 34/162.	Mycobacterium tuberculosis	70.423	17-Jun-96
		GB_BA1.MWSG142	35628	AC030005	Mycobacterium tuberculosis sequence from clone 442.	Mycobacterium tuberculosis	35.749	03-DEC-1996
		GB_BA1.MTCT790G	37617	Z14314	Melepie genes rplL, rplB, rplC, end, rpsL, rpsG, 69g, ttr, rpsL, rplC for ribosomal protein L7, RNA polymerase beta subunit, RNA polymerase beta subunit, endonuclease, ribosomal protein S7, ribosomal protein S10, ribosomal protein L3 and nrl gene.	Mycobacterium leprae	69.104	11-Feb-93
rs601305	1889	GB_GSS10.AQ242866	511	AQ242866	HS_Z041_A2_E10_TTC1 Approved Human Genomic Spem Library D	Homo sapiens	38.735	03-OCT-1998
		GB_PR2.HSU29874	6155	U29874	Homo sapiens genomic clone PlateZ241 Col-20 from genomic survey	Homo sapiens	38.731	26-Feb-96
		GB_PR2.HSU29874	6155	U29874	Human F10 ligand gene and F10 ligand alternatively spliced isoform gene, complete cds.	Homo sapiens	36.655	29-Feb-96
rs601334	507	GB_BA1.MT20H10	35890	Z92772	Human F10 ligand gene and F10 ligand alternatively spliced isoform gene, complete cds.	Mycobacterium tuberculosis	66.075	17-Jun-98

TABLE 4: ALIGNMENT RESULTS

GB_BA1.M1B1790G	376/17	Z14314	Meprase genes p1, p2b, p2C, end, p2d, p2e, p2f, p2g, p2h, p2i, p2j, p2k for ribosomal protein L7, RNA polymerase beta subunit, RNA polymerase beta subunit, endonuclease, ribosomal protein S7, ribosomal protein S72, elongation factor G, elongation factor Tu, ribosomal protein S10, ribosomal protein L3 and mkl gene.	Mycobacterium leprae	64,989	11-Feb-93
GB_BA1.MS9RPL	631	D16310	M. bovis p1L gene for ribosomal protein L7/L12.	Mycobacterium bovis	65,598	4-Feb-99
GB_BA1.SCF2A	40105	AL048587	Streptomyces coelicolor cosmid 5F2A.	Streptomyces coelicolor	40,582	24-MAY-1999
GB_BA1.SCA45	43632	AL048455	Streptomyces coelicolor cosmid 6A5.	Streptomyces coelicolor	40,582	24-MAY-1999
GB_EST30.VM02771	289	AV002771	AV002771 Mus musculus C57BL/6J kidney Mus musculus cDNA clone 0610205F04, mRNA sequence.	Mus musculus	41,957	24-May-99
GB_BA1.MT20H10	35680	Z92772	Mycobacterium tuberculosis H37Rv complete genome, segment 31/162.	Mycobacterium tuberculosis	66,508	11-Jun-98
GB_BA1.SQINISG	7235	X72787	S. gressus nusG, gpikAL gene cluster.	Streptomyces griseus	63,177	06-MAY-1998
GB_BA1.STTMBR41	7409	D50624	Streptomyces virginiae V4a gene for NusG like protein, SecE like protein and ribosomal protein, aspartate aminotransferase and adenosine deaminase.	Streptomyces virginiae	63,329	10-Feb-99
GB_BA1.SCE21	38682	AL023197	complete cds.	Mycobacterium coelicolor	65,368	4-Jun-98
GB_BA2.SRZ268111	7860	Z8611	Streptomyces coelicolor cosmid 2E1.	Streptomyces coelicolor	65,368	27-OCT-1999
GB_BA1.MITC214	39691	Z74024	Streptomyces lividans rpsP, rmd, rps, apv, apx, sqz, mat genes and a open reading frame.	Streptomyces lividans	65,368	19-Jun-98
GB_BA1.BS18UB009	208780	Z99172	Mycobacterium tuberculosis H37Rv complete genome, segment 126/162.	Mycobacterium tuberculosis	37,013	19-Jun-98
GB_PL2.GRE132478	16445	AJ132478	Bacillus subtilis complete genome (section 3 of 21) from 1598421 to 1601200.	Bacillus subtilis	44,851	26-Nov-97
GB_GSS4.AQ071168	552	AQ071168	Chlamydomonas reinhardtii ST1 gene, partial.	Chlamydomonas reinhardtii	37,200	29-Sep-99
GB_OV.FR24G11	34607	Z93780	HS_2179_42, B06_77C C1 Approved Human Genomic Sperm Library D Homo sapiens genomic clone Hlae7-129 Cde-12 Row-C, genomic survey sequence.	Homo sapiens	40,541	6-Jul-99
GB_EST36.A1881479	601	A1881479	Fugu rubripes genes encoding carthageny phosphatase synthetase III, myosin light chain, MAP2.	Fugu rubripes	37,036	22-Nov-99
GB_BA2.AE000733	15569	AE000733	600639C3 Y1 606 - Ear tissue cDNA library from Schmidt lab Zea mays cDNA, mRNA sequence.	Zea mays	38,953	21-Jul-99
GB_BA1.SCI24	41825	AL049826	Aquifex aeolicus section 55 of 109 of the complete genome.	Aquifex aeolicus	35,421	25-MAR-1998
GB_BA1.MS9GNAB	40571	L39923	Streptomyces coelicolor cosmid H24.	Streptomyces coelicolor	57,854	11-MAY-1999
GB_BA1.MS9RREP	10430	X92503	Mycobacterium leprae cosmid L222 DNA sequence, 27 CDS features.	Mycobacterium leprae	41,634	29-Apr-97
GB_OV.CC131364	2517	J13164	M. smegmatis origin of replication and genes pmh1, dnaA, dnaN, gnd, recF, gtrB, gtrA.	Mycobacterium smegmatis	39,535	26-Apr-97
GB_INT1.MN0E10841	3733	AJ010841	Cyrtus carpio steary-CoA desaturase mRNA, complete cds.	Cyrtus carpio	36,946	13-Sep-99
GB_INT1.MN0E10842	4044	AJ010842	Drosophila melanogaster rDNA for Dd protein, transcript I, partial.	Drosophila melanogaster	36,768	6-Feb-99
GB_BA1.PDEN0CURF	10425	L02354	Paracoccus denitrificans NADH dehydrogenase (URFA), (NCOB), (NCOB), (URFE), (URFE), (NCO10), (NCO11), (NCO12), (NCO13), and (NCO14) genes, complete cds., biotin [acyl-CoA carboxyl] ligase (bifA) gene, complete cds.	Paracoccus denitrificans	41,304	20-MAY-1993



## TABLE 4: ALIGNMENT RESULTS

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	GB_HJTC2.AC006169	174288	AC006169	Desopellaia neopogon chromosome 3 clone BACRBE99 (Jd89) RPO-98	Desopellaia neopogon	32,737	2-Aug-99
				48.E3 map B1A16164 strain y, on h/w sp. *** SEQUENCING IN PROGRESS ***	uncloned pieces		
ra01663	2691	GB_BA1.MTCY104	6000	X94224	M.smeagmatis gylB and gylA genes	67,476	12-Feb-97
		GB_BA1.MTCY104	39160	Z80323	Mycobacterium tuberculosis H37Rv complete genome, segment 21/82	66,428	17-Jun-98
		GB_BA1.MTCY104	5119	Z80323	M.smeagmatis gylB and gylA genes	67,090	Mycobacterium tuberculosis
ra01688	953	GB_BA1.MTCY104	39160	Z80323	Mycobacterium tuberculosis H37Rv complete genome, segment 21/82	74,397	17-Jun-98
		GB_BA1.MTCY104	10430	X92503	M.smeagmatis origin replication and genes ppnH, dnaA, dnaN, gnd, refC	74,711	26-Aug-97
		GB_BA1.MTCY104	5119	X92503	gylB, gylA		
ra01689	1239	GB_BA1.MTCY104	10430	X92503	M.smeagmatis gylB and gylA genes	63,410	13-MAR-1996
		GB_BA1.MTCY104	5119	X92503	M.smeagmatis origin replication and genes ppnH, dnaA, dnaN, gnd, refC	63,410	26-Aug-97
		GB_BA1.MTCY104	6000	X94224	M.smeagmatis gylB and gylA genes	62,969	12-Feb-97
		GB_BA1.MTCY104	5119	X94077	M.smeagmatis gylB and gylA genes	62,886	13-MAR-1996
ra01718	609	GB_CSS1.ACQ47371	688	ACQ47371	CITB1-E1-256513.1 TR CITB1-E1	36,976	23-Apr-99
		GB_CSS1.ACQ47371	688	ACQ47371	genomic survey sequence		
		GB_CSS1.ACQ47371	264	AV068888	Mus musculus small intestine C57BL/6J adult Mus musculus cDNA Mus musculus	40,000	24-Jun-99
		GB_CSS1.ACQ47371	204008	ACQ08277	done 2010307A09, mRNA sequence	39,130	04-OCT-1999
ra01736	2891	GB_BA1.MTCY104	58280	AF159282	uncloned pieces		
		GB_P12.AF159282	2290	AF159282	Mycobacterium tuberculosis H37Rv complete genome, segment 13/162	38,918	18-Jun-98
		GB_P12.AF159282	483	AF159282	Candida albicans foppy-glutamine synthetase (fops) gene, complete cds	34,684	22-Jun-98
		GB_P12.AF159282	483	AF159282	RPC111-16784.1 JRPC111 Homo sapiens genomic clone RPC11-1.61784, genomic survey sequence	39,005	23-MAR-1999
ra01739	720	GB_PRC3.HS03036	51476	AL021153	Homo sapiens DNA sequence from BAC 6039f on chromosome 22q11.2-12.1, Contains EST and STS	35,484	23-Nov-99
		GB_PRC3.HS03036	1845	UT307	Cane family beta 1 adenylyl receptor (dops1a) gene, complete cds	39,818	31-DEC-1997
		GB_PRC3.HS03036	51476	AL021153	Homo sapiens DNA sequence from BAC 6039f on chromosome 22q11.2-12.1, Contains EST and STS	36,376	23-Nov-99
ra01740	1545	GB_BA1.U0016	42831	U0016	Mycobacterium lipase (lipase) B1937	57,820	01-MAR-1994
		GB_BA1.U0016	1332	UT3935	Pseudomonas aeruginosa glyoxylate (gylC) gene, complete cds	39,322	13-Nov-98
		GB_BA1.U0016	42842	Z87861	Candida albicans foppy-glutamine synthetase (fops) gene, complete cds	35,267	2-Sep-99
ra01772	5061	GB_BA1.U0016	10792	AC001493	Candida albicans foppy-glutamine synthetase (fops) gene, complete cds	46,571	20-Jan-99
		GB_BA1.U0016	555	Z82862	Y26911.1 Scarae melleoocyte ZNH41 Homo sapiens cDNA clone	38,561	4-Jan-96
		GB_BA1.U0016	628	Z82864	Y26911.1 Scarae melleoocyte ZNH41 Homo sapiens cDNA clone	38,118	4-Jan-96
ra01786	807	GB_P11.AB006707	82315	AB006707	IMAC-28603.5, mRNA sequence	37,641	20-Nov-99
		GB_P11.AB006707	157310	AC006324	Arabisopsis italiana genome DNA, chromosome 5, P1 clone: IMC05, complete sequence	36,802	11-Nov-99
		GB_P11.AB006707	2692	UC9166	Arabisopsis italiana DNA repair protein homing (XtRb) mRNA, complete cds	38,808	6-Apr-98
ra01824	945	GB_EST19.AA780333	371	AA780333	w75b10.11 Stratagene mouse skin (#837313) Mus musculus cDNA clone	44,211	23-Jan-98
		GB_EST19.AA780333	34105	AA086807	IMAGE:1228219.5, mRNA sequence	36,374	11-OCT-1999
		GB_EST19.AA780333	34105	AA086807	Homo sapiens genomic region containing hypervariable minisatellites chromosome 8p24.3 of Homo sapiens		

# TABLE 4: ALIGNMENT RESULTS

GB_HITG3.ACO08129.0.110000	AC008129	Homo sapiens clone R0C11-47310. *** SEQUENCING IN PROGRESS ***	130 undated pieces	36.877	24-Jul-99
GB_CSS1.CNS008LB.929	AL005711	Drosophila melanogaster genome survey sequence T7 end of BAC # R0C113.01 of R0C1-98 library from Drosophila melanogaster (full fly), genomic survey sequence.	Drosophila melanogaster	35.589	3-Jun-99
GB_ROMUS.GVCA.153	MB0955	Mouse Ig gamma H-chain D region, 5' flank.	Mus musculus	43.421	27-Apr-93
GB_BAC.AE001014	AE001014	Archaeoglobus fulgidus section 33 of 172 of the complete genome.	Archaeoglobus fulgidus	38.377	15-DEC-1997
GB_ZNC.ACO003070	132171	Drosophila melanogaster, chromosome RR, region 44B-44C, BAC clones BACR00N11 and BACR40A15, complete sequence.	Drosophila melanogaster	34.845	3-Aug-99
GB_ZNC.ACO003070	132171	Drosophila melanogaster, chromosome 4R, region 44B-44C, BAC clones BACR00N11 and BACR40A15, complete sequence.	Drosophila melanogaster	37.697	3-Aug-99
GB_HITG1.HGA.9613	45302	Homo sapiens chromosome 17 clone cosmid 51.5 map p11. *** SEQUENCING IN PROGRESS *** in undated pieces.	Homo sapiens	38.717	11-Nov-98
GB_EST15.MA520493	AA520493	TEST276108.1 T7ME48 Invivo Bradycell cDNA size selected Toxoplasma gondii cDNA clone h276108.1.5, mRNA sequence.	Toxoplasma gondii	38.413	16-Jul-97
GB_GSS10.AQ225693	448	HS_2008_B2_B08_17 ClT Approved Human Genomic Sperm Library D	Homo sapiens	37.374	26-Sep-98
GB_PRC3.ACO05262	44235	Homo sapiens chromosome 19, cosmid 123990, complete sequence.	Homo sapiens	34.345	6-Jul-98
GB_OV.CHKNTC	1185	Chicken cardiac tropomyosin T from cDNA, complete cds	Gallus gallus	41.674	28-Apr-93
GB_OV.CHKNTC	927	Chicken tropomyosin T from cDNA, complete cds	Gallus gallus	40.065	28-Apr-93
GB_OV.CHKNTC	1185	Thermus thermophilus T from cDNA, complete cds	Thermus thermophilus	42.097	28-Apr-93
GB_BA1.ABO16498	566	Thermus thermophilus T from cDNA, complete cds	Thermus thermophilus	53.691	9-Apr-99
GB_PRC4.ACO02531	197900	Homo sapiens chromosome Y, clone 48C.0.8, complete sequence.	Homo sapiens	33.628	13-OCT-1999
GB_HITG3.ACO08019	190459	Mus musculus, *** SEQUENCING IN PROGRESS *** 16 undated pieces.	Mus musculus	35.022	16-Nov-99
GB_BA1.SCE21	38862	Streptomyces coelicolor cosmid 2E1.	Streptomyces coelicolor	66.047	4-Jun-99
GB_BA1.MTC2174	39991	Mycobacterium tuberculosis H37Rv complete genome, segment 120162.	Mycobacterium tuberculosis	66.047	15-OCT-1999
GB_BA2.AFC04101	2162	Streptomyces coelicolor ribosomal protein S2 (rpsB) and elongation factor Ts (efl) genes, complete cds.	Streptomyces coelicolor	65.814	15-OCT-1999
GB_BA1.MSRP.L	648	Mycobacterium smegmatis rplD gene.	Mycobacterium smegmatis	68.833	04-DEC-1987
GB_BA1.MSNGY42	36526	Mycobacterium tuberculosis sequence from clone y42.	Mycobacterium tuberculosis	35.313	03-DEC-1986
GB_BA1.MTC210	36804	Mycobacterium tuberculosis H37Rv complete genome, segment 34162.	Mycobacterium tuberculosis	66.590	17-Jun-98
GB_BA1.MSNTC210	36804	Mycobacterium bovis BCG DNA for ribosomal S10 operon.	Mycobacterium bovis BCG	68.137	04-DEC-1987
GB_BA1.MSNTC210	36804	Mycobacterium tuberculosis H37Rv complete genome, segment 34162.	Mycobacterium tuberculosis	65.952	17-Jun-98
GB_BA1.MSNGY42	36526	Mycobacterium tuberculosis sequence from clone y42.	Mycobacterium tuberculosis	38.765	03-DEC-1986
GB_BA1.MTC210	36804	Mycobacterium tuberculosis H37Rv complete genome, segment 34162.	Mycobacterium tuberculosis	71.157	17-Jun-98
GB_BA1.MSNGY42	36526	Mycobacterium tuberculosis H37Rv complete genome, segment 34162.	Mycobacterium tuberculosis	38.179	03-DEC-1986
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GB_PRC4.ACO04921	150332	Homo sapiens P4C clone DJ089E09 from Tq11.23-q21.1, complete sequence.	Homo sapiens	37.822	28-Aug-97
GB_HITG6.ACO08076	200000	Homo sapiens chromosome 4, *** SEQUENCING IN PROGRESS *** 16 undated pieces.	Homo sapiens	41.880	02-DEC-1999
GB_PRC4.ACO04921	150332	Homo sapiens P4C clone DJ089E09 from Tq11.23-q21.1, complete sequence.	Homo sapiens	37.885	14-Jan-99

[illegible]

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Attorney Docket No.: BGI-130CP

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TABLE 4: ALIGNMENT RESULTS

ra02764	GB_BA1:MYC130 GB_BA1:SC4H2	32514 39400	Z73902 AL022288	Mycobacterium tuberculosis H37Rv complete genome, segment 59762. Streptomyces coelicolor cosmid 4H2.	Mycobacterium tuberculosis Streptomyces coelicolor	39,419 56,729	17-Jun-98 6-Apr-98
ra02819	1070 GB_GSS14:AO54967.4	479	AO54967.4	RP01-11-413C1.TV:RP01-11 Homo sapiens genomic clone RP01-11-413C1, genomic survey sequence.	Homo sapiens	40,705	28-MAY-1998
	GB_GSS14:AO54967.4	479	AO54967.4	RP01-11-413C1.TV:RP01-11 Homo sapiens genomic clone RP01-11-413C1, genomic survey sequence.	Homo sapiens	38,896	28-MAY-1998
ra02826	558 GB_BA1:MY20H10 GB_BA1:SGNUSG GB_BA1:STMGBA1	35980 7235 7409	Z92772 X72787 D50624	Mycobacterium tuberculosis H37Rv complete genome, segment 311162. S. griseus nusG, rplKAL gene cluster. Streptomyces virginiae virA gene for NusG like protein, SecE like protein and ribosomal protein, aspartate aminotransferase and adenosine deaminase, complete cds.	Mycobacterium tuberculosis Streptomyces griseus Streptomyces virginiae	67,387 65,946 65,766	17-Jun-98 06-MAY-1998 10-Feb-99
ra02833	906 EM_PAT11161	3521	E11161	Genomic DNA including an autonomous replication sequences (ars)	Cornebacterium glutamicum	93,343	08-OCT-1997 (Ref. 52, Created)
	GB_BA2:MAU19185	3952	U19185	Mycobacterium avium H9rh1 (rrnH1) and DnaA (dnaA) genes, complete cds, and DnaK (dnaK) gene, partial cds.	Mycobacterium avium	46,333	08-DEC-1998
	GB_BA1:MLUDNAA	4171	MS4006	M. luteus ribonuclease P (rnpA), 50S ribosomal subunit protein L34 (rrnH1), DNA biosynthesis initiation protein (dnaA), and DNA polymerase III beta subunit (dnaN) genes, complete cds.	Micrococcus luteus	46,540	16-Feb-94

2025010622 16:52:20

**DECLARATION, PETITION AND POWER OF ATTORNEY FOR PATENT APPLICATION**

As a below named inventor, I hereby declare that:

My residence, post office address and citizenship are as stated below next to my name,

I believe I am the original, first and sole inventor (if only one name is listed below) or an original, first and joint inventor (if plural names are listed below) of the subject matter which is claimed and for which a patent is sought on the invention entitled:

**CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS INVOLVED  
IN DNA REPLICATION, PROTEIN SYNTHESIS, AND PATHOGENESIS**

the specification of which:

  X   is attached hereto.

           was filed on                                  as Application Serial No.                                 

and was amended on                                   
(if applicable)

I do not know and do not believe that the subject matter of this application was known or used by others in the United States or patented or described in a printed publication in any country before my invention thereof, or patented or described in a printed publication in any country or in public use or on sale in the United States more than one year prior to the date of this application, or first patented or caused to be patented or made the subject of an inventor's certificate by me or my legal representatives or assigns in a country foreign to the United States prior to the date of this application on an application filed more than twelve months (six months if this application is for a design) before the filing of this application; and I acknowledge my duty to disclose information of which I am aware which is material to the examination of this application, that no application for patent or inventor's certificate on the subject matter of this application has been filed by me or my representatives or assigns in any country foreign to the United States, except those identified below, and that I have reviewed and understand the contents of the specification, including the claims as amended by any amendment referred to herein.

I acknowledge the duty to disclose to the Office all information known to me to be material to patentability as defined in Title 37, Code of Federal Regulations, §1.56.



## CLAIM OF BENEFIT OF EARLIER FOREIGN APPLICATION(S)

I hereby claim priority benefits under Title 35, United States Code, §119 of any foreign application(s) for patent or inventor's certificate listed below, and have also identified below any foreign application(s) for patent or inventor's certificate filed by me on the same subject matter having a filing date before that of the application(s) from which priority is claimed.

Check one:

☒ no such applications have been filed.

☐ such applications have been filed as follows

EARLIEST FOREIGN APPLICATION(S), IF ANY, FILED WITHIN 12 MONTHS  
(6 MONTHS FOR DESIGN) PRIOR TO THIS U.S. APPLICATION

Country	Application Number	Date of Filing (month,day,year)	Priority Claimed Under 35 USC 119
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			<input type="checkbox"/> Yes <input type="checkbox"/> No

ALL FOREIGN APPLICATION(S), IF ANY FILED MORE THAN 12 MONTHS  
(6 MONTHS FOR DESIGN) PRIOR TO THIS U.S. APPLICATION


## CLAIM FOR BENEFIT OF U.S. PROVISIONAL APPLICATION(S)

I hereby claim the benefit under 35 U.S.C. §119(e) of any United States provisional application(s) listed below.

60/144,448

(Application Serial No.)

July 16, 1999

(Filing Date)

60/149,402

(Application Serial No.)

August 17, 1999

(Filing Date)

## CLAIM FOR BENEFIT OF EARLIER U.S./PCT APPLICATION(S)

I hereby claim the benefit under Title 35, United States Code, §120 of any earlier United States application(s) or PCT international application(s) designating the United States listed below and, insofar as the subject matter of each of the claims of this application is not disclosed in the earlier application(s) in the manner provided by the first paragraph of Title 35, United States Code, §112, I acknowledge the duty to disclose to the Office all information known to me to be material to patentability as defined in Title 37, Code of Federal Regulations, §1.56 which became available between the filing date(s) of the earlier application(s) and the national or PCT international filing date of this application. As to subject matter of this application which is common to my earlier application(s), if any, described below, I do not know and do not believe that the same was known or used by others in the United States or patented or described in a printed publication in any country before my invention thereof, or patented or described in a printed publication in any country or in public use or on sale in the United States more than one year prior to the date(s) of said earlier application(s), or first patented or caused to be patented or made the subject of an inventor's certificate by me or my legal representatives or assigns in a country foreign to the United States prior to the date(s) of said earlier application(s) on an application filed more than twelve months (six months if this application is for a design) before the filing of said earlier application(s); and I acknowledge that no application for patent or inventor's certificate on said subject matter has been filed by me or my representatives or assigns in any country foreign to the United States except those identified herein.

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 (Application Serial No.)

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 (Filing Date)

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 (Status)  
 (patented,pending,aband.)

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 (Application Serial No.)

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 (Filing Date)

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 (Status)  
 (patented,pending,aband.)

POWER OF ATTORNEY: As a named inventor, I hereby appoint the following attorneys and/or agents to prosecute this application and transact all business in the Patent and Trademark Office connected therewith.

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Anthony A. Laurentano	Reg. No. 38,220	David J. Rikkers	Reg. No. 43,882
Jane E. Remillard	Reg. No. 38,872	Chi Suk Kim	Reg. No. 42,728
Jeremiah Lynch	Reg. No. 17,425	Maria Laccotripe Zacharakis	Limited Recognition
Kevin J. Canning	Reg. No. 35,470		Under 37 C.F.R. § 10.9(b)
David A. Lane, Jr.	Reg. No. 39,261	Debra J. Milasincic	Reg. No. P46,931
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Direct Telephone Calls to: (name and telephone number)

Giulio A. DeConti, Jr., Esq., (617) 227-7400

Wherefore I petition that letters patent be granted to me for the invention or discovery described and claimed in the attached specification and claims, and hereby subscribe my name to said specification and claims and to the foregoing declaration, power of attorney, and this petition.

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful false statements may jeopardize the validity of the application or any patent issued thereon.

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 Kroger, Burkhard  
 Schroder, Hartwig  
 Zelder, Oskar  
 Haberhauer, Gregor  
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&lt;213&gt; Corynebacterium glutamicum

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1315

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Phe Ile Glu Arg Lys Phe Thr Gly Asp Asp Ala His His Asn Leu Leu	345	350	355	
cag cgt cct cgc gat gtt cca gtc cgc acc tca ctc ggt gtc atg gcg				1219
Gln Arg Pro Arg Asp Val Pro Val Arg Thr Ser Leu Gly Val Met Ala	360	365	370	
ctt gtc ttc tac atc ctg ctt acc gtt tct ggt ggt aac gat gtt tac				1267
Leu Val Phe Tyr Ile Leu Thr Val Ser Gly Gly Asn Asp Val Tyr	375	380	385	
gca atg cag ttc cat gtt tca ctg aac gcg atg acc tgg atc ggt cgt				1315
Ala Met Gln Phe His Val Ser Leu Asn Ala Met Thr Trp Ile Gly Arg	390	395	400	405
atc ggc ctc atc gtt gga cca gct att gca tac ttc atc act tac cga				1363
Ile Gly Leu Ile Val Gly Pro Ala Ile Ala Tyr Phe Ile Thr Tyr Arg	410	415	420	
ctg tgc atc ggc ttg cag cgc tct gac cgc gag gtc ctg gag cac ggc				1411
Leu Cys Ile Gly Leu Gln Arg Ser Asp Arg Glu Val Leu Glu His Gly	425	430	435	
atc gag acc ggt atc atc aag cag atg cca aat ggt gcc ttc att gaa				1459
Ile Glu Thr Gly Ile Ile Lys Gln Met Pro Asn Gly Ala Phe Ile Glu	440	445	450	
gtt cac cag cca ctt ggc cca gtt gat gac cat ggt cac cca atc cca				1507
Val His Gln Pro Leu Gly Pro Val Asp Asp His Gly His Pro Ile Pro	455	460	465	
ctg cca tac gct ggc gct gcg gtt cca aag cag atg aac cag ctt ggt				1555
Leu Pro Tyr Ala Gly Ala Ala Val Pro Lys Gln Met Asn Gln Leu Gly	470	475	480	485
tac gct gag gtt gaa acc cgc ggt gga ttc ttc gga cct gat cca gaa				1603
Tyr Ala Glu Val Glu Thr Arg Gly Gly Phe Phe Gly Pro Asp Pro Glu	490	495	500	
gac atc cgt gcg aag gct aag gaa att gag cac gca aac cac att gag				1651
Asp Ile Arg Ala Lys Ala Lys Glu Ile Glu His Ala Asn His Ile Glu	505	510	515	
gaa gcg aac act ctt cgt gca ctc aac gag gca aac att gag cgt gac				1699
Glu Ala Asn Thr Leu Arg Ala Leu Asn Glu Ala Asn Ile Glu Arg Asp	520	525	530	
aag aat gag ggc aag aac tagtttctag gacttcattct ctg				1740
Lys Asn Glu Gly Lys Asn	535			

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&lt;211&gt; 539

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 12

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Ala Ser Gly Ile Arg Arg Gln Ile Asn Lys Val Phe Pro Thr His Trp  
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Ser Phe Met Leu Gly Glu Ile Ala Leu Tyr Ser Phe Ile Val Leu Leu  
 35 40 45

Leu Thr Gly Val Tyr Leu Thr Leu Phe Phe Asp Pro Ser Ile Thr Lys  
 50 55 60

Val Ile Tyr Asp Gly Gly Tyr Leu Pro Leu Asn Gly Val Glu Met Ser  
 65 70 75 80

Arg Ala Tyr Ala Thr Ala Leu Asp Ile Ser Phe Glu Val Arg Gly Gly  
 85 90 95

Leu Phe Ile Arg Gln Met His His Trp Ala Ala Leu Leu Phe Val Val  
 100 105 110

Ser Met Leu Val His Met Leu Arg Ile Phe Phe Thr Gly Ala Phe Arg  
 115 120 125

Arg Pro Arg Glu Ala Asn Trp Ile Ile Gly Val Val Leu Ile Ile Leu  
 130 135 140

Gly Met Ala Glu Gly Phe Met Gly Tyr Ser Leu Pro Asp Asp Leu Leu  
 145 150 155 160

Ser Gly Val Gly Leu Arg Ile Met Ser Ala Ile Ile Val Gly Leu Pro  
 165 170 175

Ile Ile Gly Thr Trp Met His Trp Leu Ile Phe Gly Gly Asp Phe Pro  
 180 185 190

Ser Asp Leu Met Leu Asp Arg Phe Tyr Ile Ala His Val Leu Ile Ile  
 195 200 205

Pro Ala Ile Leu Leu Gly Leu Ile Ala Ala His Leu Ala Leu Val Trp  
 210 215 220

Tyr Gln Lys His Thr Gln Phe Pro Gly Ala Gly Arg Thr Glu Asn Asn  
 225 230 235 240

Val Ile Gly Ile Arg Ile Met Pro Leu Phe Ala Val Lys Ala Val Ala  
 245 250 255

Phe Gly Leu Ile Val Phe Gly Phe Leu Ala Leu Leu Ala Gly Val Thr  
 260 265 270

Thr Ile Asn Ala Ile Trp Asn Leu Gly Pro Tyr Asn Pro Ser Gln Val  
 275 280 285

Ser Ala Gly Ser Gln Pro Asp Val Tyr Met Leu Trp Thr Asp Gly Ala  
 290 295 300

Ala Arg Val Met Pro Ala Trp Glu Leu Tyr Leu Gly Asn Tyr Thr Ile  
 305 310 315 320

Pro Ala Val Phe Trp Val Ala Val Met Leu Gly Ile Leu Val Val Leu

325 330 335

Leu Val Thr Tyr Pro Phe Ile Glu Arg Lys Phe Thr Gly Asp Asp Ala  
340 345 350

His His Asn Leu Leu Gln Arg Pro Arg Asp Val Pro Val Arg Thr Ser  
355 360 365

Leu Gly Val Met Ala Leu Val Phe Tyr Ile Leu Leu Thr Val Ser Gly  
370 375 380

Gly Asn Asp Val Tyr Ala Met Gln Phe His Val Ser Leu Asn Ala Met  
385 390 395 400

Thr Trp Ile Gly Arg Ile Gly Leu Ile Val Gly Pro Ala Ile Ala Tyr  
405 410 415

Phe Ile Thr Tyr Arg Leu Cys Ile Gly Leu Gln Arg Ser Asp Arg Glu  
420 425 430

Val Leu Glu His Gly Ile Glu Thr Gly Ile Ile Lys Gln Met Pro Asn  
435 440 445

Gly Ala Phe Ile Glu Val His Gln Pro Leu Gly Pro Val Asp Asp His  
450 455 460

Gly His Pro Ile Pro Leu Pro Tyr Ala Gly Ala Ala Val Pro Lys Gln  
465 470 475 480

Met Asn Gln Leu Gly Tyr Ala Glu Val Glu Thr Arg Gly Gly Phe Phe  
485 490 495

Gly Pro Asp Pro Glu Asp Ile Arg Ala Lys Ala Lys Glu Ile Glu His  
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Ala Asn His Ile Glu Glu Ala Asn Thr Leu Arg Ala Leu Asn Glu Ala  
515 520 525

Asn Ile Glu Arg Asp Lys Asn Glu Gly Lys Asn  
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Met Ser Leu Ser Ile  
1 5

agt ttt cat aaa att gca ctc tct gcc acc acc ttg ctt ggc gct gtc 163  
Ser Phe His Lys Ile Ala Leu Ser Ala Thr Thr Leu Leu Gly Ala Val



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gca atc tct gcc tgt gcg cta gta act caa gca cct cct att aac gca				211
Ala Ile Ser Ala Cys Ala Leu Val Thr Gln Ala Pro Pro Ile Asn Ala	25	30	35	
gcc ccg gtt act gcc agc agc tca tta agc ttc acc ctc gac ctg gcc				259
Ala Pro Val Thr Gly Ser Ser Leu Ser Phe Thr Leu Asp Leu Gly	40	45	50	
acc acc acc cct acc agc atc gac aca gta aaa ctc act cag caa gca				307
Thr Thr Thr Pro Thr Ser Ile Asp Thr Val Lys Leu Thr Gln Gln Ala	55	60	65	
caa aat caa gcg gca cca cgc gtt gca gcg agc ctg gtg cgc gtg gtt				355
Gln Asn Gln Ala Ala Pro Arg Val Ala Ala Ser Leu Val Arg Val Val	70	75	80	85
gac gcc gac acc att gtc gtg aac tat cag ggt gct cag aaa act gtt				403
Asp Gly Asp Thr Ile Val Val Asn Tyr Gln Gly Ala Gln Lys Thr Val	90	95	100	
cgt atg atc ggt att gat tcc ccc gaa acc aaa cac ccc acc aag cct				451
Arg Met Ile Gly Ile Asp Ser Pro Glu Thr Lys His Pro Thr Lys Pro	105	110	115	
gtg gcc ttc tac gga cca gaa tct tca cag aat ctc acc acc atg ctg				499
Val Gly Phe Tyr Gly Pro Glu Ser Ser Gln Asn Leu Thr Thr Met Leu	120	125	130	
cgc ggt gcc acc atc aca cta gaa ttt gat tcc acc caa gcc cgc gaa				547
Arg Gly Ala Thr Ile Thr Leu Glu Phe Asp Ser Thr Gln Ala Arg Glu	135	140	145	
gat caa tac gga cgc ctg ctt gct tat gtc tgg tac acc aag gcc gat				595
Asp Gln Tyr Gly Arg Leu Leu Ala Tyr Val Trp Tyr Thr Lys Gly Asp	150	155	160	165
agc ggt ctt aag ctt gcc aat ttg gaa caa att gcc tca gcc tct gct				643
Ser Gly Leu Lys Leu Ala Asn Leu Glu Gln Ile Ala Ser Gly Ser Ala	170	175	180	
gct gaa tac agc ttc gac acc cgc tac aac cac cgc aat att ttc cta				691
Ala Glu Tyr Ser Phe Asp Thr Arg Tyr Asn His Arg Asn Ile Phe Leu	185	190	195	
cgt gca caa acc ctt gcc aag gca agc agt cta ggt atg tgg ggt				736
Arg Ala Gln Thr Leu Ala Lys Ala Ser Ser Leu Gly Met Trp Gly	200	205	210	
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Pro Pro Ile Asn Ala Ala Pro Val Thr Gly Ser Ser Ser Leu Ser Phe  
35 40 45

Thr Leu Asp Leu Gly Thr Thr Thr Pro Thr Ser Ile Asp Thr Val Lys  
50 55 60

Leu Thr Gln Gln Ala Gln Asn Gln Ala Ala Pro Arg Val Ala Ala Ser  
65 70 75 80

Leu Val Arg Val Val Asp Gly Asp Thr Ile Val Val Asn Tyr Gln Gly  
85 90 95

Ala Gln Lys Thr Val Arg Met Ile Gly Ile Asp Ser Pro Glu Thr Lys  
100 105 110

His Pro Thr Lys Pro Val Gly Phe Tyr Gly Pro Glu Ser Ser Gln Asn  
115 120 125

Leu Thr Thr Met Leu Arg Gly Ala Thr Ile Thr Leu Glu Phe Asp Ser  
130 135 140

Thr Gln Ala Arg Glu Asp Gln Tyr Gly Arg Leu Leu Ala Tyr Val Trp  
145 150 155 160

Tyr Thr Lys Gly Asp Ser Gly Leu Lys Leu Ala Asn Leu Glu Gln Ile  
165 170 175

Ala Ser Gly Ser Ala Ala Glu Tyr Ser Phe Asp Thr Arg Tyr Asn His  
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Arg Asn Ile Phe Leu Arg Ala Gln Thr Leu Ala Lys Ala Ser Ser Leu  
195 200 205

Gly Met Trp Gly  
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Met Val Ala Arg Arg  
1 5

aga ctg gac gca gaa ctt gtt cgt cga aag atc gca cga tca agg gaa 163  
Arg Leu Asp Ala Glu Leu Val Arg Arg Lys Ile Ala Arg Ser Arg Glu  
10 15 20

cac His	gcg Ala	ggt Val	gaa Glu	atg Met	atc Ile	cgc Arg	ggt Gly	cgg Arg	cgc Arg	gtc Val	ttt Phe	ggt Val	gca Ala	gga Gly	atg Met	211
ctt Leu	gct Ala	tta Leu	aag Lys	ccc Pro	gca Ala	aca Thr	gtc Val	gtg Val	gaa Glu	cca Pro	gag Glu	gtg Val	tct Ser	att Ile	cgt Arg	259
gtg Val	gaa Glu	gaa Glu	gat Asp	gct Ala	agt Ser	gaa Glu	gat Asp	tgg Trp	gca Ala	tcc Ser	cgc Arg	ggt Gly	gcg Ala	cac His	aag Lys	307
ctt Leu	ctt Leu	ggt Gly	gcg Ala	ctg Leu	gaa Glu	tct Ser	ttt Phe	gag Glu	ccc Pro	ttg Leu	ggg Gly	ctc Leu	aag Lys	gtc Val	aag Lys	355
ggc Gly	cgt Arg	cgc Arg	gtg Val	cta Leu	gat Asp	gcc Ala	ggc Gly	gct Ala	tcg Ser	aca Thr	ggc Gly	gga Gly	ttt Phe	acg Thr	gac Asp	403
gtg Val	ttg Leu	cta Leu	cgt Leu	cga Arg	gaa Glu	gcg Ala	tct Ser	gaa Glu	gta Val	gtg Val	gca Ala	gta Val	gac Val	gtg Val	ggc Gly	451
tac Tyr	gga Gly	cag Gln	ctt Leu	att Ile	tgg Trp	cgc Arg	ctg Leu	caa Gln	aac Asn	gac Asp	gac Asp	cgc Asp	gtg Val	cgc Arg	gtg Val	499
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gaa Glu	tgc Cys	gac Asp	atg Met	atg Met	gtg Val	ggc Gly	gat Asp	ctc Leu	tca Ser	ttt Phe	att Ile	tcg Ser	ctt Leu	aaa Lys	ctc Leu	595
acg Thr	ttg Leu	ccg Pro	gcg Ala	atc Ile	gcc Ala	aag Lys	gtc Val	cta Leu	agc Ser	gac Asp	ggc Gly	gct Ala	gat Asp	cta Leu	tta Leu	643
ccc Pro	atg Met	gtc Val	aag Lys	cca Pro	caa Gln	ttt Phe	gaa Glu	gga Val	aaa Gly	gac Lys	cga Asp	ttg Arg	ggc Leu	agt Gly	ser	691
ggc Gly	ggc Gly	gtg Val	gtg Val	cgc Arg	tca Ser	cca Glu	gag Glu	ttg Leu	cgc Arg	gca Ala	gaa Glu	ggt Val	acc Thr	gcg Val	gat Asp	739
gtc Val	gcg Ala	aaa Lys	ttt Phe	gcg Ala	gcc Ala	act Thr	ttg Leu	ggc Gly	ctg Leu	agc Ser	ttg Leu	aag Lys	cat His	ggt Val	ggt Val	787
gca Ala	tcc Ser	ccg Pro	ctg Leu	ccc Pro	ggc Gly	ccg Pro	tca Ser	ggc Gly	aac Asn	gta Val	gaa Glu	tac Tyr	ttc Phe	ctg Leu	tgg Trp	835
ctg Leu	gtt Val	aaa Lys	gat Asp	ggt Gly	ggc Gly	gct Ala	tca Ser	atg Met	ccg Pro	gat Asp	gac Asp	cag Gln	caa Gln	ttg Leu	tcg Ser	883

gca atg att gac acg gct gta aag gaa ggt ccg caa taatgactgc 929  
Ala Met Ile Asp Thr Ala Val Lys Glu Gly Pro Gln  
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acccacgaac gct 942

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20 25 30

Phe Val Ala Gly Met Leu Ala Leu Lys Pro Ala Thr Val Val Glu Pro  
35 40 45

Glu Val Ser Ile Arg Val Glu Glu Asp Ala Ser Glu Asp Trp Ala Ser  
50 55 60

Arg Gly Ala His Lys Leu Leu Gly Ala Leu Glu Ser Phe Glu Pro Leu  
65 70 75 80

Gly Leu Lys Val Lys Gly Arg Arg Val Leu Asp Ala Gly Ala Ser Thr  
85 90 95

Gly Gly Phe Thr Asp Val Leu Leu Arg Arg Glu Ala Ser Glu Val Val  
100 105 110

Ala Val Asp Val Gly Tyr Gly Gln Leu Ile Trp Arg Leu Gln Asn Asp  
115 120 125

Asp Arg Val Arg Val Val Asp Arg Thr Asn Ile Arg Tyr Met Thr Leu  
130 135 140

Glu Asp Thr Gly Gly Glu Cys Asp Met Met Val Gly Asp Leu Ser Phe  
145 150 155 160

Ile Ser Leu Lys Leu Thr Leu Pro Ala Ile Ala Lys Val Leu Ser Asp  
165 170 175

Gly Ala Asp Leu Leu Pro Met Val Lys Pro Gln Phe Glu Val Gly Lys  
180 185 190

Asp Arg Leu Gly Ser Gly Gly Val Val Arg Ser Pro Glu Leu Arg Ala  
195 200 205

Glu Val Thr Ala Asp Val Ala Lys Phe Ala Ala Thr Leu Gly Leu Ser

Leu Lys His Val Val Ala Ser Pro Leu Pro Gly Pro Ser Gly Asn Va  
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Glu Tyr Phe Leu Trp Leu Val Lys Asp Gly Gly Ala Ser Met Pro Asn  
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Gln

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cgc gtc ttt gtt gca gga atg ctt gct tta aag ccc gca aca gtc gtg	Arg Val Phe Val Ala Gly Met Leu Ala Leu Lys Pro Ala Thr Val Val 10 15 20	163
gaa cca gag gtg tct att cgt gtg gaa gaa gat gct agt gaa gat tgg	Glu Pro Glu Val Ser Ile Arg Val Glu Glu Asp Ala Ser Glu Asp Trp 25 30 35	211
gca tcc cgc ggt gcg cac aag ctt ctt ggt gcg ctg gaa tct ttt gag	Ala Ser Arg Gly Ala His Lys Leu Leu Gly Ala Leu Glu Ser Phe Glu 40 45 50	259
ccc ttg ggg ctc aag gtc aag ggc cgt cgc gtg cta gat gcc ggc gct	Pro Leu Gly Leu Lys Val Lys Gly Arg Arg Val Leu Asp Ala Gly Ala 55 60 65	307
tcg aca ggc gga ttt acg gac gtg ttg cta cgt cga gaa gcg tct gaa	Ser Thr Gly Gly Phe Thr Asp Val Leu Leu Arg Arg Glu Ala Ser Glu 70 75 80 85	355
gta gtg gca gta gac gtg ggc tac gga cag ctt att tgg cgc ctg caa	Val Val Ala Val Asp Val Gly, Tyr Gly Gln Leu Ile Trp Arg Leu Gln 90 95 100	403
aac gac gac cgc gtg cgc gtg gtg gac cgc acc aac atc aga tac atg	Asn Asp Asp Arg Val Arg Val Val Asp Arg Thr Asn Ile Arg Tyr Met 105 110 115	451
acg ctg gaa gac acc ggc gga gaa tgc gac atg atg gtg ggc gat ctc	Thr Leu Glu Asp Thr Gly Gly Glu Cys Asp Met Met Val Gly Asp Leu 120 125 130	499
tca ttt att tcg ctt aaa ctc acg ttg ccg gcg atc gcc aag gtc cta	Ser Phe Ile Ser Leu Lys Leu Thr Leu Pro Ala Ile Ala Lys Val Leu 135 140 145	547
agc gac ggc gct gat cta tta ccc atg gtc aag cca caa ttt gaa gtc		595

Ser Asp Gly Ala Asp Leu Leu Pro Met Val Lys Pro Gln Phe Glu Val  
 150 155 160 165

gga aaa gac cga ttg ggc agt ggc ggc gtg gtg cgc tca cca gag ttg 643  
 Gly Lys Asp Arg Leu Gly Ser Gly Gly Val Val Arg Ser Pro Glu Leu  
 170 175 180

cgc gca gaa gtt acc gcg gat gtc gcg aaa ttt gcg gcc act ttg ggc 691  
 Arg Ala Glu Val Thr Ala Asp Val Ala Lys Phe Ala Ala Thr Leu Gly  
 185 190 195

ctg agc ttg aag cat gtt gtt gca tcc ccg ctg ccc ggc ccg tca ggc 739  
 Leu Ser Leu Lys His Val Val Ala Ser Pro Leu Pro Gly Pro Ser Gly  
 200 205 210

aac gta gaa tac ttc ctg tgg ctg gtt aaa gat ggt ggc gct tca atg 787  
 Asn Val Glu Tyr Phe Leu Trp Leu Val Lys Asp Gly Gly Ala Ser Met  
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ccg gat gac cag caa ttg tcg gca atg att gac acg gct gta aag gaa 835  
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 Gly Pro Gln

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Ala Ser Glu Asp Trp Ala Ser Arg Gly Ala His Lys Leu Leu Gly Ala  
 35 40 45

Leu Glu Ser Phe Glu Pro Leu Gly Leu Lys Val Lys Gly Arg Arg Val  
 50 55 60

Leu Asp Ala Gly Ala Ser Thr Gly Gly Phe Thr Asp Val Leu Leu Arg  
 65 70 75 80

Arg Glu Ala Ser Glu Val Val Ala Val Asp Val Gly Tyr Gly Gln Leu  
 85 90 95

Ile Trp Arg Leu Gln Asn Asp Asp Arg Val Arg Val Val Asp Arg Thr  
 100 105 110

Asn Ile Arg Tyr Met Thr Leu Glu Asp Thr Gly Gly Glu Cys Asp Met  
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Met Val Gly Asp Leu Ser Phe Ile Ser Leu Lys Leu Thr Leu Pro Ala  
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Ile Ala Lys Val Leu Ser Asp Gly Ala Asp Leu Leu Pro Met Val Lys  
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Pro Gln Phe Glu Val Gly Lys Asp Arg Leu Gly Ser Gly Gly Val Val  
 165 170 175

Arg Ser Pro Glu Leu Arg Ala Glu Val Thr Ala Asp Val Ala Lys Phe  
 180 185 190

Ala Ala Thr Leu Gly Leu Ser Leu Lys His Val Val Ala Ser Pro Leu  
 195 200 205

Pro Gly Pro Ser Gly Asn Val Glu Tyr Phe Leu Trp Leu Val Lys Asp  
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Gly Gly Ala Ser Met Pro Asp Asp Gln Gln Leu Ser Ala Met Ile Asp  
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Thr Ala Val Lys Glu Gly Pro Gln  
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 Leu Leu Thr Ala Val  
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ttg tct tta att gct ggt ttg gtg gtc att ggg gtg atc atc gtc ctc 163  
 Leu Ser Leu Ile Ala Gly Leu Val Val Ile Gly Val Ile Ile Val Leu  
 10 15 20

aac gga tat ttt gtg gct cag gaa ttt gcc tac atg tcc gtt gat cga 211  
 Asn Gly Tyr Phe Val Ala Gln Glu Phe Ala Tyr Met Ser Val Asp Arg  
 25 30 35

aat gag ctg cga gct ctc gct gac tct gga gat aag aag gct cgt cgc 259  
 Asn Glu Leu Arg Ala Leu Ala Asp Ser Gly Asp Lys Lys Ala Arg Arg  
 40 45 50

gct ctc agc atc act aag cgc aca tcc ttt atg ctt tct ggt gcg caa 307  
 Ala Leu Ser Ile Thr Lys Arg Thr Ser Phe Met Leu Ser Gly Ala Gln  
 55 60 65

ttg ggt atc acc gtc acc gga ctt ttg gtg ggt ttt gtg gcc gaa cct 355  
 Leu Gly Ile Thr Val Thr Gly Leu Leu Val Gly Phe Val Ala Glu Pro  
 70 75 80 85

ctg gtg ggt aac cgc tta ggt gtt ctg cta gga ggg gtg ggg gtt ccc 403  
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Ala Ala Val Ser Ile Ser Val Gly Thr Val Leu Ala Leu Ala Ile Ser			
105	110	115	
acg gtt gtc caa atg att ttt ggt gaa ctc ttt cct aag aac tac acc			499
Thr Val Val Gln Met Ile Phe Gly Glu Leu Phe Pro Lys Asn Tyr Thr			
120	125	130	
ctt gcc acg cgg ttg aag tct gcg ctg gcg ctt gcg cct tgg acc acg			547
Leu Ala Thr Pro Leu Lys Ser Ala Leu Ala Leu Ala Pro Ser Thr Thr			
135	140	145	
tgg tat ttg aaa cct cgc tgg ttg gtt gat cac att ctt tgattttgca			596
Trp Tyr Leu Lys Pro Arg Trp Leu Val Asp His Ile Leu			
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tccaacgcat tgc			609

&lt;210&gt; 20

&lt;211&gt; 162

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

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Val	Ile	Ile	Val	Leu	Asn	Gly	Tyr	Phe	Val	Ala	Gln	Glu	Phe	Ala	Tyr
	20							25					30		

Met	Ser	Val	Asp	Arg	Asn	Glu	Leu	Arg	Ala	Leu	Ala	Asp	Ser	Gly	Asp
	35					40						45			

Lys	Lys	Ala	Arg	Arg	Ala	Leu	Ser	Ile	Thr	Lys	Arg	Thr	Ser	Phe	Met
	50				55						60				

Leu	Ser	Gly	Ala	Gln	Leu	Gly	Ile	Thr	Val	Thr	Gly	Leu	Leu	Val	Gly
65				70					75					80	

Phe	Val	Ala	Glu	Pro	Leu	Val	Gly	Asn	Ala	Leu	Gly	Val	Leu	Leu	Gly
			85					90					95		

Gly	Val	Gly	Val	Pro	Ala	Ala	Val	Ser	Ile	Ser	Val	Gly	Thr	Val	Leu
			100					105					110		

Ala	Leu	Ala	Ile	Ser	Thr	Val	Val	Gln	Met	Ile	Phe	Gly	Glu	Leu	Phe
		115					120						125		

Pro	Lys	Asn	Tyr	Thr	Leu	Ala	Thr	Pro	Leu	Lys	Ser	Ala	Leu	Ala	Leu
	130				135					140					

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Ile Leu



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 <223> RXN03148

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 Met Val Ile Asn Phe 5  
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 att att tta ttt ttg atg att gca att act tca ttt ttt gta gca agt 163  
 Ile Ile Leu Phe Leu Met Ile Ala Ile Thr Ser Phe Phe Val Ala Ser 20  
 10 15  
 gaa ttt gct tta gtg aaa atc aga cga tca aga ttg gaa caa cta gaa 211  
 Glu Phe Ala Leu Val Lys Ile Arg Arg Ser Arg Leu Glu Gln Leu Glu 35  
 25 30  
 aag gaa aat gta aag aac gcc aag cta gct ctt cat gtt aca cac cat 259  
 Lys Glu Asn Val Lys Asn Ala Lys Leu Ala Leu His Val Thr His His 50  
 40 45  
 tta gat aac tat tta tca gct agt caa tta gga att acg cta acc ggt 307  
 Leu Asp Asn Tyr Leu Ser Ala Ser Gln Leu Gly Ile Thr Leu Thr Gly 65  
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 ttg atc atc ggg tgg gtc ggt gaa gga tct gtc gcg gct tta cta gaa 355  
 Leu Ile Ile Gly Trp Val Gly Glu Gly Ser Val Ala Ala Leu Leu Glu 85  
 70 75 80  
 cca gtg atc ggt aaa cta cct ttt agt tcg gct att agc agt aca atc 403  
 Pro Val Ile Gly Lys Leu Pro Phe Ser Ser Ala Ile Ser Ser Thr Ile 100  
 90 95  
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 Ser Val Ala Leu Gly Phe Ile Leu Val Thr Val Tyr Arg Cys Gly Tyr 115  
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 Trp Arg Thr Ala Ser 120

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 <212> PRT  
 <213> *Corynebacterium glutamicum*

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 Phe Phe Val Ala Ser Glu Phe Ala Leu Val Lys Ile Arg Arg Ser Arg  
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Leu Glu Gln Leu Glu Lys Glu Asn Val Lys Asn Ala Lys Leu Ala Leu  
 35 40 45

His Val Thr His His Leu Asp Asn Tyr Leu Ser Ala Ser Gln Leu Gly  
 50 55 60

Ile Thr Leu Thr Gly Leu Ile Ile Gly Trp Val Gly Glu Gly Ser Val  
 65 70 75 80

Ala Ala Leu Leu Glu Pro Val Ile Gly Lys Leu Pro Phe Ser Ser Ala  
 85 90 95

Ile Ser Ser Thr Ile Ser Val Ala Leu Gly Phe Ile Leu Val Thr Val  
 100 105 110

Tyr Arg Cys Gly Tyr Trp Arg Thr Ala Ser  
 115 120

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 <211> 846  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (101)..(823)  
 <223> RXN00562

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 Met Asp Ala Asp Pro  
 1 5

ctg att gag gat gac gtt agt gga gca gaa gta aaa gat agt tcg gat 163  
 Leu Ile Glu Asp Asp Val Ser Gly Ala Glu Val Lys Asp Ser Ser Asp  
 10 15 20

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 Glu Pro Leu Leu Ala Leu Thr Arg Tyr Val Phe Asp Arg Gly Glu Arg  
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cca gtt act cgt gga ctg ttc cac cag gtt gcg gcc att ttg agt att 259  
 Pro Val Thr Arg Gly Leu Phe His Gln Val Ala Ala Ile Leu Ser Ile  
 40 45 50

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 Val Ser Gly Ser Val Leu Ser Thr Tyr Ala Trp Met Glu Leu Val Trp  
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tgg cag gcg cta ggt gtc atg gtg tac gcc ttg gcc atg ctg gga ctg 355  
 Trp Gln Ala Leu Gly Val Met Val Tyr Ala Leu Ala Met Leu Gly Leu  
 70 75 80 85

ttt gct gtc tct gcg gcg tat cac cga gga ccg tgg cgt cga ttg cac 403  
 Phe Ala Val Ser Ala Ala Tyr His Arg Gly Pro Trp Arg Arg Leu His  
 90 95 100

acc gtg gcg tgg tgg cgc aaa gct gat cac tcc acc atc gcg gtg ttt 451  
 Thr Val Ala Trp Trp Arg Lys Ala Asp His Ser Thr Ile Ala Val Phe  
 105 110 115

atc gca gca acc tat acg cca ctg tgc ttg atc gtc tta gag ccc ggt 499  
 Ile Ala Ala Thr Tyr Thr Pro Leu Cys Leu Ile Val Leu Glu Pro Gly  
 120 125 130

acc gca gca tgg atg tta ggt att gcg tgg gtt ggt gcc att gac agc 547  
 Thr Ala Ala Trp Met Leu Gly Ile Ala Trp Val Gly Ala Ile Asp Ser  
 135 140 145

gtg atc atg aac atg gtg tgg atc aat cac cca cga tgg ctc agc gtg 595  
 Val Ile Met Asn Met Val Trp Ile Asn His Pro Arg Trp Leu Ser Val  
 150 155 160 165

ctg gtc tac ttg gcc ttg gga tgg ctc att gtg cca ctt gtc cct caa 643  
 Leu Val Tyr Leu Ala Leu Gly Trp Leu Ile Val Pro Leu Val Pro Gln  
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ttg tgg tct ggt gct ggc ccc aca gtg gtg tgg ctc ctg ctg gcc gga 691  
 Leu Trp Ser Gly Ala Gly Pro Thr Val Val Trp Leu Leu Ala Gly  
 185 190 195

ggc atc gtc tac agc gtt ggc gcg ttg gtg tac ggc ttt aaa tgg cca 739  
 Gly Ile Val Tyr Ser Val Gly Ala Leu Val Tyr Gly Phe Lys Trp Pro  
 200 205 210

gga cgc aac gca cga gtg att ggc tac cac gag cac ttc cac atc gcc 787  
 Gly Arg Asn Ala Arg Val Ile Gly Tyr His Glu His Phe His Ile Ala  
 215 220 225

acg atc gtc gca gcg att gtc cat ctg gtt gca gtg tgaatggttg 833  
 Thr Ile Val Ala Ala Ile Val His Leu Val Ala Val  
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<210> 24  
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 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 24  
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Lys Asp Ser Ser Asp Glu Pro Leu Leu Ala Leu Thr Arg Tyr Val Phe  
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Asp Arg Gly Glu Arg Pro Val Thr Arg Gly Leu Phe His Gln Val Ala  
 35 40 45

Ala Ile Leu Ser Ile Val Ser Gly Ser Val Leu Ser Thr Tyr Ala Trp  
 50 55 60

Met Glu Leu Val Trp Trp Gln Ala Leu Gly Val Met Val Tyr Ala Leu  
 65 70 75 80

Ala Met Leu Gly Leu Phe Ala Val Ser Ala Ala Tyr His Arg Gly Pro

85 90 95

Trp Arg Arg Leu His Thr Val Ala Trp Trp Arg Lys Ala Asp His Ser  
100 105 110

Thr Ile Ala Val Phe Ile Ala Ala Thr Tyr Thr Pro Leu Cys Leu Ile  
115 120 125

Val Leu Glu Pro Gly Thr Ala Ala Trp Met Leu Gly Ile Ala Trp Val  
130 135 140

Gly Ala Ile Asp Ser Val Ile Met Asn Met Val Trp Ile Asn His Pro  
145 150 155 160

Arg Trp Leu Ser Val Leu Val Tyr Leu Ala Leu Gly Trp Leu Ile Val  
165 170 175

Pro Leu Val Pro Gln Leu Trp Ser Gly Ala Gly Pro Thr Val Val Trp  
180 185 190

Leu Leu Leu Ala Gly Gly Ile Val Tyr Ser Val Gly Ala Leu Val Tyr  
195 200 205

Gly Phe Lys Trp Pro Gly Arg Asn Ala Arg Val Ile Gly Tyr His Glu  
210 215 220

His Phe His Ile Ala Thr Ile Val Ala Ala Ile Val His Leu Val Ala  
225 230 235 240

Val

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<213> Corynebacterium glutamicum

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Met Asp Ala Asp Pro  
1 5

ctg att gag gat gac gtt agt gga gca gaa gta aaa gat agt tcg gat 163  
Leu Ile Glu Asp Asp Val Ser Gly Ala Glu Val Lys Asp Ser Ser Asp  
10 15 20

gaa ccg ctt ctg gca ctg aca cgt tac gtt ttt gat cgc ggt gag ccg 211  
Glu Pro Leu Leu Ala Leu Thr Arg Tyr Val Phe Asp Arg Gly Glu Arg  
25 30 35

cca gtt act cgt gga ctg ttc cac cag gtt gcg gcc att ttg agt att 259  
Pro Val Thr Arg Gly Leu Phe His Gln Val Ala Ala Ile Leu Ser Ile  
40 45 50

gtg tca ggt tgg gtg ctc tcc acg tat gca tgg atg gaa ctg gtg tgg 307  
Val Ser Gly Ser Val Leu Ser Thr Tyr Ala Trp Met Glu Leu Val Trp  
55 60 65

tgg cag gcg cta ggt gtc atg gtg tac gcc ttg gcc atg ctg gga ctg 355  
Trp Gln Ala Leu Gly Val Met Val Tyr Ala Leu Ala Met Leu Gly Leu  
70 75 80 85

ttt gct gtc tct gcg gcg tat cac cga gga ccg tgg cgt cga ttg cac 403  
Phe Ala Val Ser Ala Ala Tyr His Arg Gly Pro Trp Arg Arg Leu His  
90 95 100

acc gtg gcg tgg tgg cgc aaa gct gat cac tcc acc atc gcg gtg ttt 451  
Thr Val Ala Trp Trp Arg Lys Ala Asp His Ser Thr Ile Ala Val Phe  
105 110 115

atc gca gca acc tat acg cca ctg tgc ttg atc gtc tta gag ccc ggt 499  
Ile Ala Ala Thr Tyr Thr Pro Leu Cys Leu Ile Val Leu Glu Pro Gly  
120 125 130

acc gca gca tgg atg tta ggt att gcg tgg gtt ggt gcc att gac agc 547  
Thr Ala Ala Trp Met Leu Gly Ile Ala Trp Val Gly Ala Ile Asp Ser  
135 140 145

gtg atc atg aac atg gtg tgg atc aat cac cca cga tgg ctc agc gtg 595  
Val Ile Met Asn Met Val Trp Ile Asn His Pro Arg Trp Leu Ser Val  
150 155 160 165

ctg gtc tac ttg gcc ttg gga tgg ctc att gtg cca ctt gtc cct caa 643  
Leu Val Tyr Leu Ala Leu Gly Trp Leu Ile Val Pro Leu Val Pro Gln  
170 175 180

ttg tgg tct ggt gct ggc ccc aca gtg gtg tgg ctc ctg ctg gcc gaa 691  
Leu Trp Ser Gly Ala Gly Pro Thr Val Val Trp Leu Leu Ala Glu  
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<211> 210  
<212> PRT  
<213> *Corynebacterium glutamicum*

<400> 26  
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Lys Asp Ser Ser Asp Glu Pro Leu Leu Ala Leu Thr Arg Tyr Val Phe  
20 25 30

Asp Arg Gly Glu Arg Pro Val Thr Arg Gly Leu Phe His Gln Val Ala  
35 40 45

Ala Ile Leu Ser Ile Val Ser Gly Ser Val Leu Ser Thr Tyr Ala Trp  
50 55 60

Met Glu Leu Val Trp Trp Gln Ala Leu Gly Val Met Val Tyr Ala Leu



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Trp	Gly	Ile	Val	Leu	Ala	Ile	Val	Val	Val	Ser	Leu	Leu	Thr	Phe	Ala	
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gta	gtg	ggc	gtg	ttt	ggc	cgc	acc	gtt	ggc	cgc	aaa	aac	cca	tat	tca	451
Val	Val	Gly	Val	Phe	Gly	Arg	Thr	Val	Gly	Arg	Lys	Asn	Pro	Tyr	Ser	
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Val	Met	Leu	Arg	Ser	Ala	Val	Val	Leu	Ser	Gly	Leu	Ala	Lys	Ile	Leu	
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Gly	Pro	Ile	Ala	Arg	Gly	Leu	Ile	Trp	Ile	Gly	Asn	Ile	Ile	Ala	Pro	
				135				140					145			
ggc	cca	ggt	ttc	cgc	aat	ggc	cct	tac	gcc	act	gaa	gtg	gaa	ctg	cgt	595
Gly	Pro	Gly	Phe	Arg	Asn	Gly	Pro	Tyr	Ala	Thr	Glu	Val	Glu	Leu	Arg	
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gag	atg	gtc	gat	atc	gcc	caa	gaa	cac	ggc	atc	gtg	gaa	att	gaa	gag	643
Glu	Met	Val	Asp	Ile	Ala	Gln	Glu	His	Gly	Ile	Val	Glu	Ile	Glu	Glu	
				170					175					180		
cgc	cgc	atg	atc	cag	tcg	gtg	ttc	gac	ctg	gca	tcc	acg	acg	gtt	cgc	691
Arg	Arg	Met	Ile	Gln	Ser	Val	Phe	Asp	Leu	Ala	Ser	Thr	Thr	Val	Arg	
				185				190					195			
cag	gtg	atg	gtg	cca	cgt	cct	gaa	atg	atc	tgg	att	gaa	tct	gga	aaa	739
Gln	Val	Met	Val	Pro	Arg	Pro	Glu	Met	Ile	Trp	Ile	Glu	Ser	Gly	Lys	
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aca	gcc	ggg	caa	gca	acc	gcg	ctg	tgc	gtg	cgc	tct	ggt	cat	tcg	cgc	787
Thr	Ala	Gly	Gln	Ala	Thr	Ala	Leu	Cys	Val	Arg	Ser	Gly	His	Ser	Arg	
				215				220					225			
atc	cca	gtc	atc	ggt	gaa	aac	gtc	gac	gac	atc	atc	ggc	atc	gtc	tac	835
Ile	Pro	Val	Ile	Gly	Glu	Asn	Val	Asp	Asp	Ile	Ile	Gly	Ile	Val	Tyr	
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ctc	aaa	gac	ttg	gtc	caa	aaa	acc	tac	tac	gcc	act	gat	ggc	gga	aag	883
Leu	Lys	Asp	Leu	Val	Gln	Lys	Thr	Tyr	Tyr	Ala	Thr	Asp	Gly	Gly	Lys	
				250					255					260		
tct	gtg	ctt	gta	gac	gag	gtc	atg	cgc	gaa	gct	acc	ttc	gtg	cca	gac	931
Ser</																

tcc att gag gat att ttg gaa gaa atc gtc ggt gaa atc gct gat gaa 1075  
 Ser Ile Glu Asp Ile Leu Glu Glu Ile Val Gly Glu Ile Ala Asp Glu  
 310 315 320 325

tat gac gcc cgc gaa gta gcc ccc atc gag aaa atc ggc gac cgc acc 1123  
 Tyr Asp Ala Arg Glu Val Ala Pro Ile Glu Lys Ile Gly Asp Arg Thr  
 330 335 340

tac cgc gtg gtc tcc cga ctc tgc ctg gaa gat ctc aaa gac cac atc 1171  
 Tyr Arg Val Val Ser Arg Leu Ser Leu Glu Asp Leu Lys Asp His Ile  
 345 350 355

gaa gaa gaa ctc gac cta gaa atc gaa ttc ggt gat gaa att gaa gat 1219  
 Glu Glu Glu Leu Asp Leu Glu Ile Glu Phe Gly Asp Glu Ile Glu Asp  
 360 365 370

cag gtc gac act gtc ggt ggc ctt att gcc ttt gaa ctt ggc cga gtg 1267  
 Gln Val Asp Thr Val Gly Gly Leu Ile Ala Phe Glu Leu Gly Arg Val  
 375 380 385

cct ctg ccg ggt gcc act gtg gaa acc tgc gga cta aag ctc acc gcc 1315  
 Pro Leu Pro Gly Ala Thr Val Glu Thr Cys Gly Leu Lys Leu Thr Ala  
 390 395 400 405

gag gga gcc aag aac cgc cgg ggt cgt ttg cgc atg cat tca gca gtc 1363  
 Glu Gly Ala Lys Asn Arg Arg Gly Arg Leu Arg Met His Ser Ala Val  
 410 415 420

gta gaa gtt ggc gag ccc agc gag gac aac gaa ggt tagtttttta 1409  
 Val Glu Val Gly Glu Pro Ser Glu Asp Asn Glu Gly  
 425 430

cagcagtagg gga 1422

<210> 28  
 <211> 433  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 28  
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Ala Val Glu Ser Ala Leu Ser Ser Val Ser Arg Ala Arg Val Glu Gln  
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Met Leu Lys Asp Glu Ala Ser Gly Ser Ala Ser Leu Leu Arg Val Ile  
 35 40 45

Asp Glu Arg Ala Leu His Ile Asn Met Leu Ile Met Leu Arg Thr Leu  
 50 55 60

Leu Asp Ala Ser Ala Ala Val Phe Ala Gly Ala Ile Ala Val Asn Val  
 65 70 75 80

Met Asp Ser Trp Ala Trp Gly Ile Val Leu Ala Ile Val Val Val Ser  
 85 90 95

Leu Leu Thr Phe Ala Val Val Gly Val Phe Gly Arg Thr Val Gly Arg



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Lys	Asn	Pro	Tyr	Ser	Val	Met	Leu	Arg	Ser	Ala	Val	Val	Leu	Ser	Gly	Lys	Asn	Pro	Tyr	Ser	Val	Met	Leu	Arg	Ser	Ala	Val	Val	Leu	Ser	Gly
115										120										125											
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130										135										140											
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145										150										155											
Glu	Val	Glu	Leu	Arg	Glu	Met	Val	Asp	Ile	Ala	Gln	Glu	His	Gly	Ile	Glu	Val	Glu	Leu	Arg	Glu	Met	Val	Asp	Ile	Ala	Gln	Glu	His	Gly	Ile
165										170										175											
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180										185										190											
Ser	Thr	Thr	Val	Arg	Gln	Val	Met	Val	Pro	Arg	Pro	Glu	Met	Ile	Trp	Ser	Thr	Thr	Val	Arg	Gln	Val	Met	Val	Pro	Arg	Pro	Glu	Met	Ile	Trp
195										200										205											
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210										215										220											
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225										230										235											
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245										250										255											
Thr	Asp	Gly	Gly	Lys	Ser	Val	Leu	Val	Asp	Glu	Val	Met	Arg	Glu	Ala	Thr	Asp	Gly	Gly	Lys	Ser	Val	Leu	Val	Asp	Glu	Val	Met	Arg	Glu	Ala
260										265										270											
Thr	Phe	Val	Pro	Asp	Ser	Lys	Ser	Leu	Asp	Ala	Leu	Leu	Gln	Glu	Met	Thr	Phe	Val	Pro	Asp	Ser	Lys	Ser	Leu	Asp	Ala	Leu	Leu	Gln	Glu	Met
275										280										285											
Gln	Glu	Asp	His	Lys	His	Ile	Ala	Ile	Leu	Val	Asp	Glu	Tyr	Gly	Gly	Gln	Glu	Asp	His	Lys	His	Ile	Ala	Ile	Leu	Val	Asp	Glu	Tyr	Gly	Gly
290										295										300											
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305										310										315											
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325										330										335											
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Gly

&lt;210&gt; 29

&lt;211&gt; 1398

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1375)

&lt;223&gt; PRXA00890

&lt;400&gt; 29

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Val Val Ala Leu Leu Phe Ser Gly Leu Leu Gly Ala Val Glu Ser Ala	
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Leu Ser Ser Val Ser Arg Ala Arg Val Glu Gln Met Leu Lys Asp Glu	
25 30 35	

gcc tcc ggg tcc gcg tcc ttg ctg cga gtc atc gac gaa cgc gca ctc	259
Ala Ser Gly Ser Ala Ser Leu Leu Arg Val Ile Asp Glu Arg Ala Leu	
40 45 50	

cac atc aac atg ctc atc atg ttg cgc acc ttg ctg gat gcc tcc gca	307
His Ile Asn Met Leu Ile Met Leu Arg Thr Leu Leu Asp Ala Ser Ala	
55 60 65	

gca gtc ttc gcc ggg gca atc gca gtc aat gtg atg gac agc tgg gcg	355
Ala Val Phe Ala Gly Ala Ile Ala Val Asn Val Met Asp Ser Trp Ala	
70 75 80 85	

tgg ggc atc gtc ctg gcc atc gtg gtg gtt tcc ctc ctg acc ttc gca	403
Trp Gly Ile Val Leu Ala Ile Val Val Val Ser Leu Leu Thr Phe Ala	
90 95 100	

gta gtg ggc gtg ttt ggc cgc acc gtt ggc cgc aaa aac cca tat tca	451
Val Val Gly Val Phe Gly Arg Thr Val Gly Arg Lys Asn Pro Tyr Ser	
105 110 115	

gtg atg ctt cgc tcc gca gtc gtg ctg agc ggt tta gct aaa atc ctt	499
Val Met Leu Arg Ser Ala Val Val Leu Ser Gly Leu Ala Lys Ile Leu	
120 125 130	

ggc ccc att gca cgt ggc ctc atc ttg atc ggc aac atc atc gcg ccc	547
Gly Pro Ile Ala Arg Gly Leu Ile Trp Ile Gly Asn Ile Ile Ala Pro	
135 140 145	

ggc cca ggt ttc cgc aat ggc cct tac gcc act gaa gtg gaa ctg cgt	595
Gly Pro Gly Phe Arg Asn Gly Pro Tyr Ala Thr Glu Val Glu Leu Arg	
150 155 160 165	

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170										175							
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185								190					195				
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Asp Glu Arg Ala Leu His Ile Asn Met Leu Ile Met Leu Arg Thr Leu  
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Leu Asp Ala Ser Ala Ala Val Phe Ala Gly Ala Ile Ala Val Asn Val  
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Met Asp Ser Trp Ala Trp Gly Ile Val Leu Ala Ile Val Val Val Ser  
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Leu Leu Thr Phe Ala Val Val Gly Val Phe Gly Arg Thr Val Gly Arg  
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Lys Asn Pro Tyr Ser Val Met Leu Arg Ser Ala Val Val Leu Ser Gly  
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Leu Ala Lys Ile Leu Gly Pro Ile Ala Arg Gly Leu Ile Trp Ile Gly  
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Asn Ile Ile Ala Pro Gly Pro Gly Phe Arg Asn Gly Pro Tyr Ala Thr  
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Glu Val Glu Leu Arg Glu Met Val Asp Ile Ala Gln Glu His Gly Ile  
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Val Glu Ile Glu Glu Arg Arg Met Ile Gln Ser Val Phe Asp Leu Ala  
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Ser Thr Thr Val Arg Gln Val Met Val Pro Arg Pro Glu Met Ile Trp  
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Ile Glu Ser Gly Lys Thr Ala Gly Gln Ala Thr Ala Leu Cys Val Arg  
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Ser Gly His Ser Arg Ile Pro Val Ile Gly Glu Asn Val Asp Asp Ile  
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Ile Gly Ile Val Tyr Leu Lys Asp Leu Val Gln Lys Thr Tyr Tyr Ala



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 Trp Pro Tyr Asn Gly Gly Thr Met Asp Thr Gly Ile Asp Leu Val Ala  
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 Tyr Asn Lys Asp Asp Asp Ala Tyr Thr Ala Ile Gln Cys Lys Phe Tyr  
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 Lys Met Leu Glu Asn Gln Thr Ile Pro Thr Asn Arg Ile Gly Leu Ser  
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Tyr	Gln	Ser	Leu	Pro	Ala	Val	His	Ala	Ala	Gln	Glu	Ala	Gly	Ala	Glu	
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Pro	Phe	Asp	Leu	Val	Ile	Cys	Asp	Glu	Ala	His	Arg	Thr	Thr	Gly	Ile	
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Thr	Leu	Ala	Gly	Glu	Asp	Pro	Ser	Asn	Phe	Thr	Arg	Ile	His	Asp	Ala	
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Ser	Tyr	Ile	Lys	Ala	Ala	Lys	Arg	Leu	Tyr	Met	Thr	Ala	Thr	Pro	Arg	
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Leu	Phe	Asp	Asp	Ser	Val	Lys	Gly	Lys	Ala	Ala	Asp	His	Ser	Ala	Glu	
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Val	Ser	Ser	Met	Asp	Asp	Glu	Ala	Ile	Tyr	Gly	Pro	Glu	Phe	His	Arg	
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Gln	Asp	Thr	Lys	Thr	Gly	Phe	Ser	Ser	Ser	Asp	Ala	Ala	Met	Glu	Arg	
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Ser	Phe	Pro	Arg	Val	Val	Asn	Ala	Tyr	Thr	Thr	Glu	Leu	Glu	Val	Lys	
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Asn	Asp	Asp	Val	Asp	Glu	His	Asn	Leu	Asn	Leu	Ser	Val	Ala	Cys	Gln	

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Met Asp Leu His Ile Asn Tyr Glu Asp Val Glu Pro Trp Asp Val Glu			
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gta aag gtc aaa gaa aaa gct gat ccc acg gat cgt gag acc tgg cgt			4723
Val Lys Val Lys Glu Lys Ala Asp Pro Thr Asp Arg Glu Thr Trp Arg			
1530	1535		1540
gtt acc aag atg aag tgg gct aag gtt cgt gat cca gag acc aag aaa			4771
Val Thr Lys Met Lys Trp Ala Lys Val Arg Asp Pro Glu Thr Lys Lys			
1545	1550		1555
ttg gtg gag gac cat acc acc ttg att tac aac agc tca atc acc atc			4819
Leu Val Glu Asp His Thr Thr Leu Ile Tyr Asn Ser Ser Ile Thr Ile			
1560	1565		1570
agc ggc atc ccc gaa gaa gct gaa aac tat caa cta ggt tca cgt tct			4867
Ser Gly Ile Pro Glu Glu Ala Glu Asn Tyr Gln Leu Gly Ser Arg Ser			
1575	1580		1585
gcc atc gca tgg ctt att gac cgt tac cag gtg aag aaa gat aag gcg			4915
Ala Ile Ala Trp Leu Ile Asp Arg Tyr Gln Val Lys Lys Asp Lys Ala			
1590	1595	1600	1605
tcc ggc att gtt aat gat ccc aat gat tgg gct gat gaa gtg ggt aac			4963
Ser Gly Ile Val Asn Asp Pro Asn Asp Trp Ala Asp Glu Val Gly Asn			
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cct cgc tac att gtg gag ctg att gct aag gtc acc cgc gtt gcc gtt			5011
Pro Arg Tyr Ile Val Glu Leu Ile Ala Lys Val Thr Arg Val Ala Val			
1625	1630		1635
gag acc atg aga att gta gag gag ctt tgagttttcc tactgcagct			5058
Glu Thr Met Arg Ile Val Glu Glu Leu			
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tcc			5061
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Asn Phe Ile Lys Ser Asp Pro Thr Leu Ser Thr Glu Phe Asp Glu Val			
35	40		45
His Arg Trp Val Asp Trp Pro Tyr Asn Gly Gly Thr Met Asp Thr Gly			
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Ile Asp Leu Val Ala Tyr Asn Lys Asp Asp Ala Tyr Thr Ala Ile			
65	70	75	80

Gln Cys Lys Phe Tyr Leu Pro Thr Thr Ser Leu Ala Lys Gly Gln Leu  
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 Asp Ser Phe Phe Glu Ala Ser Gly Arg Thr Phe Glu Thr Pro Glu Gly  
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 Thr Arg Ser Phe Ser Asn Arg Leu Val Ile Ser Thr Thr Asp Lys Trp  
 115 120 125  
 Ser Ser Asn Ala Glu Lys Met Leu Glu Asn Gln Thr Ile Pro Thr Asn  
 130 135 140  
 Arg Ile Gly Leu Ser Ala Ile Ala Glu Ser Pro Ile Asp Trp Asp Ile  
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 Ala Tyr Pro Gly Ser Glu Leu Thr Ile Asn Leu Gln Leu Lys Glu Pro  
 165 170 175  
 Tyr Ser Pro Arg Pro His Gln Gln Thr Ala Ile Glu Lys Ala Ile Glu  
 180 185 190  
 Gly Phe Gln Thr His Asp Arg Gly Lys Leu Ile Met Ala Cys Gly Thr  
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 Gly Lys Thr Phe Thr Ala Leu Arg Leu Ser Glu Glu Val Ala Arg Leu  
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 Asn Gly Asn Lys Ala Arg Ile Leu Phe Leu Val Pro Ser Ile Ser Leu  
 225 230 235 240  
 Leu Ser Gln Thr Leu Lys Glu Trp Thr Ala Gln Lys Thr Met Asp Leu  
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 Arg Pro Val Ala Val Cys Ser Asp Ser Lys Val Ser Lys Ala Ala Glu  
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 Asp Ile Ala Ala Tyr Asp Leu Glu Val Pro Val Ser Thr Asp Gly Ala  
 275 280 285  
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 Val Val Phe Ser Thr Tyr Gln Ser Leu Pro Ala Val His Ala Ala Gln  
 305 310 315 320  
 Glu Ala Gly Ala Glu Pro Phe Asp Leu Val Ile Cys Asp Glu Ala His  
 325 330 335  
 Arg Thr Thr Gly Ile Thr Leu Ala Gly Glu Asp Pro Ser Asn Phe Thr  
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 Arg Ile His Asp Ala Ser Tyr Ile Lys Ala Ala Lys Arg Leu Tyr Met  
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 Thr Ala Thr Pro Arg Leu Phe Asp Asp Ser Val Lys Gly Lys Ala Ala  
 370 375 380  
 Asp His Ser Ala Glu Val Ser Ser Met Asp Asp Glu Ala Ile Tyr Gly  
 385 390 395 400

Pro Glu Phe His Arg Leu Gly Phe Gly Glu Ala Val Glu Lys Gly Leu  
 405 410 415  
 Leu Thr Asp Tyr Lys Val Val Val Met Thr Val Asp Glu Gln Val Ala  
 420 425 430  
 Ala Ser Ala Leu Thr Val Leu Gly Ser Thr Pro Gly Glu Glu Leu Thr  
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 Arg Ser Gly Lys Glu Gln Asp Thr Lys Thr Gly Phe Ser Ser Ser Asp  
 465 470 475 480  
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 Glu Leu Glu Val Lys Asn Asp Asp Val Asp Glu His Asn Leu Asn Leu  
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 Ser Val Ala Cys Gln His Val Asp Gly Ser Met Asn Ala Leu Glu Arg  
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 545 550 555 560  
 Lys Ile Leu Thr Asn Ala Arg Cys Leu Ser Glu Gly Val Asp Val Pro  
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 Ala Leu Asp Ser Val Ile Phe Phe Asn Pro Arg Asn Ser Met Val Asp  
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 Val Val Gln Ser Val Gly Arg Val Met Arg Lys Ser Pro Gly Lys Asn  
 595 600 605  
 Tyr Gly Tyr Ile Ile Leu Pro Val Ala Val Pro Pro Gly Val Ala Pro  
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 Ser Ala Ala Leu Asn Asp Ser Arg Arg Phe Lys Val Val Trp Gln Val  
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 Ser Ile Ala Leu Asn Glu Gly Asn Ile Lys Asp Leu Pro Val Glu Thr  
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 Arg Ala Phe Arg Trp Ala Thr Asp Arg Ile His Thr Gln Gly Val Val  
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 Val Arg Leu Ser Leu Ala Gln Asp Phe Ser Glu Ile Tyr Val Phe Asn  
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 1125 1130 1135  
 Gly Asn Val Phe Asn Val Arg Val Gly Thr Gln Ile Ile Val Ala Val  
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 Lys Asn Pro Gln Leu Ser Gly Cys Arg Ile Leu Tyr Lys Asp Ile Gly  
 1155 1160 1165  
 Asp Asn Leu Ser Ala Asp Ala Lys Leu Asn Glu Ile Ala Val Ala Thr  
 1170 1175 1180  
 Ile Glu Gly Ala Glu Trp Gln Thr Ile Ser Pro Asn Glu Tyr Gly Asp  
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 Trp Ile Ser Gln Arg Ser Val Asp Phe Asp Thr Trp Pro Val Leu Gly  
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 Asp Lys Lys Asn Lys Ser Ala Leu Lys Val Phe Gln Thr Phe Ser Ala  
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 Gly Leu Lys Thr Gly Arg Asp Ala Trp Cys Tyr Gly Pro Thr Ser Ala  
 1235 1240 1245  
 Gln Val Lys Thr Asn Ile Thr Arg Leu Leu Glu Thr Tyr Glu Gln Ala  
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 Gln Gln Arg Phe Asn Ser Trp Val Val Asp Asn Gly Val Thr Ser Pro  
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 Lys Glu Ala Asp Val Asn Gln Phe Leu Lys Gln Asn Pro Asp Leu Ala  
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 Asp Ser Lys Lys Ile Ser Trp Asp Ser Asn Leu Lys Met Ser Leu Ser  
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 Arg Gly Asp Thr Phe Ser Phe Asp Pro Ser Ser Ile Gln Met Ser Leu  
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 Tyr Arg Pro Phe Phe Pro Gln Gln Thr Tyr Phe His Val Ser Leu Asn  
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 Gln Arg Arg Tyr Gln Leu Pro Ser Met Phe Pro Thr Pro Glu His Asp  
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 Asn Gln Gly Phe Tyr Ile Val Asn Pro Gly Ser Ala Lys Pro Phe Ser  
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Thr Leu Ala Thr Asn Leu Leu Pro Asp Leu Ala Met Trp Gly Ser Asn  
 1380 1385 1390  
 Ala Gly Gln Phe Phe Thr Arg Trp Thr Trp Glu Pro Ile Glu Thr Arg  
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 Glu Gly Glu Leu Asp Phe Gly Asn Gly Leu Phe Ser Thr Thr Pro Lys  
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 1425 1430 1435 1440  
 Ile Thr Asp Glu Ile Leu Lys Leu Tyr Gln Ser Ser Leu Gly Glu Asp  
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 Val Thr Lys Asp Asp Ile Phe Tyr Phe Val Tyr Ala Gln Leu His Asp  
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 Pro Ala Tyr Arg Glu Ala Tyr Ala Ala Asp Leu Lys Lys Met Leu Pro  
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 His Ile Glu Thr Pro Thr Asp Arg Ala Arg Phe Asp His Phe Val Thr  
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 1555 1560 1565  
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Thr Pro Val Glu Ile Val Asp Phe Ile Leu Arg Ala Ala Asp Asp Val	
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tcc aag aag cat ttt ggt cgt ggc tta agc gat aaa gat gtc cat gtt	144
Ser Lys Lys His Phe Gly Arg Gly Leu Ser Asp Lys Asp Val His Val	
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ctt gat cct ttc acc ggt acg ggt act ttt atg gtg cgt tta ttg cag	192
Leu Asp Pro Phe Thr Gly Thr Gly Thr Phe Met Val Arg Leu Leu Gln	
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Ser Gly Leu Ile Lys Pro Glu Asp Leu Ala Arg Lys Tyr Ala Asn Glu	
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Leu His Ala Thr Glu Ile Met Leu Leu Ala Tyr Tyr Val Ala Ala Val	
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aac att gag acc act tat ttt ggt ctc gag gga gag cgt gct ctg cgt	336
Asn Ile Glu Thr Thr Tyr Phe Gly Leu Glu Gly Glu Arg Ala Leu Arg	
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aat ggt gaa gat gcg ccg gtc tat gag ccg ttt gat ggc att gtg ttg	384
Asn Gly Glu Asp Ala Pro Val Tyr Glu Pro Phe Asp Gly Ile Val Leu	
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ggt gat acc ttc cag atg tat gaa gac gat gac aaa ctc gat cta gat	432
Gly Asp Thr Phe Gln Met Tyr Glu Asp Asp Lys Leu Asp Leu Asp	
130 135 140	
gtt ttt act gct aac aat gac cgt atg gag cgt cag aga ctt act cct	480
Val Phe Thr Ala Asn Asn Asp Arg Met Glu Arg Gln Arg Leu Thr Pro	
145 150 155 160	
gta cag gtt att gtg ggt aac ccg cct tac tct gtg ggg caa tcg agt	528
Val Gln Val Ile Val Gly Asn Pro Pro Tyr Ser Val Gly Gln Ser Ser	
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gcg aat gac aat aac gca aac ctc aag tac ccc act ctt gat cga cgt	576
Ala Asn Asp Asn Asn Ala Asn Leu Lys Tyr Pro Thr Leu Asp Arg Arg	
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att gaa gat tct tat gcg aag tat tcg acc gca aca aat aag aac tct	624
Ile Glu Asp Ser Tyr Ala Lys Tyr Ser Thr Ala Thr Asn Lys Asn Ser	
195 200 205	
ctg tac gac tcc tat tta cgt gct ttc cgg tgg gca aca gat cgt att	672
Leu Tyr Asp Ser Tyr Leu Arg Ala Phe Arg Trp Ala Thr Asp Arg Ile	
210 215 220	
cac aca caa ggg gtt gtt gct ttt gtt tct aac aac ggt tgg gtt gac	720
His Thr Gln Gly Val Val Ala Phe Val Ser Asn Asn Gly Trp Val Asp	
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 Gly Asn Thr Ala Asp Gly Val Arg Leu Ser Leu Ala Gln Asp Phe Ser  
 245 250 255

gag att tat gtt ttc aac ctt cgt ggc aat tcc cga aca ggt ggt gat 816  
 Glu Ile Tyr Val Phe Asn Leu Arg Gly Asn Ser Arg Thr Gly Gly Asp  
 260 265 270

ttg gct aag cgc gag ggc ggc aac gtc ttt aat gtc cgt gtg ggt act 864  
 Leu Ala Lys Arg Glu Gly Gly Asn Val Phe Asn Val Arg Val Gly Thr  
 275 280 285

caa atc att gtt gcc gtg aaa aac cca caa ttg tct ggt tgc agg att 912  
 Gln Ile Ile Val Ala Val Lys Asn Pro Gln Leu Ser Gly Cys Arg Ile  
 290 295 300

ctt tat aaa gat att ggt gac aat ctc agc gcg gat gcg aag ttg aac 960  
 Leu Tyr Lys Asp Ile Gly Asp Asn Leu Ser Ala Asp Ala Lys Leu Asn  
 305 310 315 320

gag att gcc gtt gcc aca att gag ggc gct gag tgg cag act att tcg 1008  
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 325 330 335

cct aat gaa tat gga gat tgg atc agc cag cgc tct gta gat ttt gat 1056  
 Pro Asn Glu Tyr Gly Asp Trp Ile Ser Gln Arg Ser Val Asp Phe Asp  
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acc tgg cct gta ctc ggt gat aag aaa aac aaa tct gca tta aag gtt 1104  
 Thr Trp Pro Val Leu Gly Asp Lys Lys Asn Lys Ser Ala Leu Lys Val  
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 370 375 380

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 Tyr Gly Pro Thr Ser Ala Gln Val Lys Thr Asn Ile Thr Arg Leu Leu  
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gaa acc tat gaa caa gct cag caa cgg ttt aat tcg tgg gtt gtg gat 1248  
 Glu Thr Tyr Glu Gln Ala Gln Gln Arg Phe Asn Ser Trp Val Val Asp  
 405 410 415

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 420 425 430

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 435 440 445

cta aaa atg tcc ttg tca cgc ggt gat act ttt tct ttt gat cca agc 1392  
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agc atc caa atg tcc ttg tat cgt cca ttt ttc cct caa cag aca tac 1440  
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Phe His Val Ser Leu Asn Gln Arg Arg Tyr Gln Leu Pro Ser Met Phe	
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ccg acc ccg gaa cat gac aac cag ggc ttt tat atc gtc aac cca ggt	1536
Pro Thr Pro Glu His Asp Asn Gln Gly Phe Tyr Ile Val Asn Pro Gly	
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Ser Ala Lys Pro Phe Ser Thr Leu Ala Thr Asn Leu Leu Pro Asp Leu	
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gct atg tgg ggt tct aac gcc gga cag ttc ttt acc cga tgg act tgg	1632
Ala Met Trp Gly Ser Asn Ala Gly Gln Phe Phe Thr Arg Trp Thr Trp	
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gaa ccc atc gaa act cga gaa ggc gaa tta gac ttc ggt aat gga ctt	1680
Glu Pro Ile Glu Thr Arg Glu Gly Glu Leu Asp Phe Gly Asn Gly Leu	
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Phe Ser Thr Thr Pro Lys Lys Gly Val Glu Gly Glu Ile Leu Asp Gly	
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tac cgg cgc gtc gat aac atc acc gac gag atc tta aag ctc tac caa	1776
Tyr Arg Arg Val Asp Asn Ile Thr Asp Glu Ile Leu Lys Leu Tyr Gln	
580 585 590	
tca agc ttg ggt gag gat gtc acc aag gat gac atc ttc tac ttt gtt	1824
Ser Ser Leu Gly Glu Asp Val Thr Lys Asp Asp Ile Phe Tyr Phe Val	
595 600 605	
tat gca cag ttg cat gat cct gcc tat cgt gag gcc tat gcg gct gat	1872
Tyr Ala Gln Leu His Asp Pro Ala Tyr Arg Glu Ala Tyr Ala Ala Asp	
610 615 620	
cta aag aag atg ctg cca cat att gaa acc cct act gat cgc gca cgc	1920
Leu Lys Lys Met Leu Pro His Ile Glu Thr Pro Thr Asp Arg Ala Arg	
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Phe Asp His Phe Val Thr Ala Gly Lys Glu Leu Met Asp Leu His Ile	
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Asn Tyr Glu Asp Val Glu Pro Trp Asp Val Glu Val Lys Val Lys Glu	
660 665 670	
aaa gct gat ccc acg gat cgt gag acc tgg cgt gtt acc aag atg aag	2064
Lys Ala Asp Pro Thr Asp Arg Glu Thr Trp Arg Val Thr Lys Met Lys	
675 680 685	
tgg gct aag gtt cgt gat cca gag acc aag aaa ttg gtg gag gac cat	2112
Trp Ala Lys Val Arg Asp Pro Glu Thr Lys Lys Leu Val Glu Asp His	
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Thr Thr Leu Ile Tyr Asn Ser Ser Ile Thr Ile Ser Gly Ile Pro Glu	
705 710 715 720	
gaa gct gaa aac tat caa cta ggt tca cgt tct gcc atc gca tgg ctt	2208

Glu Ala Glu Asn Tyr Gln Leu Gly Ser Arg Ser Ala Ile Ala Trp Leu  
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 Ile Asp Arg Tyr Gln Val Lys Lys Asp Lys Ala Ser Gly Ile Val Asn  
 740 745 750

gat ccc aat gat tgg gct gat gaa gtg ggt aac cct cgc tac att gtg 2304  
 Asp Pro Asn Asp Trp Ala Asp Glu Val Gly Asn Pro Arg Tyr Ile Val  
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gag ctg att gct aag gtc acc cgc gtt gcc gtt gag acc atg aga att 2352  
 Glu Leu Ile Ala Lys Val Thr Arg Val Ala Val Glu Thr Met Arg Ile  
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gta gag gag ctt tgagttttcc tactgcagct tcc 2387  
 Val Glu Glu Leu  
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&lt;211&gt; 788

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 34

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Ser Lys Lys His Phe Gly Arg Gly Leu Ser Asp Lys Asp Val His Val  
 35 40 45

Leu Asp Pro Phe Thr Gly Thr Gly Thr Phe Met Val Arg Leu Leu Gln  
 50 55 60

Ser Gly Leu Ile Lys Pro Glu Asp Leu Ala Arg Lys Tyr Ala Asn Glu  
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Leu His Ala Thr Glu Ile Met Leu Leu Ala Tyr Tyr Val Ala Ala Val  
 85 90 95

Asn Ile Glu Thr Thr Tyr Phe Gly Leu Glu Gly Glu Arg Ala Leu Arg  
 100 105 110

Asn Gly Glu Asp Ala Pro Val Tyr Glu Pro Phe Asp Gly Ile Val Leu  
 115 120 125

Gly Asp Thr Phe Gln Met Tyr Glu Asp Asp Asp Lys Leu Asp Leu Asp  
 130 135 140

Val Phe Thr Ala Asn Asn Asp Arg Met Glu Arg Gln Arg Leu Thr Pro  
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Val Gln Val Ile Val Gly Asn Pro Pro Tyr Ser Val Gly Gln Ser Ser  
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Ala Asn Asp Asn Asn Ala Asn Leu Lys Tyr Pro Thr Leu Asp Arg Arg  
 180 185 190

Ile Glu Asp Ser Tyr Ala Lys Tyr Ser Thr Ala Thr Asn Lys Asn Ser  
 195 200 205  
 Leu Tyr Asp Ser Tyr Leu Arg Ala Phe Arg Trp Ala Thr Asp Arg Ile  
 210 215 220  
 His Thr Gln Gly Val Val Ala Phe Val Ser Asn Asn Gly Trp Val Asp  
 225 230 235 240  
 Gly Asn Thr Ala Asp Gly Val Arg Leu Ser Leu Ala Gln Asp Phe Ser  
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 Gln Ile Ile Val Ala Val Lys Asn Pro Gln Leu Ser Gly Cys Arg Ile  
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 Glu Ile Ala Val Ala Thr Ile Glu Gly Ala Glu Trp Gln Thr Ile Ser  
 325 330 335  
 Pro Asn Glu Tyr Gly Asp Trp Ile Ser Gln Arg Ser Val Asp Phe Asp  
 340 345 350  
 Thr Trp Pro Val Leu Gly Asp Lys Lys Asn Lys Ser Ala Leu Lys Val  
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 370 375 380  
 Tyr Gly Pro Thr Ser Ala Gln Val Lys Thr Asn Ile Thr Arg Leu Leu  
 385 390 395 400  
 Glu Thr Tyr Glu Gln Ala Gln Gln Arg Phe Asn Ser Trp Val Val Asp  
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 420 425 430  
 Gln Asn Pro Asp Leu Ala Asp Ser Lys Lys Ile Ser Trp Asp Ser Asn  
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 Phe His Val Ser Leu Asn Gln Arg Arg Tyr Gln Leu Pro Ser Met Phe  
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 545 550 555 560  
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 565 570 575  
 Tyr Arg Arg Val Asp Asn Ile Thr Asp Glu Ile Leu Lys Leu Tyr Gln  
 580 585 590  
 Ser Ser Leu Gly Glu Asp Val Thr Lys Asp Asp Ile Phe Tyr Phe Val  
 595 600 605  
 Tyr Ala Gln Leu His Asp Pro Ala Tyr Arg Glu Ala Tyr Ala Ala Asp  
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 625 630 635 640  
 Phe Asp His Phe Val Thr Ala Gly Lys Glu Leu Met Asp Leu His Ile  
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 Asn Tyr Glu Asp Val Glu Pro Trp Asp Val Glu Val Lys Val Lys Glu  
 660 665 670  
 Lys Ala Asp Pro Thr Asp Arg Glu Thr Trp Arg Val Thr Lys Met Lys  
 675 680 685  
 Trp Ala Lys Val Arg Asp Pro Glu Thr Lys Lys Leu Val Glu Asp His  
 690 695 700  
 Thr Thr Leu Ile Tyr Asn Ser Ser Ile Thr Ile Ser Gly Ile Pro Glu  
 705 710 715 720  
 Glu Ala Glu Asn Tyr Gln Leu Gly Ser Arg Ser Ala Ile Ala Trp Leu  
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 Ile Asp Arg Tyr Gln Val Lys Lys Asp Lys Ala Ser Gly Ile Val Asn  
 740 745 750  
 Asp Pro Asn Asp Trp Ala Asp Glu Val Gly Asn Pro Arg Tyr Ile Val  
 755 760 765  
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&lt;210&gt; 35

&lt;211&gt; 4923

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

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&lt;221&gt; CDS

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&lt;223&gt; RXA02363

&lt;400&gt; 35

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Lys Lys Ser Phe Ser Asp Phe Phe Ser Pro Leu Ala Thr Glu Thr Glu
                               10                               15                               20

aca act att acg ctc tcg gca att gag gta gag aaa gtc aat gcc aag 211
Thr Thr Ile Thr Leu Ser Ala Ile Glu Val Glu Lys Val Asn Ala Lys
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Thr Glu Val Thr Arg Asn Ile Asp Pro Val Glu Ala Ala Glu Gln Ile
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Ser Arg Asp Tyr Arg Arg Tyr Leu Lys Thr Leu Ile Ser Pro Ser Asn
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Lys Thr Ile Ala Ala Glu Phe Asn Arg Glu Ile Asp Glu Ser Glu Asn
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Lys Ser Pro Ala Gln Leu Ile Asp Glu Gly Val Leu Ser Pro Asn Phe
                               105                               110                               115

tca cgt ctc gat gcc gca cta ccc aaa gat cgc ccg ctt tat cag cat 499
Ser Arg Leu Asp Ala Ala Leu Pro Lys Asp Arg Pro Leu Tyr Gln His
                               120                               125                               130

cag gaa gac gct ctg cga aaa atc gct agt ggc cga aac tta atc gtt 547
Gln Glu Asp Ala Leu Arg Lys Ile Ala Ser Gly Arg Asn Leu Ile Val
                               135                               140                               145

tca acc ggt aca gga tct gga aaa aca gag tct ttc ctc atc ccg atc 595
Ser Thr Gly Thr Gly Ser Gly Lys Thr Glu Ser Phe Leu Ile Pro Ile
                               150                               155                               160                               165

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Phe Asp Gln Leu Leu Arg Gln Gln Gln Ala Gly Glu Leu Asn Pro Gly
                               170                               175                               180

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Val Arg Ala Leu Leu Leu Tyr Pro Met Asn Ala Leu Ala Asn Asp Gln
                               185                               190                               195

gag aaa cgt ctc cgc gaa tta ttg gca gac acc ccg gaa att act ttt 739
Glu Lys Arg Leu Arg Glu Leu Leu Ala Asp Thr Pro Glu Ile Thr Phe

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 Ala Arg Tyr His Met Phe Val Arg Ala Val Glu Gly Ala Phe Leu Gly  
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tat aca gag caa gga aag cca atc gtg tcc ttg gac cgg caa gtg aca 1603  
 Tyr Thr Glu Gln Gly Lys Pro Ile Val Ser Leu Asp Arg Gln Val Thr  
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 Leu Gly Asp Thr Ala Arg Pro Met Tyr Glu Met Gly Ala Cys Ile Lys  
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 Cys Gly Thr Val His Ile Ser Ala His Asn Asp Ser Gly Phe Leu Val  
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 Val Leu Thr Asp Asp Phe Glu Thr Ala Asp Ile Asp Glu Asp Asp Leu  
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 Lys Asn Leu Ile Arg Arg Leu Arg Thr Asp Ser Asn Ala Ala Pro Ser  
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Cys	Lys	Gly	Lys	Leu	Lys	Glu	Ile	Asp	Thr	Phe	Leu	Pro	Glu	Tyr	Ala	
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Ser	Ala	Lys	Glu	His	Thr	Ala	Gln	Trp	Thr	Pro	Thr	Glu	Ala	Ala	Glu	
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Val	Gln	Lys	Glu	Phe	Ile	Glu	Gly	Lys	Ile	Asn	Val	Leu	Ser	Cys	Ser	
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cag 4923

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<400> 36

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 20 25 30

Lys Val Asn Ala Lys Thr Glu Val Thr Arg Asn Ile Asp Pro Val Glu

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Ile Ser Pro Ser Asn Lys Thr Ile Ala Ala Glu Phe Asn Arg Glu Ile 65 70 75 80		
Asp Glu Ser Glu Asn Leu Val Tyr Gly Pro Ile Leu Gln Leu Thr Pro 85 90 95		
Pro Tyr Ala Pro Gly Lys Ser Pro Ala Gln Leu Ile Asp Glu Gly Val 100 105 110		
Leu Ser Pro Asn Phe Ser Arg Leu Asp Ala Ala Leu Pro Lys Asp Arg 115 120 125		
Pro Leu Tyr Gln His Gln Glu Asp Ala Leu Arg Lys Ile Ala Ser Gly 130 135 140		
Arg Asn Leu Ile Val Ser Thr Gly Thr Gly Ser Gly Lys Thr Glu Ser 145 150 155 160		
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Pro Glu Ile Thr Phe Gly Arg Tyr Thr Gly Asp Thr Lys Gln Thr Arg 210 215 220		
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Pro Leu Pro Asn Glu Leu Ile Ser Arg Asp Glu Met Gln Glu Asn Pro 245 250 255		
Pro His Ile Leu Leu Thr Asn Tyr Ala Met Leu Glu Tyr Leu Leu Leu 260 265 270		
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 645 650 655  
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 Leu Leu Thr Phe Ser Asp Ser Arg Gln Ala Ala Tyr Ala Ala Pro  
 675 680 685



Tyr Leu Gln Ala Ser Tyr Thr Arg Leu Leu Glu Arg Arg Ile Leu Ile  
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Leu Gln Ser Val Met Met Arg Asn Val Pro Pro Arg Thr Ala Asn Tyr 1025 1030 1035 1040		
Val Gln Arg Ala Gly Arg Ala Gly Arg Arg Ser Gly Ser Ala Ala Phe 1045 1050 1055		
Val Leu Thr Phe Ala Lys Arg Ser Ser His Asp Leu Ala Val Phe Lys 1060 1065 1070		
Asn Pro Thr Gln Met Ile Asp Gly Glu Met Thr Val Pro Phe Leu His 1075 1080 1085		
Ile Asn Asn Ala Arg Ile Ala Arg Arg His Thr Tyr Ser Ile Ala Leu 1090 1095 1100		
Ala Ala Phe Phe Arg Glu Gln Ala Ala Gln Asn Arg Phe Trp Lys Lys 1105 1110 1115 1120		
Ala Gly Glu Phe Phe Leu Gly Thr Asp Ala Ala Pro Tyr Leu Arg Pro 1125 1130 1135		
Ala Val Ala Glu Gln Glu Ala Thr Glu Ile Leu Glu Glu Phe Leu Ser 1140 1145 1150		
Pro Val Pro Asn Tyr Ile Thr Glu Ala Leu Arg Arg Val Phe Pro Glu 1155 1160 1165		
Ser Leu His Glu Asp Leu Asp Ile Glu Asn Gln Gly Trp Val Lys Gln 1170 1175 1180		
Phe Leu Glu Ile Phe Asp Thr Thr Arg Gln Glu Ile Ser Glu Asp Phe 1185 1190 1195 1200		
Gln Thr Leu Lys Lys Met Gln Gly Arg Ala Leu Gly Ser Glu Gln Gly 1205 1210 1215		
Lys Lys Ala Asp Ala Phe Lys Arg Thr Ile Thr Thr Leu Met Asp Gln 1220 1225 1230		
Asp Leu Leu Gly Tyr Leu Ala Lys Lys Asn Met Leu Pro Lys Tyr Ser 1235 1240 1245		
Phe Pro Val Asp Thr Val Asp Leu Gln Thr Asn Phe Ser Glu Ala Gly 1250 1255 1260		
Asn Lys Val Ser Leu Ser Arg Asp Leu Gln Leu Ala Ile Thr Asp Tyr 1265 1270 1275 1280		
Ala Pro Gly Ala Glu Leu Val Ala Gly Gly Lys Leu Trp Lys Ser Ala 1285 1290 1295		
Gly Ile Arg His Leu Ala Gly Lys Lys Val Glu Thr Phe Tyr Trp Thr 1300 1305 1310		
Thr Cys Thr Glu Cys Lys His Thr Glu Thr Ser Arg Phe Gly Phe Thr 1315 1320 1325		
Ser Glu Asp Val Cys Ser Gln Cys Ser Ala Pro Ile Ser Leu Gly Lys 1330 1335 1340		

Glu Asn Lys Phe Leu Ile Pro Arg Phe Gly Phe Val Ala Asp Pro Asn  
 1345 1350 1355 1360  
 Pro Thr Glu Val Gly Thr Ala Pro Pro Val Arg Ser Ser Asn Arg Leu  
 1365 1370 1375  
 Glu Phe Val Lys Gln Phe Gly Val Lys Asp Asp Ser Glu Glu Phe Ser  
 1380 1385 1390  
 Asn Ser Asp Gly Thr Ala Thr Ala Gln Val Leu Thr Ser Ser Trp Ser  
 1395 1400 1405  
 Arg Thr Glu Met Gly Ala Leu Glu Thr Gly Pro Asn Lys Asn Gly Phe  
 1410 1415 1420  
 Trp Tyr Cys Gln Thr Cys Gly Phe Gly Thr Pro Asn Gly Ala Glu Ile  
 1425 1430 1435 1440  
 Pro Lys Ser His Arg Asn Pro Arg Thr Lys Gln Gln Cys Gly Thr Tyr  
 1445 1450 1455  
 Tyr Leu Glu Pro His Ser Leu Gly His Thr Tyr Gln Thr Asp Ile Ala  
 1460 1465 1470  
 Thr Val Ala Val Pro Ser Tyr Thr Asn Leu Asp Phe Glu Gly Trp Arg  
 1475 1480 1485  
 Ser Gly Met Tyr Ala Ile Ile Glu Ala Ala Ala Glu Cys Leu Glu Ile  
 1490 1495 1500  
 Asn Arg Asp Asp Leu Asn Gly Thr Met Ala Lys His Asp Asn Arg Pro  
 1505 1510 1515 1520  
 Thr Met Val Leu Phe Asp Thr Val Pro Gly Gly Ala Gly Ile Thr Arg  
 1525 1530 1535  
 Lys Val Arg Glu Asn Phe Pro Gln Val Leu Glu Ala Ala Ile Arg Arg  
 1540 1545 1550  
 Val Glu Thr Cys Ser Cys Gly Ile Asp Thr Ser Cys Tyr Ala Cys Leu  
 1555 1560 1565  
 Arg Ser Phe Ser Asn Gln Arg Phe His Leu Asp Leu Arg Arg Asp Ile  
 1570 1575 1580  
 Ala Leu Asp Leu Leu His His Met Ala Val Ala Met Pro Lys Ser Glu  
 1585 1590 1595 1600

<210> 37  
 <211> 2799  
 <212> DNA  
 <213> Corynebacterium glutamicum  
 <220>  
 <221> CDS  
 <222> (101)..(2776)

&lt;223&gt; RXN01606

&lt;400&gt; 37

ctccaccctg gcgaatagaa caaacaaggt tcttcgcatg aaggactacc acccagaact 60

gaagggtctaa aagctttttcc cgcccggttc aatagcgtta atg gca gaa tca aac 115  
 Met Ala Glu Ser Asn  
 1 5

gct atg gac cgg gca caa atc tct gca ctg cta gat aga gca cag cac 163  
 Ala Met Asp Arg Ala Gln Ile Ser Ala Leu Leu Asp Arg Ala Gln His  
 10 15 20

aca atc aac ctt gcc gaa caa gca aac aac gtg ctc cga ctg ttg aaa 211  
 Thr Ile Asn Leu Ala Glu Gln Ala Asn Asn Val Leu Arg Leu Leu Lys  
 25 30 35

aca ccc gga acg gcc aca gta ggg gac aac ggg aca ctc ggc acc gat 259  
 Thr Pro Gly Thr Ala Thr Val Gly Asp Asn Gly Thr Leu Gly Thr Asp  
 40 45 50

acc tat ctg atc cca tcc cgc aac atc acc tgg cct gac aac ctg tat 307  
 Thr Tyr Leu Ile Pro Ser Arg Asn Ile Thr Trp Pro Asp Asn Leu Tyr  
 55 60 65

gtc aac gtc ttt cta gac ggc atg aat gca gaa gcc acc ctt acc gat 355  
 Val Asn Val Phe Leu Asp Gly Met Asn Ala Glu Ala Thr Leu Thr Asp  
 70 75 80 85

tac gtc gca tca gtc gct tcg atc cca cgc cta tgc cag atc atc aac 403  
 Tyr Val Ala Ser Val Ala Ser Ile Pro Arg Leu Cys Gln Ile Ile Asn  
 90 95 100

gag ggc caa ggc ggc atg ttc cgc aga cta ttc aac ccc acc aag gtc 451  
 Glu Gly Gln Gly Gly Met Phe Arg Arg Leu Phe Asn Pro Thr Lys Val  
 105 110 115

caa gcc ggc gac caa gct gtc ttc gac ctc atg gtc aaa ctc gac gag 499  
 Gln Ala Gly Asp Gln Ala Val Phe Asp Leu Met Val Lys Leu Asp Glu  
 120 125 130

att tca tct acc acc cac gaa gtc tcc cgc atg ctc gag ggc gtc cac 547  
 Ile Ser Ser Thr Thr His Glu Val Ser Arg Met Leu Glu Gly Val His  
 135 140 145

gct gcc cgc acc cgc caa caa ggc gtt gca ctt ttc cca ggt att 595  
 Ala Ala Arg Thr Arg Gln Gln Gln Gly Val Ala Leu Phe Pro Gly Ile  
 150 155 160 165

cat gga gtg gga gag cgc tac atc gaa cgc gca caa cag gta ctc gcc 643  
 His Gly Val Gly Glu Arg Tyr Ile Glu Arg Ala Gln Gln Val Leu Ala  
 170 175 180

tca gcc ctc ggt atc gct gga ttc ggt gcc gaa ccc tgg gac gga cat 691  
 Ser Ala Leu Gly Ile Ala Gly Phe Gly Ala Glu Pro Trp Asp Gly His  
 185 190 195

acc ctt gcc caa cgc cgc cgg gta gtc caa cgc tac gcc caa gat cct 739  
 Thr Leu Ala Gln Ala Arg Arg Val Val Gln Arg Tyr Ala Gln Asp Pro  
 200 205 210

aac tcc gaa tac cgg ctg aaa agc gaa gcc gag aaa cac ctc aca tcc Asn Ser Glu Tyr Arg Leu Lys Ser Glu Ala Glu Lys His Leu Thr Ser 215 220 225	787
atc aac gag ctc cgc gta cag ata ctc ctc gaa caa ctc ccc gtt gat Ile Asn Glu Leu Arg Val Gln Ile Leu Leu Glu Gln Leu Pro Val Asp 230 235 240 245	835
gcc cta cgc atg gct acc gac cac cgc ctg cgc ttt gga tcc ctc gat Ala Leu Arg Met Ala Thr Asp His Arg Leu Arg Phe Gly Ser Leu Asp 250 255 260	883
tcc atc cac gtc gca acc gtc gcc gac gtc cta aaa aca cac acc tcc Ser Ile His Val Ala Thr Val Ala Asp Val Leu Lys Thr His Thr Ser 265 270 275	931
atc ctc acc acc gtg caa ggt atc ggc gcc caa acc gcg ggg cgg atg Ile Leu Thr Thr Val Gln Gly Ile Gly Ala Gln Thr Ala Gly Arg Met 280 285 290	979
aaa gcc gca gca gaa aca ctc aaa caa gaa gca cta cgc cgc caa aac Lys Ala Ala Ala Glu Thr Leu Lys Gln Glu Ala Leu Arg Arg Gln Asn 295 300 305	1027
acc tcc atc ggc gac gaa cct acc caa ccc gcc atg cgt cta atc aac Thr Ser Ile Gly Asp Glu Pro Thr Gln Pro Ala Met Arg Leu Ile Asn 310 315 320 325	1075
gtg ctg gcc cgc ttc gac caa acc gaa acc atc acg ccc gaa gaa cgc Val Leu Ala Arg Phe Asp Gln Thr Glu Thr Ile Thr Pro Glu Glu Arg 330 335 340	1123
gcc cgc cgc acc cgc gtc atc gac tac gta gaa cac ata ccc cca agc Ala Arg Arg Thr Arg Val Ile Asp Tyr Val Glu His Ile Pro Pro Ser 345 350 355	1171
ctc gac ccc tac atc gtc atc aac cca gca acg cct gag ttc aac aac Leu Asp Pro Tyr Ile Val Ile Asn Pro Ala Thr Pro Glu Phe Asn Asn 360 365 370	1219
ttc acc gac gac ctc cgc tgg atc gac gca aac ccc aac ctc ttc cac Phe Thr Asp Asp Leu Arg Trp Ile Asp Ala Asn Pro Asn Leu Phe His 375 380 385	1267
cca caa aca atc acc acc cca ccc gcc gac atc tgg gac gac tac atc Pro Gln Thr Ile Thr Thr Pro Pro Ala Asp Ile Trp Asp Asp Tyr Ile 390 395 400 405	1315
tcc cgt ccc gct cac tac caa ggc ctg cta gcc acg ctg ctc ggc cgc Ser Arg Pro Ala His Tyr Gln Gly Leu Leu Ala Thr Leu Leu Gly Arg 410 415 420	1363
gac atc gaa ggc gca gac gaa ctc ctc gac gcc acc acc ctc caa aaa Asp Ile Glu Gly Ala Asp Glu Leu Leu Asp Ala Thr Thr Leu Gln Lys 425 430 435	1411
atc aga gac ctc acc ctc gac aaa act cat ctc acc gac ctc cac ctc Ile Arg Asp Leu Thr Leu Asp Lys Thr His Leu Thr Asp Leu His Leu 440 445 450	1459
cgc gga tac caa tca ttc ggc gcc cgc ttc gcc atc atc caa aag aaa	1507

Arg Gly Tyr Gln Ser Phe Gly Ala Arg Phe Ala Ile Ile Gln Lys Lys  
 455 460 465

acc ctc ctc ggc gac gac atg gga ctc ggc aaa aca gtc caa gcc ctc 1555  
 Thr Leu Leu Gly Asp Asp Met Gly Leu Gly Lys Thr Val Gln Ala Leu  
 470 475 480 485

tcc gca gct gca cac ctt gcc gcc acc gaa aaa gac ttc cgc acc ctc 1603  
 Ser Ala Ala Ala His Leu Ala Ala Thr Glu Lys Asp Phe Arg Thr Leu  
 490 495 500

gtc gtc gta ccc gca tcc gtc att gtt aac tgg acc cgc gaa tgc aaa 1651  
 Val Val Val Pro Ala Ser Val Ile Val Asn Trp Thr Arg Glu Cys Lys  
 505 510 515

cgc ttc ctc aac ctc ccc gta ttc atc gcc cac gga gac aac aaa caa 1699  
 Arg Phe Leu Asn Leu Pro Val Phe Ile Ala His Gly Asp Asn Lys Gln  
 520 525 530

gac gcc atc aac gcc tgg tct aac acc aac gga atc gca atc tgc acc 1747  
 Asp Ala Ile Asn Ala Trp Ser Asn Thr Asn Gly Ile Ala Ile Cys Thr  
 535 540 545

tac gac ggc gtc cgc acc atg gac atc ccc gcg cgt ctg gtc att 1795  
 Tyr Asp Gly Val Arg Thr Met Asp Ile Pro Ala Pro Gly Leu Val Ile  
 550 555 560 565

gcc gat gaa gcc cac ctg atc aaa aac ccc tcc acc aaa cgc acc caa 1843  
 Ala Asp Glu Ala His Leu Ile Lys Asn Pro Ser Thr Lys Arg Thr Gln  
 570 575 580

gca ctg cgc aaa ctt atc gac gcc gcc cca tac acc ctt ctg atg acc 1891  
 Ala Leu Arg Lys Leu Ile Asp Ala Ala Pro Tyr Thr Leu Leu Met Thr  
 585 590 595

ggc aca cca cta gaa aac aaa gtg gaa gag ttt gta aat ctc gtg cgc 1939  
 Gly Thr Pro Leu Glu Asn Lys Val Glu Glu Phe Val Asn Leu Val Arg  
 600 605 610

tac atc caa cgc gag ctg atc acc cgt ggc atg tcc aaa atg cag gcc 1987  
 Tyr Ile Gln Pro Glu Leu Ile Thr Arg Gly Met Ser Lys Met Gln Ala  
 615 620 625

gag aat ttc cgc gag cgc atc gca cca gcc tat ctg cgc aga aat caa 2035  
 Glu Asn Phe Arg Glu Arg Ile Ala Pro Ala Tyr Leu Arg Arg Asn Gln  
 630 635 640 645

gct gat gtg ctt gac gaa ctc cca gag cgc acc gac tcc atc gac tgg 2083  
 Ala Asp Val Leu Asp Glu Leu Pro Glu Arg Thr Asp Ser Ile Asp Trp  
 650 655 660

atc gac ctc acc cca gaa gac cgc agc gcc tac gac gac caa gtc cgc 2131  
 Ile Asp Leu Thr Pro Glu Asp Arg Ser Ala Tyr Asp Asp Gln Val Arg  
 665 670 675

caa ggc agc tgg atg ggc atg cgc cgc tcc gcc atg ctc tca cca aca 2179  
 Gln Gly Ser Trp Met Gly Met Arg Arg Ser Ala Met Leu Ser Pro Thr  
 680 685 690

cca cgc cta act tcc gca aaa atg caa cgc atc cta gaa ctc ttc gaa 2227  
 Pro Arg Leu Thr Ser Ala Lys Met Gln Arg Ile Leu Glu Leu Phe Glu

695	700	705	
gaa gca gaa gaa cac ggc	cgc aaa gcc ctc atc	ttc acc tac ttc ctc	2275
Glu Ala Glu Glu His Gly	Arg Lys Ala Leu Ile	Phe Thr Tyr Phe Leu	
710	715	725	
gac gtc ctc gac gaa ctg	gaa aag cat cta ggc	gag cgc gtc atc ggc	2323
Asp Val Leu Asp Gly	Glu Leu Glu Lys His	Leu Gly Glu Arg Val Ile	
730	735	740	
cgc att tcc ggc gac gtg	cca gcc acc aag cgc	caa ttg ctt gtc gac	2371
Arg Ile Ser Gly Asp	Val Pro Ala Thr Lys	Arg Gln Leu Leu Val Asp	
745	750	755	
gcc ctg tcc cac tcc aaa	ccc gga tcc gcc ctc att	gcc caa atc acc	2419
Ala Leu Ser His Ser Lys	Pro Gly Ser Ala Leu Ile	Ala Gln Ile Thr	
760	765	770	
gcc ggg gga gta ggc cta	aac atc caa tcc gcg	agc cta tgc att att	2467
Ala Gly Gly Val Gly Leu	Asn Ile Gln Ser Ala	Ser Leu Cys Ile Ile	
775	780	785	
tgt gaa cct caa gta aag	cca acc atc gaa cag	cag gcc gtc gcc cga	2515
Cys Glu Pro Gln Val Lys	Pro Thr Ile Glu Gln	Gln Ala Val Ala Arg	
790	795	800	
gtc cac cgc atg ggc caa	acc gcc acc gtc caa	gtc cac cga ctc atc	2563
Val His Arg Met Gly	Gln Thr Ala Thr Val	Gln Val His Arg Leu Ile	
810	815	820	
ggc gac gaa acc gca gac	gaa cgc atg cta gaa	atc ctg gca ggc aaa	2611
Gly Asp Glu Thr Ala Asp	Glu Arg Met Leu Glu	Ile Leu Ala Gly Lys	
825	830	835	
act cac gtc ttc gac gtc	tac gcc cgg cta tct	gaa acc gca gag att	2659
Thr His Val Phe Asp	Val Tyr Ala Arg Leu	Ser Glu Thr Ala Glu Ile	
840	845	850	
cca gat gct gtg gat atc	act gaa tca cag ctg	gca gca cgg gtt att	2707
Pro Asp Ala Val Asp Ile	Thr Glu Ser Gln Leu	Ala Ala Arg Val Ile	
855	860	865	
gat gag gag cgt gca cgg	tta ggg ctt act gaa	tcc act ggc cct aaa	2755
Asp Glu Glu Arg Ala Arg	Leu Gly Leu Thr Glu	Ser Thr Gly Pro Lys	
870	875	880	
gat gaa gaa acg gcc tta	agc tagttgccta aggc	cggaat taa	2799
Asp Glu Glu Thr Ala Leu	Ser		
890			

&lt;210&gt; 38

&lt;211&gt; 892

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 38

Met Ala Glu Ser Asn Ala Met Asp Arg Ala Gln Ile Ser Ala Leu Leu

1

5

10

15

Asp Arg Ala Gln His Thr Ile Asn Leu Ala Glu Gln Ala Asn Asn Val

20										25										30										
Leu Arg Leu Leu Lys Thr Pro Gly Thr Ala Thr Val Gly Asp Asn Gly																														
35											40										45									
Thr Leu Gly Thr Asp Thr Tyr Leu Ile Pro Ser Arg Asn Ile Thr Trp																														
50											55										60									
Pro Asp Asn Leu Tyr Val Asn Val Phe Leu Asp Gly Met Asn Ala Glu																														
65	70										75										80									
Ala Thr Leu Thr Asp Tyr Val Ala Ser Val Ala Ser Ile Pro Arg Leu																														
	85										90										95									
Cys Gln Ile Ile Asn Glu Gly Gln Gly Gly Met Phe Arg Arg Leu Phe																														
	100										105										110									
Asn Pro Thr Lys Val Gln Ala Gly Asp Gln Ala Val Phe Asp Leu Met																														
	115										120										125									
Val Lys Leu Asp Glu Ile Ser Ser Thr Thr His Glu Val Ser Arg Met																														
	130										135										140									
Leu Glu Gly Val His Ala Ala Arg Thr Arg Gln Gln Gly Val Ala																														
145	150										155										160									
Leu Phe Pro Gly Ile His Gly Val Gly Glu Arg Tyr Ile Glu Arg Ala																														
	165										170										175									
Gln Gln Val Leu Ala Ser Ala Leu Gly Ile Ala Gly Phe Gly Ala Glu																														
	180										185										190									
Pro Trp Asp Gly His Thr Leu Ala Gln Ala Arg Arg Val Val Gln Arg																														
	195										200										205									
Tyr Ala Gln Asp Pro Asn Ser Glu Tyr Arg Leu Lys Ser Glu Ala Glu																														
	210										215										220									
Lys His Leu Thr Ser Ile Asn Glu Leu Arg Val Gln Ile Leu Leu Glu																														
225	230										235										240									
Gln Leu Pro Val Asp Ala Leu Arg Met Ala Thr Asp His Arg Leu Arg																														
	245										250										255									
Phe Gly Ser Leu Asp Ser Ile His Val Ala Thr Val Ala Asp Val Leu																														
	260										265										270									
Lys Thr His Thr Ser Ile Leu Thr Thr Val Gln Gly Ile Gly Ala Gln																														
	275										280										285									
Thr Ala Gly Arg Met Lys Ala Ala Ala Glu Thr Leu Lys Gln Glu Ala																														
	290										295										300									
Leu Arg Arg Gln Asn Thr Ser Ile Gly Asp Glu Pro Thr Gln Pro Ala																														
305	310										315										320									
Met Arg Leu Ile Asn Val Leu Ala Arg Phe Asp Gln Thr Glu Thr Ile																														
	325										330										335									
Thr Pro Glu Glu Arg Ala Arg Arg Thr Arg Val Ile Asp Tyr Val Glu																														
	340										345										350									



His Ile Pro Pro Ser Leu Asp Pro Tyr Ile Val Ile Asn Pro Ala Thr  
 355 360 365  
 Pro Glu Phe Asn Asn Phe Thr Asp Asp Leu Arg Trp Ile Asp Ala Asn  
 370 375 380  
 Pro Asn Leu Phe His Pro Gln Thr Ile Thr Thr Pro Pro Ala Asp Ile  
 385 390 395 400  
 Trp Asp Asp Tyr Ile Ser Arg Pro Ala His Tyr Gln Gly Leu Leu Ala  
 405 410 415  
 Thr Leu Leu Gly Arg Asp Ile Glu Gly Ala Asp Glu Leu Leu Asp Ala  
 420 425 430  
 Thr Thr Leu Gln Lys Ile Arg Asp Leu Thr Leu Asp Lys Thr His Leu  
 435 440 445  
 Thr Asp Leu His Leu Arg Gly Tyr Gln Ser Phe Gly Ala Arg Phe Ala  
 450 455 460  
 Ile Ile Gln Lys Lys Thr Leu Leu Gly Asp Asp Met Gly Leu Gly Lys  
 465 470 475 480  
 Thr Val Gln Ala Leu Ser Ala Ala Ala His Leu Ala Ala Thr Glu Lys  
 485 490 495  
 Asp Phe Arg Thr Leu Val Val Val Pro Ala Ser Val Ile Val Asn Trp  
 500 505 510  
 Thr Arg Glu Cys Lys Arg Phe Leu Asn Leu Pro Val Phe Ile Ala His  
 515 520 525  
 Gly Asp Asn Lys Gln Asp Ala Ile Asn Ala Trp Ser Asn Thr Asn Gly  
 530 535 540  
 Ile Ala Ile Cys Thr Tyr Asp Gly Val Arg Thr Met Asp Ile Pro Ala  
 545 550 555 560  
 Pro Gly Leu Val Ile Ala Asp Glu Ala His Leu Ile Lys Asn Pro Ser  
 565 570 575  
 Thr Lys Arg Thr Gln Ala Leu Arg Lys Leu Ile Asp Ala Ala Pro Tyr  
 580 585 590  
 Thr Leu Leu Met Thr Gly Thr Pro Leu Glu Asn Lys Val Glu Glu Phe  
 595 600 605  
 Val Asn Leu Val Arg Tyr Ile Gln Pro Glu Leu Ile Thr Arg Gly Met  
 610 615 620  
 Ser Lys Met Gln Ala Glu Asn Phe Arg Glu Arg Ile Ala Pro Ala Tyr  
 625 630 635 640  
 Leu Arg Arg Asn Gln Ala Asp Val Leu Asp Glu Leu Pro Glu Arg Thr  
 645 650 655  
 Asp Ser Ile Asp Trp Ile Asp Leu Thr Pro Glu Asp Arg Ser Ala Tyr  
 660 665 670

Asp Asp Gln Val Arg Gln Gly Ser Trp Met Gly Met Arg Arg Ser Ala  
675 680 685

Met Leu Ser Pro Thr Pro Arg Leu Thr Ser Ala Lys Met Gln Arg Ile  
690 695 700

Leu Glu Leu Phe Glu Glu Ala Glu Glu His Gly Arg Lys Ala Leu Ile  
705 710 715 720

Phe Thr Tyr Phe Leu Asp Val Leu Asp Glu Leu Glu Lys His Leu Gly  
725 730 735

Glu Arg Val Ile Gly Arg Ile Ser Gly Asp Val Pro Ala Thr Lys Arg  
740 745 750

Gln Leu Leu Val Asp Ala Leu Ser His Ser Lys Pro Gly Ser Ala Leu  
755 760 765

Ile Ala Gln Ile Thr Ala Gly Gly Val Gly Leu Asn Ile Gln Ser Ala  
770 775 780

Ser Leu Cys Ile Ile Cys Glu Pro Gln Val Lys Pro Thr Ile Glu Gln  
785 790 795 800

Gln Ala Val Ala Arg Val His Arg Met Gly Gln Thr Ala Thr Val Gln  
805 810 815

Val His Arg Leu Ile Gly Asp Glu Thr Ala Asp Glu Arg Met Leu Glu  
820 825 830

Ile Leu Ala Gly Lys Thr His Val Phe Asp Val Tyr Ala Arg Leu Ser  
835 840 845

Glu Thr Ala Glu Ile Pro Asp Ala Val Asp Ile Thr Glu Ser Gln Leu  
850 855 860

Ala Ala Arg Val Ile Asp Glu Glu Arg Ala Arg Leu Gly Leu Thr Glu  
865 870 875 880

Ser Thr Gly Pro Lys Asp Glu Glu Thr Ala Leu Ser  
885 890

<210> 39

<211> 731

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(708)

<223> FRXA01797

<400> 39

ggg tct ata gcg tgg att gac ctc acc cca gaa gac cgc agc gcc tac 48  
Gly Ser Ile Ala Trp Ile Asp Leu Thr Pro Glu Asp Arg Ser Ala Tyr  
1 5 10 15

gac gac caa gtc cgc caa ggc agc tgg atg ggc atg cgc cgc tcc gcc 96  
Asp Asp Gln Val Arg Gln Gly Ser Trp Met Gly Met Arg Arg Ser Ala  
20 25 30

atg ctc tca cca aca cca cgc cta act tcc gca aaa atg caa cgc atc 144  
 Met Leu Ser Pro Thr Pro Arg Leu Thr Ser Ala Lys Met Gln Arg Ile  
 35 40 45  
 cta gaa ctc ttc gaa gaa gca gaa gaa cac ggc cgc aaa gcc ctc atc 192  
 Leu Glu Leu Phe Glu Glu Ala Glu Glu His Gly Arg Lys Ala Leu Ile  
 50 55 60  
 ttc acc tac ttc ctc gac gtc ctc gac gaa ctg gaa aag cat cta ggc 240  
 Phe Thr Tyr Phe Leu Asp Val Leu Asp Glu Leu Lys His Leu Gly  
 65 70 75 80  
 gag cgc gtc atc ggc cgc att tcc ggc gac gtg cca gcc acc aag cgc 288  
 Glu Arg Val Ile Gly Arg Ile Ser Gly Asp Val Pro Ala Thr Lys Arg  
 85 90 95  
 caa ttg ctt gtc gac gcc ctg tcc cac tcc aaa ccc gga tcc gcc ctc 336  
 Gln Leu Leu Val Asp Ala Leu Ser His Ser Lys Pro Gly Ser Ala Leu  
 100 105 110  
 att gcc caa atc acc gcc ggc gga gta ggc cta aac atc caa tcc gcg 384  
 Ile Ala Gln Ile Thr Ala Gly Gly Val Gly Leu Asn Ile Gln Ser Ala  
 115 120 125  
 agc cta tgc att att tgt gaa cct caa gta aag cca acc atc gaa cag 432  
 Ser Leu Cys Ile Ile Cys Glu Pro Gln Val Lys Pro Thr Ile Glu Gln  
 130 135 140  
 cag gcc gtc gcc cga gtc cac cgc atg ggc caa acc gcc acc gtc caa 480  
 Gln Ala Val Ala Arg Val His Arg Met Gly Gln Thr Ala Thr Val Gln  
 145 150 155 160  
 gtc cac cga ctc atc ggc gac gaa acc gca gac gaa cgc atg cta gaa 528  
 Val His Arg Leu Ile Gly Asp Glu Thr Ala Asp Glu Arg Met Leu Glu  
 165 170 175  
 atc ctg gca ggc aaa act cac gtc ttc gac gtc tac gcc cgg cta tct 576  
 Ile Leu Ala Gly Lys Thr His Val Phe Asp Val Tyr Ala Arg Leu Ser  
 180 185 190  
 gaa acc gca gag att cca gat gct gtg gat atc act gaa tca cag ctg 624  
 Glu Thr Ala Glu Ile Pro Asp Ala Val Asp Ile Thr Glu Ser Gln Leu  
 195 200 205  
 gca gca cgg gtt att gat gag gag cgt gca cgg tta ggg ctt act gaa 672  
 Ala Ala Arg Val Ile Asp Glu Glu Arg Ala Arg Leu Gly Leu Thr Glu  
 210 215 220  
 tcc act ggc cct aaa gat gaa gaa acg gcc tta agc tagttgccta 718  
 Ser Thr Gly Pro Lys Asp Glu Glu Thr Ala Ser  
 225 230 235  
 aggccggaat taa 731

&lt;210&gt; 40

&lt;211&gt; 236

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 40

Gly Ser Ile Ala Trp Ile Asp Leu Thr Pro Glu Asp Arg Ser Ala Tyr  
 1 5 10 15

Asp Asp Gln Val Arg Gln Gly Ser Trp Met Gly Met Arg Arg Ser Ala  
 20 25 30

Met Leu Ser Ser Pro Thr Pro Arg Leu Thr Ser Ala Lys Met Gln Arg Ile  
 35 40 45

Leu Glu Leu Phe Glu Glu Ala Glu Glu His Gly Arg Lys Ala Leu Ile  
 50 55 60

Phe Thr Tyr Phe Leu Asp Val Leu Asp Glu Leu Glu Lys His Leu Gly  
 65 70 75 80

Glu Arg Val Ile Gly Arg Ile Ser Gly Asp Val Pro Ala Thr Lys Arg  
 85 90 95

Gln Leu Leu Val Asp Ala Leu Ser His Ser Lys Pro Gly Ser Ala Leu  
 100 105 110

Ile Ala Gln Ile Thr Ala Gly Gly Val Gly Leu Asn Ile Gln Ser Ala  
 115 120 125

Ser Leu Cys Ile Ile Cys Glu Pro Gln Val Lys Pro Thr Ile Glu Gln  
 130 135 140

Gln Ala Val Ala Arg Val His Arg Met Gly Gln Thr Ala Thr Val Gln  
 145 150 155 160

Val His Arg Leu Ile Gly Asp Glu Thr Ala Asp Glu Arg Met Leu Glu  
 165 170 175

Ile Leu Ala Gly Lys Thr His Val Phe Asp Val Tyr Ala Arg Leu Ser  
 180 185 190

Glu Thr Ala Glu Ile Pro Asp Ala Val Asp Ile Thr Glu Ser Gln Leu  
 195 200 205

Ala Ala Arg Val Ile Asp Glu Glu Arg Ala Arg Leu Gly Leu Thr Glu  
 210 215 220

Ser Thr Gly Pro Lys Asp Glu Glu Thr Ala Leu Ser  
 225 230 235

&lt;210&gt; 41

&lt;211&gt; 1299

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1276)

&lt;223&gt; RXN01030

&lt;400&gt; 41

cctccccgc cacacgcccc agaggggttc tttttcatcc tttttaaat atacttatat 60  
 gtattaatcc cctctttgtg cagcatagga gactactgct atg acc tca aca acc 115

	Met	Thr	Ser	Thr	Thr	
	1				5	
caa cct ggc aca aca cct gag ctc agc gca gac act cat tct gag ccc						163
Gln Pro Gly Thr Thr Pro Glu Leu Ser Ala Asp Thr His Ser Glu Pro	10				20	
tggt gat gtc gtc atc gaa aac acc ctt gaa cct ttt caa aaa gtc gtt						211
Trp Asp Val Val Ile Glu Asn Thr Leu Glu Pro Phe Gln Lys Val Val	25				35	
cgt caa ttt att att gac cgc ccc tat tcc ggc att ttc ctc acc atg						259
Arg Gln Phe Ile Ile Asp Arg Pro Tyr Ser Gly Ile Phe Leu Thr Met	40				50	
ggg ggc ggc aaa aca ctc act acc ctc tcc gca ttg acc tat atc cag						307
Gly Gly Gly Lys Thr Leu Thr Thr Leu Ser Ala Leu Thr Tyr Ile Gln	55				65	
cca cct gga cac att ctg gtt gtc gcg cct cta aat atc tct cga ctc						355
Pro Pro Gly His Ile Leu Val Val Ala Pro Leu Asn Ile Ser Arg Leu	70				85	
acc tgg ccc gaa gag gtt cgc aag tgg aat atc cct gtt aac gca atc						403
Thr Trp Pro Glu Glu Val Arg Lys Thr Asn Ile Pro Val Asn Ala Ile	90				100	
tcg ctg atc acc aat gag cgc ggc acc aaa ctc acc cgc gcc aaa cgc						451
Ser Leu Ile Thr Asn Glu Arg Gly Thr Lys Leu Thr Arg Ala Lys Arg	105				115	
ctc aaa ctc tat gag gaa aca gcg acc aca cca cca acg ctg tat tac						499
Leu Lys Leu Tyr Glu Glu Thr Ala Thr Thr Pro Pro Thr Leu Tyr Tyr	120				130	
atc acc att aat ctg ctc gaa gat att gtc aat tac ttt ggt gat agg						547
Ile Thr Ile Asn Leu Leu Glu Asp Ile Val Asn Tyr Phe Gly Asp Arg	135				145	
tggt ccg ttt tgg aca gtc att att gat gag tca cag aca atc tct gat						595
Trp Pro Phe Trp Thr Val Ile Ile Asp Glu Ser Gln Thr Ile Ser Asp	150				165	
ata tcc tcc aag cgc act aga gcg ctc ttt tct gtg cga ccc tat atc						643
Ile Ser Ser Lys Arg Thr Arg Ala Leu Phe Ser Val Arg Pro Tyr Ile	170				180	
ggc aga cta att ctg ctc acc gga acc ccc agc gcc aac aag ttc gac						691
Gly Arg Leu Ile Leu Leu Thr Gly Thr Pro Ser Ala Asn Lys Phe Asp	185				195	
tcc att tac gcc caa gtc gca gtg cta gat tat ggt gcc agc ctg ggt						739
Ser Ile Tyr Ala Gln Val Ala Val Leu Asp Tyr Gly Ala Ser Leu Gly	200				210	
gac aac atc gac gta ttc cga gcc aga tgg tgt gcg ccc gac att att						787
Asp Asn Ile Asp Val Phe Arg Ala Arg Trp Cys Ala Pro Asp Ile Ile	215				225	
acc gat aaa caa gtg cgt cgc tgg aag ccg gct aac aag cag gct gaa						835
Thr Asp Lys Gln Val Arg Arg Trp Lys Pro Ala Asn Lys Gln Ala Glu						

230	235	240	245	
gca gag gtg tac cgc act att agc cac ctg gtc atg tct gcc gtc aac				883
Ala Glu Val Tyr Arg Thr Ile Ser His Leu Val Met Ser Ala Val Asn	250	255	260	
acg gat att aag ctg cca ccg ctg cat ttt gtt gat cac gag gta cac				931
Thr Asp Ile Lys Leu Pro Pro Leu His Phe Val Asp His Glu Val His	265	270	275	
atg agc gac gat gag cac cgc gac tac gag ctc ttc aaa aag gac gcg				979
Met Ser Asp Asp Glu His Arg Asp Tyr Glu Leu Phe Lys Lys Asp Ala	280	285	290	
gtg ctt gct gca ttg ctc gat atg gct gaa gag aat gag ggt gcc gaa				1027
Val Leu Ala Ala Leu Leu Asp Met Ala Glu Glu Asn Glu Gly Gly Glu	295	300	305	
ggc gct gat gac act gac gct gct gat tca gcg aca acg acc cca cct				1075
Gly Ala Asp Asp Thr Asp Ala Ala Asp Ser Ala Thr Thr Pro Pro	310	315	320	325
gcg tca tca cag cca aca aac cct gcc atc ccc gct gga ctg ctt cag				1123
Ala Ser Ser Gln Pro Thr Asn Pro Ala Ile Pro Ala Gly Leu Leu Gln	330	335	340	
gca ata caa caa acc cag gac acc aat ggt cgc gcc atc gcg cct gtg				1171
Ala Ile Gln Gln Thr Gln Asp Thr Asn Gly Arg Ala Ile Ala Pro Val	345	350	355	
acc aca gct gaa ctt gat cat ttt gat gat ctg cca gta cag cgc caa				1219
Thr Thr Ala Glu Leu Asp His Phe Asp Asp Leu Pro Val Gln Arg Gln	360	365	370	
gaa gat ctt gcc acc tta gtt gtt atc tct gct gtt cac gca agc gac				1267
Glu Asp Leu Gly Thr Leu Val Val Ile Ser Ala Val His Ala Ser Asp	375	380	385	
tct gcg gca tgaaactgct gcaatacgca ggt				1299
Ser Ala Ala				
390				
<210> 42				
<211> 392				
<212> PRT				
<213> Corynebacterium glutamicum				
<400> 42				
Met Thr Ser Thr Thr Gln Pro Gly Thr Thr Pro Glu Leu Ser Ala Asp				
1 5 10 15				
Thr His Ser Glu Pro Trp Asp Val Val Ile Glu Asn Thr Leu Glu Pro				
20 25 30				
Phe Gln Lys Val Val Arg Gln Phe Ile Ile Asp Arg Pro Tyr Ser Gly				
35 40 45				
Ile Phe Leu Thr Met Gly Gly Gly Lys Thr Leu Thr Thr Leu Ser Ala				
50 55 60				

Leu Thr Tyr Ile Gln Pro Pro Gly His Ile Leu Val Val Ala Pro Leu  
 65 70 75 80  
 Asn Ile Ser Arg Leu Thr Trp Pro Glu Glu Val Arg Lys Trp Asn Ile  
 85 90 95  
 Pro Val Asn Ala Ile Ser Leu Ile Thr Asn Glu Arg Gly Thr Lys Leu  
 100 105 110  
 Thr Arg Ala Lys Arg Leu Lys Leu Tyr Glu Glu Thr Ala Thr Thr Pro  
 115 120 125  
 Pro Thr Leu Tyr Tyr Ile Thr Ile Asn Leu Leu Glu Asp Ile Val Asn  
 130 135 140  
 Tyr Phe Gly Asp Arg Trp Pro Phe Trp Thr Val Ile Ile Asp Glu Ser  
 145 150 155 160  
 Gln Thr Ile Ser Asp Ile Ser Ser Lys Arg Thr Arg Ala Leu Phe Ser  
 165 170 175  
 Val Arg Pro Tyr Ile Gly Arg Leu Ile Leu Leu Thr Gly Thr Pro Ser  
 180 185 190  
 Ala Asn Lys Phe Asp Ser Ile Tyr Ala Gln Val Ala Val Leu Asp Tyr  
 195 200 205  
 Gly Ala Ser Leu Gly Asp Asn Ile Asp Val Phe Arg Ala Arg Trp Cys  
 210 215 220  
 Ala Pro Asp Ile Ile Thr Asp Lys Gln Val Arg Arg Trp Lys Pro Ala  
 225 230 235 240  
 Asn Lys Gln Ala Glu Ala Glu Val Tyr Arg Thr Ile Ser His Leu Val  
 245 250 255  
 Met Ser Ala Val Asn Thr Asp Ile Lys Leu Pro Pro Leu His Phe Val  
 260 265 270  
 Asp His Glu Val His Met Ser Asp Asp Glu His Arg Asp Tyr Glu Leu  
 275 280 285  
 Phe Lys Lys Asp Ala Val Leu Ala Ala Leu Leu Asp Met Ala Glu Glu  
 290 295 300  
 Asn Glu Gly Gly Glu Gly Ala Asp Asp Thr Asp Ala Ala Asp Ser Ala  
 305 310 315 320  
 Thr Thr Thr Pro Pro Ala Ser Ser Gln Pro Thr Asn Pro Ala Ile Pro  
 325 330 335  
 Ala Gly Leu Leu Gln Ala Ile Gln Gln Thr Gln Asp Thr Asn Gly Arg  
 340 345 350  
 Ala Ile Ala Pro Val Thr Thr Ala Glu Leu Asp His Phe Asp Asp Leu  
 355 360 365  
 Pro Val Gln Arg Gln Glu Asp Leu Gly Thr Leu Val Val Ile Ser Ala  
 370 375 380  
 Val His Ala Ser Asp Ser Ala Ala

385

390

<210> 43

<211> 1299

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101) . . (1276)

<223> FRXA01030

<400> 43

cctccccggc cacacgcccc agaggggttc tttttcatcc tttttaaaat atacttatat 60

gtattaaatcc cctctttgtg cagcatagga gactactgct atg acc tca aca acc 115  
Met Thr Ser Thr Thr  
1 5

caa cct ggc aca aca cct gag ctc agc gca gac act cat tct gag ccc 163  
Gln Pro Gly Thr Thr Pro Glu Leu Ser Ala Asp Thr His Ser Glu Pro  
10 15 20

tgg gat gtc gtc atc gaa aac acc ctt gaa cct ttt caa aaa gtc gtt      211  
Trp Asp Val Val Ile Glu Asn Thr Leu Glu Pro Phe Gln Lys Val Val

25                          30                          35

cgt caa ttt att att gac cgc ccc tat tcc ggc att ttc ctc acc atg 259  
Arg Gln Phe Ile Ile Asp Arg Pro Tyr Ser Gly Ile Phe Leu Thr Met  
40 45 50

ggt ggc ggc aaa aca ctc act acc ctc tcc gca ttg acc tat atc cag 307  
Gly Gly Gly Lys Thr Leu Thr Thr Leu Ser Ala Leu Thr Tyr Ile Gln  
55 60 65

cca cct gga cac att ctg gtt gtc gcg cct cta aat atc tct cga ctc 355  
Pro Pro Gly His Ile Leu Val Val Ala Pro Leu Asn Ile Ser Arg Leu  
70 75 80 85

acc tgg ccc gaa gag gtt cgc aag tgg aat atc cct gtt aac gca atc 403  
Thr Trp Pro Glu Glu Val Arg Lys Trp Asn Ile Pro Val Asn Ala Ile  
90 95 100

tcg ctg atc acc aat gag cgc ggc acc aaa ctc acc cgc gcc aaa cgc 451  
Ser Leu Ile Thr Asn Glu Arg Gly Thr Lys Leu Thr Arg Ala Lys Arg  
105 110 115

ctc aaa ctc tat gag gaa aca gcg acc aca cca cca acg ctg tat tac 499  
Leu Lys Leu Tyr Glu Glu Thr Ala Thr Thr Pro Pro Thr Leu Tyr Tyr  
120 125 130

atc acc att aat ctg ctc gaa gat att gtc aat tac ttt ggt gat agg 547  
Ile Thr Ile Asn Leu Leu Glu Asp Ile Val Asn Tyr Phe Gly Asp Arg  
135 140 145

tgg ccg ttt tgg aca gtc att att gat gag tca cag aca atc tct gat 595  
 Trp Pro Phe Trp Thr Val Ile Ile Asp Glu Ser Gln Thr Ile Ser Asp  
 150 155 160 165

ata tcc tcc aag cgc act aga gcg ctc ttt tct gtg cga ccc tat atc 643



Ile Ser Ser Lys Arg Thr Arg Ala Leu Phe Ser Val Arg Pro Tyr Ile  
170 175 180

ggc aga cta att ctg ctc acc gga acc ccc agc gcc aac aag ttc gac 691  
Gly Arg Leu Ile Leu Leu Thr Gly Thr Pro Ser Ala Asn Lys Phe Asp  
185 190 195

tcc att tac gcc caa gtc gca gtg cta gat tat ggt gcc agc ctg ggt 739  
Ser Ile Tyr Ala Gln Val Ala Val Leu Asp Tyr Gly Ala Ser Leu Gly  
200 205 210

gac aac atc gac gta ttc cga gcc aga tgg tgt gcg ccc gac att att 787  
Asp Asn Ile Asp Val Phe Arg Ala Arg Trp Cys Ala Pro Asp Ile Ile  
215 220 225

acc gat aaa caa gtg cgt cgc tgg aag ccg gct aac aag cag gct gaa 835  
Thr Asp Lys Gln Val Arg Arg Trp Lys Pro Ala Asn Lys Gln Ala Glu  
230 235 240 245

gca gag gtg tac cgc act att agc cac ctg gtc atg tct gcc gtc aac 883  
Ala Glu Val Tyr Arg Thr Ile Ser His Leu Val Met Ser Ala Val Asn  
250 255 260

acg gat att aag ctg cca ccg ctg cat ttt gtt gat cac gag gta cac 931  
Thr Asp Ile Lys Leu Pro Pro Leu His Phe Val Asp His Glu Val His  
265 270 275

atg agc gac gat gag cac cgc gac tac gag ctc ttc aaa aag gac gcg 979  
Met Ser Asp Asp Glu His Arg Asp Tyr Glu Leu Phe Lys Lys Asp Ala  
280 285 290

gtg ctt gct gca ttg ctc gat atg gct gaa gag aat gag ggt ggc gaa 1027  
Val Leu Ala Ala Leu Leu Asp Met Ala Glu Glu Asn Glu Gly Gly Glu  
295 300 305

ggc gct gat gac act gac gct gct gat tca gcg aca acg acc cca cct 1075  
Gly Ala Asp Asp Thr Asp Ala Ala Asp Ser Ala Thr Thr Thr Pro Pro  
310 315 320 325

gcg tca tca cag cca aca aac cct gcc atc ccc gct gga ctg ctt cag 1123  
Ala Ser Ser Gln Pro Thr Asn Pro Ala Ile Pro Ala Gly Leu Leu Gln  
330 335 340

gca ata caa caa acc cag gac acc aat ggt cgc gcc atc gcg cct gtg 1171  
Ala Ile Gln Gln Thr Gln Asp Thr Asn Gly Arg Ala Ile Ala Pro Val  
345 350 355

acc aca gct gaa ctt gat cat ttt gat gat ctg cca gta cag cgc caa 1219  
Thr Thr Ala Glu Leu Asp His Phe Asp Asp Leu Pro Val Gln Arg Gln  
360 365 370

gaa gat ctt ggc acc tta gtt gtt atc tct gct gtt cac gca agc gac 1267  
Glu Asp Leu Gly Thr Leu Val Val Ile Ser Ala Val His Ala Ser Asp  
375 380 385

tct gcg gca tgaaactgct gcaatacgca ggt 1299  
Ser Ala Ala  
390

&lt;211&gt; 392

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 44

Met Thr Ser Thr Thr Gln Pro Gly Thr Thr Pro Glu Leu Ser Ala Asp  
 1 5 10 15

Thr His Ser Glu Pro Trp Asp Val Val Ile Glu Asn Thr Leu Glu Pro  
 20 25 30

Phe Gln Lys Val Val Arg Gln Phe Ile Ile Asp Arg Pro Tyr Ser Gly  
 35 40 45

Ile Phe Leu Thr Met Gly Gly Lys Thr Leu Thr Thr Leu Ser Ala  
 50 55 60

Leu Thr Tyr Ile Gln Pro Pro Gly His Ile Leu Val Val Ala Pro Leu  
 65 70 75 80

Asn Ile Ser Arg Leu Thr Trp Pro Glu Glu Val Arg Lys Trp Asn Ile  
 85 90 95

Pro Val Asn Ala Ile Ser Leu Ile Thr Asn Glu Arg Gly Thr Lys Leu  
 100 105 110

Thr Arg Ala Lys Arg Leu Lys Leu Tyr Glu Glu Thr Ala Thr Thr Pro  
 115 120 125

Pro Thr Leu Tyr Tyr Ile Thr Ile Asn Leu Leu Glu Asp Ile Val Asn  
 130 135 140

Tyr Phe Gly Asp Arg Trp Pro Phe Trp Thr Val Ile Ile Asp Glu Ser  
 145 150 155 160

Gln Thr Ile Ser Asp Ile Ser Ser Lys Arg Thr Arg Ala Leu Phe Ser  
 165 170 175

Val Arg Pro Tyr Ile Gly Arg Leu Ile Leu Leu Thr Gly Thr Pro Ser  
 180 185 190

Ala Asn Lys Phe Asp Ser Ile Tyr Ala Gln Val Ala Val Leu Asp Tyr  
 195 200 205

Gly Ala Ser Leu Gly Asp Asn Ile Asp Val Phe Arg Ala Arg Trp Cys  
 210 215 220

Ala Pro Asp Ile Ile Thr Asp Lys Gln Val Arg Arg Trp Lys Pro Ala  
 225 230 235 240

Asn Lys Gln Ala Glu Ala Glu Val Tyr Arg Thr Ile Ser His Leu Val  
 245 250 255

Met Ser Ala Val Asn Thr Asp Ile Lys Leu Pro Pro Leu His Phe Val  
 260 265 270

Asp His Glu Val His Met Ser Asp Asp Glu His Arg Asp Tyr Glu Leu  
 275 280 285

Phe Lys Lys Asp Ala Val Leu Ala Ala Leu Leu Asp Met Ala Glu Glu  
 290 295 300

Asn Glu Gly Gly Glu Gly Ala Asp Asp Thr Asp Ala Ala Asp Ser Ala 305 310 315 320  
 Thr Thr Thr Pro Pro Ala Ser Ser Gln Pro Thr Asn Pro Ala Ile Pro 325 330 335  
 Ala Gly Leu Leu Gln Ala Ile Gln Gln Thr Gln Asp Thr Asn Gly Arg 340 345 350  
 Ala Ile Ala Pro Val Thr Thr Ala Glu Leu Asp His Phe Asp Asp Leu 355 360 365  
 Pro Val Gln Arg Gln Glu Asp Leu Gly Thr Leu Val Val Ile Ser Ala 370 375 380  
 Val His Ala Ser Asp Ser Ala Ala 385 390

<210> 45  
 <211> 720  
 <212> DNA  
 <213> *Corynebacterium glutamicum*

<220>  
 <221> CDS  
 <222> (101)..(697)  
 <223> RXA01739

<400> 45  
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 cctgggcgcg agataaaca aactaaggga gctttttaca gtg atc aat ttg cag 115  
 Val Ile Asn Leu Gln 5  
 1  
 gac ctc gac gag gat caa cgc atc gct gct tct gcg cct cgc gga cca 163  
 Asp Leu Asp Glu Asp Gln Arg Ile Ala Ser Ala Pro Arg Gly Pro 20  
 10 15  
 gtg tgc att ctc gcc gga gcc gcc acg ggt aaa act cga acg att act 211  
 Val Cys Ile Leu Ala Gly Ala Gly Thr Gly Lys Thr Arg Thr Ile Thr 35  
 25 30  
 tat cgc atc gcg cat ctg att gat cag ggt ttt gtg agc ccg aat cgt 259  
 Tyr Arg Ile Ala His Leu Ile Asp Gln Gly Phe Val Ser Pro Asn Arg 50  
 40 45  
 gtt ctt gct gtg acg ttt aca tcc cgc gcg gca ggg gag atg cgt cat 307  
 Val Leu Ala Val Thr Phe Thr Ser Arg Ala Ala Gly Glu Met Arg His 65  
 55 60  
 cgc ttg aat ctc atg ggg atc ggt gcc gtg cag gca agg aca ttc cac 355  
 Arg Leu Asn Leu Met Gly Ile Gly Gly Val Gln Ala Arg Thr Phe His 85  
 70 75 80  
 gca gca gcg agg aag cag ttg ttg tat ttc tgg cct cag gtg gcg ggt 403  
 Ala Ala Ala Arg Lys Gln Leu Leu Tyr Phe Trp Pro Gln Val Ala Gly 100  
 90 95

aat ctg ccg tgg cgc ctg ttg gat aat aag ttt caa ctt gtg ggt cgt 451  
 Asn Leu Pro Trp Arg Leu Leu Asp Asn Lys Phe Gln Leu Val Gly Arg  
 105 110 115

gcg gtt cgt ggt cgc cgg ttg gaa tcg cag act gaa aaa gtt cgc gat 499  
 Ala Val Arg Gly Ala Arg Leu Glu Ser Gln Thr Glu Lys Val Arg Asp  
 120 125 130

att ttg ggt gaa att gag tgg cgc aag cgc tcg ttg att aca cct gag 547  
 Ile Leu Gly Glu Ile Glu Trp Ala Lys Ala Ser Leu Ile Thr Pro Glu  
 135 140 145

cag tat ccg gat cgt ttg ggt acg agg acc cct ccg cgc ccc cgc gag 595  
 Gln Tyr Pro Asp Arg Leu Gly Thr Arg Thr Pro Pro Ala Pro Ala Glu  
 150 155 160 165

aaa atc gct gag gtg tat cag cga tac gaa aac atg aag gca acc cct 643  
 Lys Ile Ala Glu Val Tyr Gln Arg Tyr Glu Asn Met Lys Ala Thr Pro  
 170 175 180

gag ggg atg ttg ctt gat ttc gac gat ctg ttg ctt cac acc gcc ggg 691  
 Glu Gly Met Leu Leu Asp Phe Asp Asp Leu Leu Leu His Thr Ala Gly  
 185 190 195

gcg ttg tagaattccc cgcggtggc gga 720  
 Ala Leu

<210> 46  
 <211> 199  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 46  
 Val Ile Asn Leu Gln Asp Leu Asp Glu Asp Gln Arg Ile Ala Ala Ser  
 1 5 10 15

Ala Pro Arg Gly Pro Val Cys Ile Leu Ala Gly Ala Gly Thr Gly Lys  
 20 25 30

Thr Arg Thr Ile Thr Tyr Arg Ile Ala His Leu Ile Asp Gln Gly Phe  
 35 40 45

Val Ser Pro Asn Arg Val Leu Ala Val Thr Phe Thr Ser Arg Ala Ala  
 50 55 60

Gly Glu Met Arg His Arg Leu Asn Leu Met Gly Ile Gly Gly Val Gln  
 65 70 75 80

Ala Arg Thr Phe His Ala Ala Ala Arg Lys Gln Leu Leu Tyr Phe Trp  
 85 90 95

Pro Gln Val Ala Gly Asn Leu Pro Trp Arg Leu Leu Asp Asn Lys Phe  
 100 105 110

Gln Leu Val Gly Arg Ala Val Arg Gly Ala Arg Leu Glu Ser Gln Thr  
 115 120 125

Glu Lys Val Arg Asp Ile Leu Gly Glu Ile Glu Trp Ala Lys Ala Ser  
 130 135 140

Leu Ile Thr Pro Glu Gln Tyr Pro Asp Arg Leu Gly Thr Arg Thr Pro  
145 150 155 160

Pro Ala Pro Ala Glu Lys Ile Ala Glu Val Tyr Gln Arg Tyr Glu Asn  
165 170 175

Met Lys Ala Thr Pro Glu Gly Met Leu Leu Asp Phe Asp Asp Leu Leu  
180 185 190

Leu His Thr Ala Gly Ala Leu  
195

<210> 47

<211> 1992

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)...(1969)

<223> RXA02359

<400> 47

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ggaggagcaa ctccgggacg ccgtcggaagt acccaccacca gtg gag ctg ccc agc 115  
Val Glu Leu Pro Ser 5  
1

cct ggt gag gcg ctc gca cat gca ggg cac acc cca gaa gtc ctg gaa 163  
Pro Gly Glu Ala Leu Ala His Ala Gly His Thr Pro Glu Val Leu Glu 20  
10 15

gcc gag ctc ggc att gac ccg gct gcc acc cgt att gtg ttg gaa ctt 211  
Ala Glu Leu Gly Ile Asp Pro Ala Ala Thr Arg Ile Val Leu Glu Thr 35  
25 30

gcc tca gag gat gac atc gca gca gcg ctt cct agc agc ccg acg tgg 259  
Ala Ser Glu Asp Asp Ile Ala Ala Ala Leu Pro Ser Ser Pro Thr Trp 50  
40 45

gaa aaa gac gca ctt atc ggc ctt gtc gcc ggt ttg agc att gaa gat 307  
Glu Lys Asp Ala Leu Ile Gly Leu Val Ala Gly Leu Ser Ile Glu Asp 65  
55 60

atc cgc gaa tcg ctc gct atc ccc gca cct tcc aca gag ccg gat acc 355  
Ile Arg Glu Ser Leu Ala Ile Pro Ala Pro Ser Thr Glu Pro Asp Thr 85  
70 75 80

cgc agc gaa gat acc agg ctc att gct ggg ctt aaa acc cca gca gcg 403  
Arg Ser Glu Asp Thr Arg Leu Ile Ala Gly Leu Lys Thr Pro Ala Ala 100  
90 95

caa atg gac ttt gcc tat ttg gat acc cca aat agc aat gac ctg cgc 451  
Gln Met Asp Phe Ala Tyr Leu Asp Thr Pro Asn Ser Asn Asp Leu Arg 115  
105 110

cgc gtt att gaa act gaa ggt ttt gat agc tgg cgc gtg tat atc gac 499  
Arg Val Ile Glu Thr Glu Gly Phe Asp Ser Trp Arg Val Tyr Ile Asp

002223 002223 002223

120	125	130	
ccc agc cag cgc tcc tta gtc acc cgc aac ttc agc gga tcg ggt cgc Pro Ser Gln Arg Ser Leu Val Thr Arg Asn Phe Ser Gly Ser Gly Arg 135 140 145			547
gtt ttt ggt gga gct ggc acc ggc aaa acc gtg gtg gta gtc cac cgt Val Phe Gly Gly Ala Gly Thr Gly Lys Thr Val Val Val Val His Arg 150 155 160 165			595
gcc aac cgc ctg gtc act tct gat gga cac ctt gag acc gac gat aag Ala Asn Arg Leu Val Thr Ser Asp Gly His Leu Glu Thr Asp Asp Lys 170 175 180			643
acg cct cga gtc ctg ctc acc acc tat acc cgc ggt ttg gcc gat gcg Thr Pro Arg Val Leu Leu Thr Thr Tyr Thr Arg Gly Leu Ala Asp Ala 185 190 195			691
ttg aaa tcc tcc atg aac gcg ctt aat ccc act ttc ccc gag gca gaa Leu Lys Ser Ser Met Asn Ala Leu Asn Pro Thr Phe Pro Glu Ala Glu 200 205 210			739
aaa ccc ggt agt cct ggc ttg tgg atc agc gga att gat gcc ttg gca Lys Pro Gly Ser Pro Gly Leu Trp Ile Ser Gly Ile Asp Ala Leu Ala 215 220 225			787
aat aag gtg gtt gcg cta gca aac acc gcc gaa cgt gag gca gca acc Asn Lys Val Val Ala Leu Ala Asn Thr Ala Glu Arg Glu Ala Ala Thr 230 235 240 245			835
act gct atc ttg ggg cgt gca gcc ggc aga atc acc cca ttc atc ggc Thr Ala Ile Leu Gly Arg Ala Ala Gly Arg Ile Thr Pro Phe Ile Gly 250 255 260			883
aac ggc gaa caa gaa ttt tgg atc gac gcg atc att tcc gca gat ccc Asn Gly Glu Gln Glu Phe Trp Ile Asp Ala Ile Ile Ser Ala Asp Pro 265 270 275			931
ggc gat cta tca gaa gaa atc agc aat act gaa ttc ctc gcc caa gag Gly Asp Leu Ser Glu Glu Ile Ser Asn Thr Glu Phe Leu Ala Gln Glu 280 285 290			979
ttt gaa acc gta atc cta gcc cgc gga atc acc caa gaa aag gac tat Phe Glu Thr Val Ile Leu Ala Arg Gly Ile Thr Gln Glu Lys Asp Tyr 295 300 305			1027
ctg cgt gca cct cgt ccc ggc cgt ggt acc cca cta aac cgc gta caa Leu Arg Ala Pro Arg Pro Gly Arg Gly Thr Pro Leu Asn Arg Val Gln 310 315 320 325			1075
cgc aaa aaa gtg tgg gcg att att cag caa ttc atg act tcc tgt gcg Arg Lys Lys Val Trp Ala Ile Ile Gln Gln Phe Met Thr Ser Cys Ala 330 335 340			1123
cgc gaa gga aag atg tcc tgg cca gcg ctt tcc tcc atc gcc gca aac Arg Glu Gly Lys Met Ser Trp Pro Ala Leu Ser Ser Ile Ala Ala Asn 345 350 355			1171
atc ctg gag cag cgc gcc gcc gcc ggc cag gcc cgg cta ttt gac cat Ile Leu Glu Gln Arg Ala Ala Ala Gly Gln Gly Arg Leu Phe Asp His 360 365 370			1219

gtg ctt atc gac gag gcc cag gac ttc cac gcc gga cat tgg ctc tta 1267  
Val Leu Ile Asp Glu Ala Gln Asp Phe His Ala Gly His Trp Leu Leu  
375 380 385

ctc agg gct gcg gta gcc gaa ggt ccc aat gac atc ttc ttg gct gag 1315  
Leu Arg Ala Ala Val Ala Glu Gly Pro Asn Asp Ile Phe Leu Ala Glu  
390 395 400 405

gat tca cac cag cgc atc tac ggc caa cat cat gtg cta agc cgt ttt 1363  
Asp Ser His Gln Arg Ile Tyr Gly Gln His His Val Leu Ser Arg Phe  
410 415 420

ggg att tcc acc cgc ggt cgg gcg tct aag cga ctc acc ctt aac tac 1411  
Gly Ile Ser Thr Arg Gly Arg Ala Ser Lys Arg Leu Thr Leu Asn Tyr  
425 430 435

cgc acc acc gcc gaa aac ctc agt tac gca ctt ggc atg ctc acc ggt 1459  
Arg Thr Thr Ala Glu Asn Leu Ser Tyr Ala Leu Gly Met Leu Thr Gly  
440 445 450

gaa tgg acc gac gcc gaa ggc gaa acg gac aca att gag cac tat cgc 1507  
Glu Trp Thr Asp Ala Glu Gly Glu Thr Asp Thr Ile Glu His Tyr Arg  
455 460 465

tca gcg cgt aag ggc ccc aag cca cac ctc tac caa ttt gaa tct gag 1555  
Ser Ala Arg Lys Gly Pro Lys Pro His Leu Tyr Gln Phe Glu Ser Glu  
470 475 480 485

acc gac gag ttc gaa gca atc gct gag ctc atc aag gtg tgg cag gac 1603  
Thr Asp Glu Phe Glu Ala Ile Ala Glu Leu Ile Lys Val Trp Gln Asp  
490 495 500

agg acc acc gat gta cgc atc ggc att ttg gca cgc acc cgt cct ttg 1651  
Arg Thr Thr Asp Val Arg Ile Gly Ile Leu Ala Arg Thr Arg Pro Leu  
505 510 515

atc aac cgc gtg gtt aat gcg ctc tct gag cag ggc atc gat gcc gtc 1699  
Ile Asn Arg Val Val Asn Ala Leu Ser Glu Gln Gly Ile Asp Ala Val  
520 525 530

aag acg caa aat gcc gaa ctt gca gcc cac gaa act gtc agt gta atg 1747  
Lys Thr Gln Asn Ala Glu Leu Ala Ala His Glu Thr Val Ser Val Met  
535 540 545

aca atg cac gga gct aaa ggc atg gag ttt acc cat gtc atc ttg atc 1795  
Thr Met His Gly Ala Lys Gly Met Glu Phe Thr His Val Ile Leu Ile  
550 555 560 565

gga atg ggc cgt gac ctc att cct ttg caa tac acc atg caa ggt tta 1843  
Gly Met Gly Arg Asp Leu Ile Pro Leu Gln Tyr Thr Met Gln Gly Leu  
570 575 580

ggc gag gcc gag cgt aac gac gcc caa cag cgc gaa cgc tcc ttg ctc 1891  
Gly Glu Ala Glu Arg Asn Asp Ala Gln Gln Arg Glu Arg Ser Leu Leu  
585 590 595

tac gtt gca gct tct cgt gca cgt gat gcc ctt gtt ctc acc acg cat 1939  
Tyr Val Ala Ala Ser Arg Ala Arg Asp Ala Leu Val Leu Thr Thr His  
600 605 610

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gtt

1992

<210> 48

<211> 623

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 48

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 20 25 30

Ile Val Leu Glu Leu Ala Ser Glu Asp Asp Ile Ala Ala Ala Leu Pro  
 35 40 45

Ser Ser Pro Thr Trp Glu Lys Asp Ala Leu Ile Gly Leu Val Ala Gly  
 50 55 60

Leu Ser Ile Glu Asp Ile Arg Glu Ser Leu Ala Ile Pro Ala Pro Ser  
 65 70 75 80

Thr Glu Pro Asp Thr Arg Ser Glu Asp Thr Arg Leu Ile Ala Gly Leu  
 85 90 95

Lys Thr Pro Ala Ala Gln Met Asp Phe Ala Tyr Leu Asp Thr Pro Asn  
 100 105 110

Ser Asn Asp Leu Arg Arg Val Ile Glu Thr Glu Gly Phe Asp Ser Trp  
 115 120 125

Arg Val Tyr Ile Asp Pro Ser Gln Arg Ser Leu Val Thr Arg Asn Phe  
 130 135 140

Ser Gly Ser Gly Arg Val Phe Gly Gly Ala Gly Thr Gly Lys Thr Val  
 145 150 155 160

Val Val Val His Arg Ala Asn Arg Leu Val Thr Ser Asp Gly His Leu  
 165 170 175

Glu Thr Asp Asp Lys Thr Pro Arg Val Leu Leu Thr Thr Tyr Thr Arg  
 180 185 190

Gly Leu Ala Asp Ala Leu Lys Ser Ser Met Asn Ala Leu Asn Pro Thr  
 195 200 205

Phe Pro Glu Ala Glu Lys Pro Gly Ser Pro Gly Leu Trp Ile Ser Gly  
 210 215 220

Ile Asp Ala Leu Ala Asn Lys Val Val Ala Leu Ala Asn Thr Ala Glu  
 225 230 235 240

Arg Glu Ala Ala Thr Thr Ala Ile Leu Gly Arg Ala Ala Gly Arg Ile  
 245 250 255



Thr Pro Phe Ile Gly Asn Gly Glu Gln Glu Phe Trp Ile Asp Ala Ile  
 260 265 270  
 Ile Ser Ala Asp Pro Gly Asp Leu Ser Glu Glu Ile Ser Asn Thr Glu  
 275 280 285  
 Phe Leu Ala Gln Glu Phe Glu Thr Val Ile Leu Ala Arg Gly Ile Thr  
 290 295 300  
 Gln Glu Lys Asp Tyr Leu Arg Ala Pro Arg Pro Gly Arg Gly Thr Pro  
 305 310 315 320  
 Leu Asn Arg Val Gln Arg Lys Lys Val Trp Ala Ile Ile Gln Gln Phe  
 325 330 335  
 Met Thr Ser Cys Ala Arg Glu Gly Lys Met Ser Trp Pro Ala Leu Ser  
 340 345 350  
 Ser Ile Ala Ala Asn Ile Leu Glu Gln Arg Ala Ala Ala Gly Gln Gly  
 355 360 365  
 Arg Leu Phe Asp His Val Leu Ile Asp Glu Ala Gln Asp Phe His Ala  
 370 375 380  
 Gly His Trp Leu Leu Leu Arg Ala Ala Val Ala Glu Gly Pro Asn Asp  
 385 390 395 400  
 Ile Phe Leu Ala Glu Asp Ser His Gln Arg Ile Tyr Gly Gln His His  
 405 410 415  
 Val Leu Ser Arg Phe Gly Ile Ser Thr Arg Gly Arg Ala Ser Lys Arg  
 420 425 430  
 Leu Thr Leu Asn Tyr Arg Thr Thr Ala Glu Asn Leu Ser Tyr Ala Leu  
 435 440 445  
 Gly Met Leu Thr Gly Glu Trp Thr Asp Ala Glu Gly Glu Thr Asp Thr  
 450 455 460  
 Ile Glu His Tyr Arg Ser Ala Arg Lys Gly Pro Lys Pro His Leu Tyr  
 465 470 475 480  
 Gln Phe Glu Ser Glu Thr Asp Glu Phe Glu Ala Ile Ala Glu Leu Ile  
 485 490 495  
 Lys Val Trp Gln Asp Arg Thr Thr Asp Val Arg Ile Gly Ile Leu Ala  
 500 505 510  
 Arg Thr Arg Pro Leu Ile Asn Arg Val Val Asn Ala Leu Ser Glu Gln  
 515 520 525  
 Gly Ile Asp Ala Val Lys Thr Gln Asn Ala Glu Leu Ala Ala His Glu  
 530 535 540  
 Thr Val Ser Val Met Thr Met His Gly Ala Lys Gly Met Glu Phe Thr  
 545 550 555 560  
 His Val Ile Leu Ile Gly Met Gly Arg Asp Leu Ile Pro Leu Gln Tyr  
 565 570 575  
 Thr Met Gln Gly Leu Gly Glu Ala Glu Arg Asn Asp Ala Gln Gln Arg

580

585

590

Glu Arg Ser Leu Leu Tyr Val Ala Ala Ser Arg Ala Arg Asp Ala Leu  
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Val Leu Thr Thr His Thr Glu Pro Ser Glu Leu Leu Pro Arg Val  
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<211> 2884

<212> DNA

<213> Corynebacterium glutamicum

<220>

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Met Ser Glu Tyr Lys  
1 5

cca ccc att cca tcg gat cca caa gtt cgg ctg att aag cca aca tcc 163  
Pro Pro Ile Pro Ser Asp Pro Gln Val Arg Leu Ile Lys Pro Thr Ser  
10 15 20

aag ctt cgt cct cgt tcg tgg gag ggc gaa gtt tcg cat tta gtt aaa 211  
Lys Leu Arg Pro Arg Ser Trp Glu Gly Glu Val Ser His Leu Val Lys  
25 30 35

caa ggc acc ggt ttg tgg cgg gtg act ggt gag gcg ggc tcg ggg gtg 259  
Gln Gly Thr Gly Leu Trp Arg Val Thr Gly Glu Ala Gly Ser Gly Val  
40 45 50

agc tcc gct gtt gtc gat act gtc ctt gaa cgc att cgc caa ggg tgg 307  
Ser Ser Ala Val Val Asp Thr Val Leu Glu Arg Ile Arg Gln Gly Trp  
55 60 65

gag ccg tca tcg atg ttg gtt gtc gcc acg tcg aaa gag gcg gcg agt 355  
Glu Pro Ser Ser Met Leu Val Val Ala Thr Ser Lys Glu Ala Ala Ser  
70 75 80 85

cgc ttg agg caa gag atc tcg gaa tcc gta gcc cag atg gat tat gtg 403  
Arg Leu Arg Gln Glu Ile Ser Glu Ser Val Ala Gln Met Asp Tyr Val  
90 95 100

tcg gag ggg ccg ttg gtg cga tcg gtg cac tcg gtg gct ttc gcg ctg 451  
Ser Glu Gly Pro Leu Val Arg Ser Val His Ser Val Ala Phe Ala Leu  
105 110 115

att cgt gat gcg tcg gat gat gat gtg cgg ttg att acg ggc gct gag 499  
Ile Arg Asp Ala Ser Asp Asp Asp Val Arg Leu Ile Thr Gly Ala Glu  
120 125 130

caa gat gcg gtg att cgg gag ttg ctg cgt ggt cat gct gat gat ggt 547  
Gln Asp Ala Val Ile Arg Glu Leu Leu Arg Gly His Ala Asp Asp Gly  
135 140 145

cgt ggg ggg tgg ccg cag gag cag cgt gag ggt ttg cgg atg gtg ggg 595  
 Arg Gly Gly Trp Pro Gln Glu Gln Arg Glu Gly Leu Arg Met Val Gly  
 150 155 160 165

ttc gct agg cag ttg cgt gac ttt ttg ctt cgt gcg gtg gag cgt ggt 643  
 Phe Ala Arg Gln Leu Arg Asp Phe Leu Leu Arg Ala Val Glu Arg Gly  
 170 175 180

gtg ggc cct gat gag ttg gtg gaa ttg ggg gag cga ttt gag cgc gcc 691  
 Val Gly Pro Asp Glu Leu Val Glu Leu Gly Glu Arg Phe Glu Arg Ala  
 185 190 195

aat tgg gtt gct gcg ggt gag ttc ctt cgt gag tac aag cag gtg atg 739  
 Asn Trp Val Ala Ala Gly Glu Phe Leu Arg Glu Tyr Lys Gln Val Met  
 200 205 210

aag ctg tcg ggg gcg cat agt ttt tct gcg tct gag ttg gtg act gaa 787  
 Lys Leu Ser Gly Ala His Ser Phe Ser Ala Ser Glu Leu Val Thr Glu  
 215 220 225

gcg ctg cgt ggt cct gag ccg tcg gtg aag tat cgc ggt gtg ttt att 835  
 Ala Leu Arg Gly Pro Glu Pro Ser Val Lys Tyr Arg Gly Val Phe Ile  
 230 235 240 245

gat gat gcg cag cat ttg gat ccg aag tcg gcg gaa ctt gtg tcg cgg 883  
 Asp Asp Ala Gln His Leu Asp Pro Lys Ser Ala Glu Leu Val Ser Arg  
 250 255 260

ttt ttc cct gag gcg gag ttg gct gtg gtg gcg ggt gat ccg cag cag 931  
 Phe Phe Pro Glu Ala Glu Leu Ala Val Val Ala Gly Asp Pro Gln Gln  
 265 270 275

tcg gtg ttt agg ttc cgt ggt gcg aat ccg gat ttt ctc acc aag ttg 979  
 Ser Val Phe Arg Phe Arg Gly Ala Asn Pro Asp Phe Leu Thr Lys Leu  
 280 285 290

agt gtg gat cac gag gtg gtg ttg aag ggg agg agg aaa gcg tcg aca 1027  
 Ser Val Asp His Glu Val Val Leu Lys Gly Arg Arg Lys Ala Ser Thr  
 295 300 305

agc att gtc gtg gca gag acc gag tcg gcg cat gcg gac ctg ctt gct 1075  
 Ser Ile Val Val Ala Glu Thr Glu Ser Ala His Ala Asp Leu Leu Ala  
 310 315 320 325

gac acg gtg cgg cgc gcg cat ctc att gat ggg cgc agc tgg tcg gag 1123  
 Asp Thr Val Arg Arg Ala His Leu Ile Asp Gly Arg Ser Trp Ser Glu  
 330 335 340

atc gct gtt atc gtg cgc tcg gcc ggc atg att gcg ccg att tgg cgc 1171  
 Ile Ala Val Ile Val Arg Ser Ala Gly Met Ile Ala Pro Ile Trp Arg  
 345 350 355

acc ctg ctg gcc gcc gcc gtg ccc gtg cac atc agc ccg act gat gtg 1219  
 Thr Leu Leu Ala Ala Gly Val Pro Val His Ile Ser Pro Thr Asp Val  
 360 365 370

gtg ctc gcc gaa caa cgt atc gtt gcc gca atg att ctc ggg ctg cgc 1267  
 Val Leu Ala Glu Gln Arg Ile Val Ala Ala Met Ile Leu Gly Leu Arg  
 375 380 385

gcg ctg acg gaa tgc ctc aac gcc atc gag ttg gag gat ctt ctc cta 1315  
 Ala Leu Thr Glu Ser Leu Asn Ala Ile Glu Leu Glu Asp Leu Leu Leu  
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 gga ccg atc ggt ggc gcc gat ccg gtg act ctg cgt cgt ttg ctg cgc 1363  
 Gly Pro Ile Gly Gly Ala Asp Pro Val Thr Leu Arg Arg Leu Leu Arg  
 410 415 420  
 ggg ttg cgg cag gcg gag atg aag atg ggt ggg cag agg cga gcg atc 1411  
 Gly Leu Arg Gln Ala Glu Met Lys Met Gly Gly Gln Arg Arg Ala Ile  
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 gag gtg ctc aga agc ctg ctc gca gag tgc gat gcg gag atg ttg gcc 1459  
 Glu Val Leu Arg Ser Leu Leu Ala Glu Ser Asp Ala Glu Met Leu Gly  
 440 445 450  
 ttt ttg acc gat cgt gag ctg aat ttg ctc gag ccg gtg cga tct gtg 1507  
 Phe Leu Thr Asp Arg Glu Leu Asn Leu Leu Glu Arg Val Arg Ser Val  
 455 460 465  
 ttg gaa gcg ggt cgt gaa gcg ctc gcg gaa cac gcc agt atc gaa gag 1555  
 Leu Glu Ala Gly Arg Glu Ala Leu Ala Glu His Gly Ser Ile Glu Glu  
 470 475 480 485  
 gtg ttg tgg gcg ctg tgg tgc gcg acc gat ctg tgc aac tgc ttg tcc 1603  
 Val Leu Trp Ala Leu Trp Ser Ala Thr Asp Leu Ser Asn Ser Leu Ser  
 490 495 500  
 gcg atc agc ctt cga ggc gcc gca tgc ggg tcc cag gcc gat cgc gat 1651  
 Ala Ile Ser Leu Arg Gly Gly Ala Ser Gly Ser Gln Ala Asp Arg Asp  
 505 510 515  
 ttg gat gcg atg atg gcg ctt ttc gac gcc gcc gcc gac tac gtg gag 1699  
 Leu Asp Ala Met Met Ala Leu Phe Asp Ala Ala Gly Asp Tyr Val Glu  
 520 525 530  
 cgc tac ccg tca gcg gcc gtg ccg agt ttc att ctg cat att tct gag 1747  
 Arg Tyr Pro Ser Ala Gly Val Arg Ser Phe Ile Leu His Ile Ser Glu  
 535 540 545  
 cag gaa ctt ccg acc gcc atg cgt gag cga cgc gcc gcg atc ccg gag 1795  
 Gln Glu Leu Pro Thr Gly Met Arg Glu Arg Arg Gly Ala Ile Pro Glu  
 550 555 560 565  
 gcc gtc gag gtg ctg acg gcg cac gcg acg acg ggt cgt gag tgg aag 1843  
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 570 575 580  
 cgc gtg atc gtt gct gag gtg cag gag gcc agt tgg ccg tgc ctc ggt 1891  
 Arg Val Ile Val Ala Glu Val Gln Glu Gly Ser Trp Pro Ser Leu Gly  
 585 590 595  
 gaa act gcc acg ctg ctt ggt cag gaa gag ttc gtc gat ttg gtg gat 1939  
 Glu Thr Gly Thr Leu Leu Gly Gln Glu Glu Phe Val Asp Leu Val Asp  
 600 605 610  
 gag ggt att gat ccc gat atc atc att tcc cga tcc gcc gaa cga ctg 1987  
 Glu Gly Ile Asp Pro Asp Ile Ile Ile Ser Arg Ser Ala Glu Arg Leu  
 615 620 625  
 gcg gag gaa cgc cga ctg ttc tac ctc gcc acc acc aga tcc acc gaa 2035

Ala Glu Glu Arg Arg Leu Phe Tyr Leu Ala Thr Thr Arg Ser Thr Glu	635	640	645	
630				
tcg ctc ctg gtt acc gct gtg aat tcc ccc gac tcc gac gaa gtc cgc				2083
Ser Leu Leu Val Thr Ala Val Asn Ser Pro Asp Ser Asp Glu Val Arg	650	655	660	
gaa ccc tcc cgg ttt ttg gaa ttg ctg agt caa ccg atc gtt gtt ctc				2131
Glu Pro Ser Arg Phe Leu Glu Leu Leu Ser Gln Pro Ile Val Val Leu	665	670	675	
gag ggg gag gaa gct tcg gcg atc gcg gaa ccg gag gag att ggg cat				2179
Glu Gly Glu Glu Ala Ser Ala Ile Ala Glu Pro Glu Glu Ile Gly His	680	685	690	
cgg ttg ttg tcg att cct gcg atg gtt gct gag ttg cgt cgt gtg gtg				2227
Arg Leu Leu Ser Ile Pro Ala Met Val Ala Glu Leu Arg Arg Val Val	695	700	705	
aat gat ccg cgg gat ccg cgt cgg aag cag gct gcg agg cag ttg tcg				2275
Asn Asp Pro Arg Asp Pro Arg Arg Lys Gln Ala Ala Arg Gln Leu Ser	710	715	720	725
agg ctt gcg gag gcg ggg att ccg ggt gcg aat cct gcc gag tgg acg				2323
Arg Leu Ala Glu Ala Gly Ile Pro Gly Ala Asn Pro Ala Glu Trp Thr	730	735	740	
aat ctg cgc act ccg tcg act gat gag gag ttg atc aag ggg gcg gtg				2371
Asn Leu Arg Thr Pro Ser Thr Asp Glu Glu Leu Ile Lys Gly Ala Val	745	750	755	
tcg ttg tcg ccg tcg cgg att gag cag ttg ttg aat tgt ccg ctg cgc				2419
Ser Leu Ser Pro Ser Arg Ile Glu Gln Leu Leu Asn Cys Pro Leu Arg	760	765	770	
gct gtg ttg gat cgt ttg gac agt gag gag gaa acg ccg atc gcg atg				2467
Ala Val Leu Asp Arg Leu Asp Ser Glu Glu Glu Thr Pro Ile Ala Met	775	780	785	
ctc aag ggc acc ttg gtg cac gcg ttt gcg gag gcg gtc gcc ggt ggc				2515
Leu Lys Gly Thr Leu Val His Ala Phe Ala Glu Ala Val Ala Gly Gly	790	795	800	805
gtc gat gcg gcg ctc gcc gaa gag aag gtg acc agc gcc tac atg cag				2563
Val Asp Ala Ala Leu Ala Glu Glu Lys Val Thr Ser Ala Tyr Met Gln	810	815	820	
ctg gcg aac gtg ccg agc tgg tcg cgc gaa agc acc gaa att gct ttt				2611
Leu Ala Asn Val Pro Ser Trp Ser Arg Glu Ser Thr Glu Ile Ala Phe	825	830	835	
cga cgc atc ctc tca cgt acc gat acc tgg ctg aag act tct cgc gcc				2659
Arg Arg Ile Leu Ser Arg Thr Asp Thr Trp Leu Lys Thr Ser Arg Ala	840	845	850	
gat ttt acg gaa gtg gga acg gag atg gac gta tcg gtg acc atc gat				2707
Asp Phe Thr Glu Val Gly Thr Glu Met Asp Val Ser Val Thr Ile Asp	855	860	865	
gac tcc gta tcg atc cgt ggt gcg atg gac cgt ttg gag cga aac aaa				2755
Asp Ser Val Ser Ile Arg Gly Arg Met Asp Arg Leu Glu Arg Asn Lys				

870	875	880	885	
tcc ggc gag ttg	gtg gtt gtt gat ttc aaa acg ggc aaa act caa atc			2803
Ser Gly Glu Leu	Val Val Val Asp Phe Lys Thr Gly Lys Thr Gln Ile		900	
	890	895		
gct gca aaa gac atg ggc gat cac cca cag ttg ttt gcg tat caa ttg				2851
Ala Ala Lys Asp Met Gly Asp His Pro Gln Leu Phe Ala Tyr Gln Leu			915	
	905	910		
gcg ttg tcg aaa ggc gtg ctg cat ggt gac aaa				2884
Ala Leu Ser Lys Gly Val Leu His Gly Asp Lys				
	920	925		

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 <212> PRT  
 <213> Corynebacterium glutamicum

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 Ser His Leu Val Lys Gln Gly Thr Gly Leu Trp Arg Val Thr Gly Glu  
 35 40 45  
 Ala Gly Ser Gly Val Ser Ser Ala Val Val Asp Thr Val Leu Glu Arg  
 50 55 60  
 Ile Arg Gln Gly Trp Glu Pro Ser Ser Met Leu Val Val Ala Thr Ser  
 65 70 75 80  
 Lys Glu Ala Ala Ser Arg Leu Arg Gln Glu Ile Ser Glu Ser Val Ala  
 85 90 95  
 Gln Met Asp Tyr Val Ser Glu Gly Pro Leu Val Arg Ser Val His Ser  
 100 105 110  
 Val Ala Phe Ala Leu Ile Arg Asp Ala Ser Asp Asp Val Arg Leu  
 115 120 125  
 Ile Thr Gly Ala Glu Gln Asp Ala Val Ile Arg Glu Leu Leu Arg Gly  
 130 135 140  
 His Ala Asp Asp Gly Arg Gly Gly Trp Pro Gln Glu Gln Arg Glu Gly  
 145 150 155 160  
 Leu Arg Met Val Gly Phe Ala Arg Gln Leu Arg Asp Phe Leu Leu Arg  
 165 170 175  
 Ala Val Glu Arg Gly Val Gly Pro Asp Glu Leu Val Glu Leu Gly Glu  
 180 185 190  
 Arg Phe Glu Arg Ala Asn Trp Val Ala Ala Gly Glu Phe Leu Arg Glu  
 195 200 205  
 Tyr Lys Gln Val Met Lys Leu Ser Gly Ala His Ser Phe Ser Ala Ser

210	215	220
Glu Leu Val Thr Glu Ala Leu Arg Gly Pro Glu Pro Ser Val Lys Tyr 225 230 235 240		
Arg Gly Val Phe Ile Asp Asp Ala Gln His Leu Asp Pro Lys Ser Ala 245 250 255		
Glu Leu Val Ser Arg Phe Phe Pro Glu Ala Glu Leu Ala Val Val Ala 260 265 270		
Gly Asp Pro Gln Gln Ser Val Phe Arg Phe Arg Gly Ala Asn Pro Asp 275 280 285		
Phe Leu Thr Lys Leu Ser Val Asp His Glu Val Val Leu Lys Gly Arg 290 295 300		
Arg Lys Ala Ser Thr Ser Ile Val Val Ala Glu Thr Glu Ser Ala His 305 310 315 320		
Ala Asp Leu Leu Ala Asp Thr Val Arg Arg Ala His Leu Ile Asp Gly 325 330 335		
Arg Ser Trp Ser Glu Ile Ala Val Ile Val Arg Ser Ala Gly Met Ile 340 345 350		
Ala Pro Ile Trp Arg Thr Leu Leu Ala Ala Gly Val Pro Val His Ile 355 360 365		
Ser Pro Thr Asp Val Val Leu Ala Glu Gln Arg Ile Val Ala Ala Met 370 375 380		
Ile Leu Gly Leu Arg Ala Leu Thr Glu Ser Leu Asn Ala Ile Glu Leu 385 390 395 400		
Glu Asp Leu Leu Leu Gly Pro Ile Gly Gly Ala Asp Pro Val Thr Leu 405 410 415		
Arg Arg Leu Leu Arg Gly Leu Arg Gln Ala Glu Met Lys Met Gly Gly 420 425 430		
Gln Arg Arg Ala Ile Glu Val Leu Arg Ser Leu Leu Ala Glu Ser Asp 435 440 445		
Ala Glu Met Leu Gly Phe Leu Thr Asp Arg Glu Leu Asn Leu Leu Glu 450 455 460		
Arg Val Arg Ser Val Leu Glu Ala Gly Arg Glu Ala Leu Ala Glu His 465 470 475 480		
Gly Ser Ile Glu Glu Val Leu Trp Ala Leu Trp Ser Ala Thr Asp Leu 485 490 495		
Ser Asn Ser Leu Ser Ala Ile Ser Leu Arg Gly Gly Ala Ser Gly Ser 500 505 510		
Gln Ala Asp Arg Asp Leu Asp Ala Met Met Ala Leu Phe Asp Ala Ala 515 520 525		
Gly Asp Tyr Val Glu Arg Tyr Pro Ser Ala Gly Val Arg Ser Phe Ile 530 535 540		

Leu His Ile Ser Glu Gln Glu Leu Pro Thr Gly Met Arg Glu Arg Arg  
 545 550 555 560  
 Gly Ala Ile Pro Glu Ala Val Glu Val Leu Thr Ala His Ala Thr Thr  
 565 570 575  
 Gly Arg Glu Trp Lys Arg Val Ile Val Ala Glu Val Gln Glu Gly Ser  
 580 585 590  
 Trp Pro Ser Leu Gly Glu Thr Gly Thr Leu Leu Gly Gln Glu Glu Phe  
 595 600 605  
 Val Asp Leu Val Asp Glu Gly Ile Asp Pro Asp Ile Ile Ile Ser Arg  
 610 615 620  
 Ser Ala Glu Arg Leu Ala Glu Glu Arg Arg Leu Phe Tyr Leu Ala Thr  
 625 630 635 640  
 Thr Arg Ser Thr Glu Ser Leu Leu Val Thr Ala Val Asn Ser Pro Asp  
 645 650 655  
 Ser Asp Glu Val Arg Glu Pro Ser Arg Phe Leu Glu Leu Leu Ser Gln  
 660 665 670  
 Pro Ile Val Val Leu Glu Gly Glu Glu Ala Ser Ala Ile Ala Glu Pro  
 675 680 685  
 Glu Glu Ile Gly His Arg Leu Leu Ser Ile Pro Ala Met Val Ala Glu  
 690 695 700  
 Leu Arg Arg Val Val Asn Asp Pro Arg Asp Pro Arg Arg Lys Gln Ala  
 705 710 715 720  
 Ala Arg Gln Leu Ser Arg Leu Ala Glu Ala Gly Ile Pro Gly Ala Asn  
 725 730 735  
 Pro Ala Glu Trp Thr Asn Leu Arg Thr Pro Ser Thr Asp Glu Glu Leu  
 740 745 750  
 Ile Lys Gly Ala Val Ser Leu Ser Pro Ser Arg Ile Glu Gln Leu Leu  
 755 760 765  
 Asn Cys Pro Leu Arg Ala Val Leu Asp Arg Leu Asp Ser Glu Glu Glu  
 770 775 780  
 Thr Pro Ile Ala Met Leu Lys Gly Thr Leu Val His Ala Phe Ala Glu  
 785 790 795 800  
 Ala Val Ala Gly Gly Val Asp Ala Ala Leu Ala Glu Glu Lys Val Thr  
 805 810 815  
 Ser Ala Tyr Met Gln Leu Ala Asn Val Pro Ser Trp Ser Arg Glu Ser  
 820 825 830  
 Thr Glu Ile Ala Phe Arg Arg Ile Leu Ser Arg Thr Asp Thr Trp Leu  
 835 840 845  
 Lys Thr Ser Arg Ala Asp Phe Thr Glu Val Gly Thr Glu Met Asp Val  
 850 855 860



Ser Val Thr Ile Asp Asp Ser Val Ser Ile Arg Gly Arg Met Asp Arg  
865 870 875 880

Leu Glu Arg Asn Lys Ser Gly Glu Leu Val Val Val Asp Phe Lys Thr  
885 890 895

Gly Lys Thr Gln Ile Ala Ala Lys Asp Met Gly Asp His Pro Gln Leu  
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Phe Ala Tyr Gln Leu Ala Leu Ser Lys Gly Val Leu His Gly Asp Lys  
915 920 925

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<212> DNA  
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Met Ser Glu Tyr Lys  
1 5

cca ccc att cca tcg gat cca caa gtt cgg ctg att aag cca aca tcc 163  
Pro Pro Ile Pro Ser Asp Pro Gln Val Arg Leu Ile Lys Pro Thr Ser  
10 15 20

aag ctt cgt cct cgt tcg tgg gag ggc gaa gtt tcg cat tta gtt aaa 211  
Lys Leu Arg Pro Arg Ser Trp Glu Gly Glu Val Ser His Leu Val Lys  
25 30 35

caa ggc acc ggt ttg tgg cgg gtg act ggt gag gcg ggc tcg ggg gtg 259  
Gln Gly Thr Gly Leu Trp Arg Val Thr Gly Glu Ala Gly Ser Gly Val  
40 45 50

agc tcc gct gtt gtc gat act gtc ctt gaa cgc att cgc caa ggg tgg 307  
Ser Ser Ala Val Val Asp Thr Val Leu Glu Arg Ile Arg Gln Gly Trp  
55 60 65

gag ccg tca tcg atg ttg gtt gtc gcc acg tcg aaa gag gcg gcg agt 355  
Glu Pro Ser Ser Met Leu Val Val Ala Thr Ser Lys Glu Ala Ala Ser  
70 75 80 85

cgc ttg agg caa gag atc tcg gaa tcc gta gcc cag atg gat tat gtg 403  
Arg Leu Arg Gln Glu Ile Ser Glu Ser Val Ala Gln Met Asp Tyr Val  
90 95 100

tcg gag ggg ccg ttg gtg cga tcg gtg cac tcg gtg gct ttc gcg ctg 451  
Ser Glu Gly Pro Leu Val Arg Ser Val His Ser Val Ala Phe Ala Leu  
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 Ser Gly Glu Leu Val Val Val Asp Phe Lys Thr Gly Lys Thr Gln Ile  
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 Tyr Lys Gln Val Met Lys Leu Ser Gly Ala His Ser Phe Ser Ala Ser  
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Pro Ile Val Val Leu Glu Gly Glu Glu Ala Ser Ala Ile Ala Glu Pro			675				680					685		
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Ala Arg Gln Leu Ser Arg Leu Ala Glu Ala Gly Ile Pro Gly Ala Asn			725					730					735	
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Cys	Val	Val	Ser	Trp	Trp	Glu	Gly	Glu	Glu	Gly	Asp	Val	Glu	Lys	Gln	
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Lys	Pro	Ala	Glu	Gly	Val	Phe	Pro	Gln	Leu	Leu	Ala	Ala	Asp	Ser	Ser	
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Gly	Leu	Glu	Ser	Leu	Trp	Glu	Lys	Glu	Val	Ser	Ala	Leu	Ile	Asp	Glu	
			740				745						750			
cac	cg	cg	ctt	tcc	aac	ccc	atc	gtc	gaa	gtc	gaa	acg	ccc	cg	gaa	2304
His	Arg	Arg	Leu	Ser	Asn	Pro	Ile	Val	Glu	Val	Glu	Thr	Pro	Arg	Glu	
		755					760					765				
ctc	acg	gcc	acc	gac	ctc	gtc	tct	atg	aaa	aac	aat	ccc	gaa	cag	ttc	2352
Leu	Thr	Ala	Thr	Asp	Leu	Val	Ser	Met	Lys	Asn	Asn	Pro	Glu	Gln	Phe	
		770				775						780				
gcc	cga	cga	atg	cgt	cg	cct	gtc	ccg	ttc	aaa	cca	aac	acc	tac	gca	2400
Ala	Arg	Arg	Met	Arg	Arg	Pro	Val	Pro	Phe	Lys	Pro	Lys	Thr	Tyr	Ala	
		785			790					795					800	
aaa	cg	ggc	aca	ctg	ttc	cac	caa	tgg	ctc	gaa	gat	cgg				

835	840	845	
tgg gaa aac cgc aca ccg gaa ttc gtc gaa cat ccc ttc gaa gta acg			2592
Trp Glu Asn Arg Thr Pro Glu Phe Val Glu His Pro Phe Glu Val Thr			
850	855	860	
atc ggc gaa cac gtc atc cgc ggc cgc atg gac gcc gtc ttc cac acc			2640
Ile Gly Glu His Val Ile Arg Gly Arg Met Asp Ala Val Phe His Thr			
865	870	875	880
gat ggc acc tgg atg gtg gtc gac tgg aaa acc gga cgc acc cca acc			2688
Asp Gly Thr Trp Met Val Val Asp Trp Lys Thr Gly Arg Thr Pro Thr			
885	890	895	
ggc ccc gaa atg gac gca gcg atc atc cag ctc gct gtc tat aga ctc			2736
Gly Pro Glu Met Asp Ala Ala Ile Ile Gln Leu Ala Val Tyr Arg Leu			
900	905	910	
gcc tgg gca cga ctc aaa ggc ctc gaa cct gaa gaa gtc cgc gca gca			2784
Ala Trp Ala Arg Leu Lys Gly Leu Glu Pro Glu Glu Val Arg Ala Ala			
915	920	925	
ttc cat tac gtc gcc cac gat cac acc ttt gag cgc aac gat ctg cgc			2832
Phe His Tyr Val Ala His Asp His Thr Phe Glu Pro Asn Asp Leu Pro			
930	935	940	
act caa gaa gaa cta gcc cgg ctg ctc agt cag gaa tgaatgcgcct			2878
Thr Gln Glu Glu Leu Ala Arg Leu Leu Ser Gln Glu			
945	950	955	
aagatcaaac aag			2891
<210> 54			
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<212> PRT			
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<400> 54			
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Gly Leu Leu Leu Pro Val Glu Pro Ser Ala Arg Leu Ile Thr Gln Thr			
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Glu Leu Tyr His Ile Ala Arg Asn Val Val Asn Asn Tyr Asp Gly Glu			
35	40	45	
Leu Thr Ala Thr Gln Thr Pro Ala Thr Val Thr Glu Tyr Leu Leu Lys			
50	55	60	
Leu Val Ser Glu Met Asp Asn His Met Val Thr Ala Glu Asp Ile Arg			
65	70	75	80
Glu Glu Ser Asp Pro Phe Ile Lys Leu Phe Asp Glu Leu Pro Lys Gly			
85	90	95	
Lys Gly Gln Arg Asp Asn Leu Asn Ala Glu Met Thr Lys Trp Arg Asp			
100	105	110	
Thr Gln Val Ala Arg Leu Gln Tyr Leu Pro Leu Val Lys Ala Leu Lys			

115	120	125
Glu Glu Leu His Asn Gln Ala Val Val Thr Phe Gly Glu Gln Met Ser 130 135 140		
Lys Ala Ala His Leu Ala Ser Thr His Pro Gln Val Gly Tyr Ser Gln 145 150 155 160		
Arg Arg Arg Phe Arg Val Val Met Leu Asp Glu Tyr Gln Asp Thr Ser 165 170 175		
His Ser Gln Arg Val Leu Leu Ser Ser Leu Phe Gly Gly Thr Asp Pro 180 185 190		
Gly Leu Thr Val Asn Ala Val Gly Asp Pro Met Gln Ala Ile Tyr Gly 195 200 205		
Trp Arg Gly Ala Thr Ala Ala Asn Leu Glu Asn Phe Val Asp Asp Phe 210 215 220		
Pro Val Ile His Leu Asp Gly Lys Thr Arg Ala Pro Lys Asn Glu Leu 225 230 235 240		
Thr Thr Ser Trp Arg Asn Pro Pro Glu Val Leu Thr Leu Ala Asn Ala 245 250 255		
Val Ser Arg Glu Val Leu Gly Ser Pro Asp Ala Pro Thr Arg Thr Val 260 265 270		
Gln Pro Leu Gln Pro Arg Glu Gly Ala Pro Thr Gly Glu Val Ser Leu 275 280 285		
Gly Trp Phe Gly Thr Ala Ala Gln Glu Arg Glu Phe Val Ala Asp Glu 290 295 300		
Met Val Lys His Trp Asn Ala Arg Glu Glu Lys Gly Thr Phe Thr Ala 305 310 315 320		
Ala Val Leu Val Arg Lys Lys Arg His Ser Ala Pro Met Ala Glu Glu 325 330 335		
Leu Thr Lys Arg Gly Ile Pro Val Glu Ile Val Gly Leu Ser Gly Leu 340 345 350		
Leu Asp Ile Pro Glu Ile Ala Asp Leu Ile Ser Leu Ala Thr Met Leu 355 360 365		
Val Arg Pro His Asp Asn Arg Ala Ala Leu Arg Ile Leu Ala Gly Pro 370 375 380		
His Val Gly Leu Gly Val Ala Asp Leu Gln Arg Leu Gln Gly Arg Ala 385 390 395 400		
Arg Asn Ile Ala Gly Arg Val Ser Arg Glu Arg Arg Glu Lys Asn Pro 405 410 415		
Asp Pro Leu Ala Glu Leu Asp Ala Ile Ile Glu Glu Ala Thr Ala Ile 420 425 430		
Glu Pro Glu Ala Val Val Gly Leu Ala Asp Ala Val Ala Asp Leu Gly 435 440 445		

Glu Gly Asp Arg Phe Ser Glu Glu Gly Leu Ser Arg Leu Lys Arg Leu  
 450 455 460  
 Ala Thr Gln Leu Arg Tyr Leu Arg Lys Tyr Ser Leu Gly Arg Ser Val  
 465 470 475 480  
 Ala Asp Ile Phe Ala Asp Ile Glu Thr Val Phe Asn Ile Arg Thr Glu  
 485 490 495  
 Val Leu Ser Arg Gln Asp Pro His Ala Asp Gly Ala Ala Gly Thr Val  
 500 505 510  
 His Leu Asp Lys Phe Ala Glu Glu Val Ala Ser His Gly Gly Ile Gly  
 515 520 525  
 Leu Pro Glu Leu Leu Asp Tyr Phe Glu Leu Ala Lys Asp Gln Glu Glu  
 530 535 540  
 Gly Leu Glu Pro Gly Glu Val Thr Val Arg Ser Asp Arg Val Gln Ile  
 545 550 555 560  
 Leu Thr Val His Lys Ala Lys Gly Leu Glu Trp Asp Ile Val Ser Val  
 565 570 575  
 Leu His Ala Asp Ala Ser Thr Tyr Asp Ala Lys Ala Ser Thr Trp Leu  
 580 585 590  
 Lys Asn Val Thr Met Ile Pro Ser Ser Leu Arg Gly Asp Ala Gly Thr  
 595 600 605  
 Gly Ala Pro Glu Met Asp Thr Ser Glu Ala Asp Asp Arg Lys Ala Leu  
 610 615 620  
 Glu Asp Ser Gly Lys Glu Tyr Thr Ser Glu Val Arg Glu Gly Leu Arg  
 625 630 635 640  
 Glu Glu Asn Ser Arg Leu Phe Tyr Val Gly Ile Thr Arg Ser Glu Arg  
 645 650 655  
 Val Leu Leu Val Thr Gly Ser Ala Leu Asp Glu Ser Gly Thr Lys Ala  
 660 665 670  
 Lys Val Pro Tyr Gly His Leu Glu Ile Leu Arg Asp Lys Ala Pro Glu  
 675 680 685  
 Cys Val Val Ser Trp Trp Glu Gly Glu Glu Gly Asp Val Glu Lys Gln  
 690 695 700  
 Lys Pro Ala Glu Gly Val Phe Pro Gln Leu Leu Ala Ala Asp Ser Ser  
 705 710 715 720  
 Gly Ala Asp Leu Val Arg Gly Pro Arg Ala Glu Pro Asn Asn Glu Gly  
 725 730 735  
 Gly Leu Glu Ser Leu Trp Glu Lys Glu Val Ser Ala Leu Ile Asp Glu  
 740 745 750  
 His Arg Arg Leu Ser Asn Pro Ile Val Glu Val Glu Thr Pro Arg Glu  
 755 760 765

Leu Thr Ala Thr Asp Leu Val Ser Met Lys Asn Asn Pro Glu Gln Phe  
770 775 780

Ala Arg Arg Met Arg Arg Pro Val Pro Phe Lys Pro Asn Thr Tyr Ala  
785 790 795 800

Lys Arg Gly Thr Leu Phe His Gln Trp Leu Glu Asp Arg Phe Gly Ser  
805 810 815

Thr Ala Leu Leu Asp Glu Thr Glu Leu Pro Gly Ile Asp Glu Asp Tyr  
820 825 830

Ser Asp Asp Ala Phe Ile Glu Leu Arg Asp Ala Phe Leu Gly Ser Thr  
835 840 845

Trp Glu Asn Arg Thr Pro Glu Phe Val Glu His Pro Phe Glu Val Thr  
850 855 860

Ile Gly Glu His Val Ile Arg Gly Arg Met Asp Ala Val Phe His Thr  
865 870 875 880

Asp Gly Thr Trp Met Val Val Asp Trp Lys Thr Gly Arg Thr Pro Thr  
885 890 895

Gly Pro Glu Met Asp Ala Ala Ile Ile Gln Leu Ala Val Tyr Arg Leu  
900 905 910

Ala Trp Ala Arg Leu Lys Gly Leu Glu Pro Glu Glu Val Arg Ala Ala  
915 920 925

Phe His Tyr Val Ala His Asp His Thr Phe Glu Pro Asn Asp Leu Pro  
930 935 940

Thr Gln Glu Glu Leu Ala Arg Leu Leu Ser Gln Glu  
945 950 955

<210> 55

<211> 2412

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(2389)

<223> RXA00095

<400> 55

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gactatgcgt gtccacccca cctagtaggt tattggggta atg aat act tct cct 115  
Met Asn Thr Ser Pro 5

ttt acc cca ggt tcc ccc gat ctc atc gat ggc ttg aat gag caa cag 163  
Phe Thr Pro Gly Ser Pro Asp Leu Ile Asp Gly Leu Asn Glu Gln Gln 10 15 20

cgt gct gct gtg gag cat atc ggt tct ccg ctg ctg att gtc gct ggt 211  
Arg Ala Ala Val Glu His Ile Gly Ser Pro Leu Leu Ile Val Ala Gly 25 30 35

gct ggt tca ggc aag act gct gtg ttg acc agg cgt att gct tat tta 259  
Ala Gly Ser Gly Lys Thr Ala Val Leu Thr Arg Arg Ile Ala Tyr Leu  
40 45 50

atg cgt tac cgt ggt gtg cat ccg cag caa att ttg gcc att acc ttt 307  
Met Arg Tyr Arg Gly Val His Pro Gln Gln Ile Leu Ala Ile Thr Phe  
55 60 65

acc aat aag gct gcc gct gag atg cgt gag cgt gtc agt cag ctg gtg 355  
Thr Asn Lys Ala Ala Glu Met Arg Glu Arg Val Ser Gln Leu Val  
70 75 80 85

ggc ccg gtt gcg gag cgc atg tgg gtg gct acg ttc cac tcg gtg tgt 403  
Gly Pro Val Ala Glu Arg Met Trp Val Ala Thr Phe His Ser Val Cys  
90 95 100

gtg cgt att ttg cgt cag cag gcg cag ttg gtg gag ggg ctg aac act 451  
Val Arg Ile Leu Arg Gln Gln Ala Gln Leu Val Glu Gly Leu Asn Thr  
105 110 115

aac ttc act att tat gat tcg gat gat tcg agg cgt ttg ctc acg atg 499  
Asn Phe Thr Ile Tyr Asp Ser Asp Asp Ser Arg Arg Leu Leu Thr Met  
120 125 130

atc gcc aag gat ctg gag ttg gat att aag aag ttc tcg gcg cgt acg 547  
Ile Ala Lys Asp Leu Glu Leu Asp Ile Lys Lys Phe Ser Ala Arg Thr  
135 140 145

ttg ctg ggt gct att tct aat ttg aaa aat gag ttg gtt act ccg cag 595  
Leu Leu Gly Ala Ile Ser Asn Leu Lys Asn Glu Leu Val Thr Pro Gln  
150 155 160 165

gag gct ctt gcg gat gct gaa cgc acg cac aat cct tat gaa aca gtc 643  
Glu Ala Leu Ala Asp Ala Glu Arg Thr His Asn Pro Tyr Glu Thr Val  
170 175 180

gtg gcc agg gcg ttt tcg gag tat cag agc agg ctt cgc cgt gcc aac 691  
Val Ala Arg Ala Phe Ser Glu Tyr Gln Ser Arg Leu Arg Arg Ala Asn  
185 190 195

gct gtg gat ttt gat gat ttg att ggg gag act gtt cgg att ttc cgg 739  
Ala Val Asp Phe Asp Asp Leu Ile Gly Glu Thr Val Arg Ile Phe Arg  
200 205 210

gag cat cca cct gtt gcg gag tat tac cgc aga cgt ttc cgc cac gtg 787  
Glu His Pro Pro Val Ala Glu Tyr Tyr Arg Arg Arg Phe Arg His Val  
215 220 225

ctg atc gat gag tat cag gac acc aac cac gct cag tat gag ctg att 835  
Leu Ile Asp Glu Tyr Gln Asp Thr Asn His Ala Gln Tyr Glu Leu Ile  
230 235 240 245

tct acg ctc gtc ggc aag cct gac cag gat ccg tct gag ctg tgt gtt 883  
Ser Thr Leu Val Gly Lys Pro Asp Gln Asp Pro Ser Glu Leu Cys Val  
250 255 260

gtg ggt gat tcg gat cag tct att tat gct ttc cgt ggc gcc acg atc 931  
Val Gly Asp Ser Asp Gln Ser Ile Tyr Ala Phe Arg Gly Ala Thr Ile  
265 270 275



cgc aac att gaa gag ttt gag cgc gat ttc tcc aac gcc cgc acc att 979  
 Arg Asn Ile Glu Glu Phe Glu Arg Asp Phe Ser Asn Ala Arg Thr Ile  
 280 285 290

ttg ctg gag cag aat tac cgt tcc acc cag acg att ctt tct gct gcc 1027  
 Leu Leu Glu Gln Asn Tyr Arg Ser Thr Gln Thr Ile Leu Ser Ala Ala  
 295 300 305

aac gcg gtg att tct caa aat gag aac cgt cga cct aaa aac ctg tgg 1075  
 Asn Ala Val Ile Ser Gln Asn Glu Asn Arg Arg Pro Lys Asn Leu Trp  
 310 315 320 325

act gcg ctg ggg gag ggc gag cag atc att ggt tat gtt gcc gac aat 1123  
 Thr Ala Leu Gly Glu Gly Glu Gln Ile Ile Gly Tyr Val Ala Asp Asn  
 330 335 340

gag cac gat gaa gcc cgt ttt att gct agt gag atc gac aat tta gtt 1171  
 Glu His Asp Glu Ala Arg Phe Ile Ala Ser Glu Ile Asp Asn Leu Val  
 345 350 355

gac cac ggc atg agc tat tcc gac atc gcg atc atg tac cgc acg aac 1219  
 Asp His Gly Met Ser Tyr Ser Asp Ile Ala Ile Met Tyr Arg Thr Asn  
 360 365 370

aat tcc tcg cgc gca cta gag gat gtc ttc atg cgc acc ggc gtc ccc 1267  
 Asn Ser Ser Arg Ala Leu Glu Asp Val Phe Met Arg Thr Gly Val Pro  
 375 380 385

tac aaa gta gtc ggc ggc acg aag ttc tac gaa cgc aaa gaa atc cgt 1315  
 Tyr Lys Val Val Gly Gly Thr Lys Phe Tyr Glu Arg Lys Glu Ile Arg  
 390 395 400 405

gac atc atc gct tac ctg cgc gtt tta gaa aac ccc gat gac acc gtc 1363  
 Asp Ile Ile Ala Tyr Leu Arg Val Leu Glu Asn Pro Asp Asp Thr Val  
 410 415 420

aac ctg cgt cgc atc atc aac acc ccc aag cgc ggc atc ggc gat cgc 1411  
 Asn Leu Arg Arg Ile Ile Asn Thr Pro Lys Arg Gly Ile Gly Asp Arg  
 425 430 435

gcg cag gcg ttc atc gcg ctg cac agc gag aac aat cag atc agc ttc 1459  
 Ala Gln Ala Phe Ile Ala Leu His Ser Glu Asn Asn Gln Ile Ser Phe  
 440 445 450

ggg caa gcg ctt ctg gac gcc gcc ctg ggc aag gtc gac ctg ctt gga 1507  
 Gly Gln Ala Leu Leu Asp Ala Ala Leu Gly Lys Val Asp Leu Leu Gly  
 455 460 465

gcg cgc ggc aag aat gcg gcg att aag ttc aat gag ctt ttc gac gcc 1555  
 Ala Arg Gly Lys Asn Ala Ala Ile Lys Phe Asn Glu Leu Phe Asp Ala  
 470 475 480 485

ctg cgc tcc gaa ctg ccc acc atg gtc aat gag gtc acc ggc ctg cca 1603  
 Leu Arg Ser Glu Leu Pro Thr Met Val Asn Glu Val Thr Gly Leu Pro  
 490 495 500

gac atc ggc caa gtc atc agt cgc atc ctg gac atc act ggc tac aag 1651  
 Asp Ile Gly Gln Val Ile Ser Arg Ile Leu Asp Ile Thr Gly Tyr Lys  
 505 510 515

gca gaa ctt gag gca tcc aac gac cct caa gat ggc gca cgc cta gac 1699

Ala Glu Leu Glu Ala Ser Asn Asp Pro Gln Asp Gly Ala Arg Leu Asp  
520 525 530

aac ctg aac gag ctt gtc tcc gtg gcc cgc gag ttc tcc tcc gac gcc 1747  
Asn Leu Asn Glu Leu Val Ser Val Ala Arg Glu Phe Ser Ser Asp Ala  
535 540 545

gca aac cgc atg gtt aat gaa gtt cca gaa ggc gaa gcc caa cgc ggc 1795  
Ala Asn Arg Met Val Asn Glu Val Pro Glu Gly Glu Ala Gln Pro Gly  
550 555 560 565

agc tta cag gca ttc ttg gag cga gtc tcc ctg gtt gcc gac gcc gac 1843  
Ser Leu Gln Ala Phe Leu Glu Arg Val Ser Leu Val Ala Asp Ala Asp  
570 575 580

caa atc ccc gat tcc gac aac ggc gta gtc acc ctc atg acc ctg cat 1891  
Gln Ile Pro Asp Ser Asp Asn Gly Val Val Thr Leu Met Thr Leu His  
585 590 595

acc gcc aag ggc ctt gaa ttc ccc atc gtg ttc ctc aca ggc tgg gaa 1939  
Thr Ala Lys Gly Leu Glu Phe Pro Ile Val Phe Leu Thr Gly Trp Glu  
600 605 610

gac gga cag ttc cca cac ctg cgt tcc ctt ggt gat gcc aaa gaa ctt 1987  
Asp Gly Gln Phe Pro His Leu Arg Ser Leu Gly Asp Ala Lys Glu Leu  
615 620 625

gcc gag gaa cgc cgc ctc gcc tac gtg ggt atc acc cgc gcc cgc aag 2035  
Ala Glu Glu Arg Arg Leu Ala Tyr Val Gly Ile Thr Arg Ala Arg Lys  
630 635 640 645

cgc ctc tac atg acc aga gcc atg ctg cgt agc tcc tgg ggc aac cgc 2083  
Arg Leu Tyr Met Thr Arg Ala Met Leu Arg Ser Ser Trp Gly Asn Pro  
650 655 660

gtg acc aac cca cgc tca cgt ttc ctc caa gaa gtg ccc gca gaa ctc 2131  
Val Thr Asn Pro Pro Ser Arg Phe Leu Gln Glu Val Pro Ala Glu Leu  
665 670 675

atc gat tgg agg cgc gaa gaa ccc cag atg tct tcc gcc tgg gct cct 2179  
Ile Asp Trp Arg Arg Glu Glu Pro Gln Met Ser Ser Ala Trp Ala Pro  
680 685 690

cga ccc acc cga agc atc ccc acc aaa act cgc acc aac aat aag cag 2227  
Arg Pro Thr Arg Ser Ile Pro Thr Lys Thr Arg Thr Asn Asn Lys Gln  
695 700 705

ttg gat ctg tcg gtg ggg gat cgc gtc aat cac gac aag tac ggc ttg 2275  
Leu Asp Leu Ser Val Gly Asp Arg Val Asn His Asp Lys Tyr Gly Leu  
710 715 720 725

gga acc gtg ctc tct tca gat ggc agc ggc ccc cga gcc acc gtc acc 2323  
Gly Thr Val Leu Ser Ser Asp Gly Ser Gly Pro Arg Ala Thr Val Thr  
730 735 740

atc gat ttc ggt tcc tcc ggc aag gtt aga ttg atg ctt ctt ggt ggc 2371  
Ile Asp Phe Gly Ser Ser Gly Lys Val Arg Leu Met Leu Leu Gly Gly  
745 750 755

gtc cgc atg gag aag cta tagccccaat cgcggcgac acc 2412  
Val Pro Met Glu Lys Leu

760

<210> 56  
 <211> 763  
 <212> PRT  
 <213> *Corynebacterium glutamicum*

&lt;400&gt; 56

Met Asn Thr Ser Pro Phe Thr Pro Gly Ser Pro Asp Leu Ile Asp Gly  
 1 5 10 15

Leu Asn Glu Gln Gln Arg Ala Ala Val Glu His Ile Gly Ser Pro Leu  
 20 25 30

Leu Ile Val Ala Gly Ala Gly Ser Gly Lys Thr Ala Val Leu Thr Arg  
 35 40 45

Arg Ile Ala Tyr Leu Met Arg Tyr Arg Gly Val His Pro Gln Gln Ile  
 50 55 60

Leu Ala Ile Thr Phe Thr Asn Lys Ala Ala Ala Glu Met Arg Glu Arg  
 65 70 75 80

Val Ser Gln Leu Val Gly Pro Val Ala Glu Arg Met Trp Val Ala Thr  
 85 90 95

Phe His Ser Val Cys Val Arg Ile Leu Arg Gln Gln Ala Gln Leu Val  
 100 105 110

Glu Gly Leu Asn Thr Asn Phe Thr Ile Tyr Asp Ser Asp Asp Ser Arg  
 115 120 125

Arg Leu Leu Thr Met Ile Ala Lys Asp Leu Glu Leu Asp Ile Lys Lys  
 130 135 140

Phe Ser Ala Arg Thr Leu Leu Gly Ala Ile Ser Asn Leu Lys Asn Glu  
 145 150 155 160

Leu Val Thr Pro Gln Glu Ala Leu Ala Asp Ala Glu Arg Thr His Asn  
 165 170 175

Pro Tyr Glu Thr Val Val Ala Arg Ala Phe Ser Glu Tyr Gln Ser Arg  
 180 185 190

Leu Arg Arg Ala Asn Ala Val Asp Phe Asp Asp Leu Ile Gly Glu Thr  
 195 200 205

Val Arg Ile Phe Arg Glu His Pro Pro Val Ala Glu Tyr Tyr Arg Arg  
 210 215 220

Arg Phe Arg His Val Leu Ile Asp Glu Tyr Gln Asp Thr Asn His Ala  
 225 230 235 240

Gln Tyr Glu Leu Ile Ser Thr Leu Val Gly Lys Pro Asp Gln Asp Pro  
 245 250 255

Ser Glu Leu Cys Val Val Gly Asp Ser Asp Gln Ser Ile Tyr Ala Phe  
 260 265 270

Arg Gly Ala Thr Ile Arg Asn Ile Glu Glu Phe Glu Arg Asp Phe Ser

275	280	285
Asn Ala Arg Thr Ile Leu Leu Glu Gln Asn Tyr Arg Ser Thr Gln Thr 290 295 300		
Ile Leu Ser Ala Ala Asn Ala Val Ile Ser Gln Asn Glu Asn Arg Arg 305 310 315 320		
Pro Lys Asn Leu Trp Thr Ala Leu Gly Glu Gly Glu Gln Ile Ile Gly 325 330 335		
Tyr Val Ala Asp Asn Glu His Asp Glu Ala Arg Phe Ile Ala Ser Glu 340 345 350		
Ile Asp Asn Leu Val Asp His Gly Met Ser Tyr Ser Asp Ile Ala Ile 355 360 365		
Met Tyr Arg Thr Asn Asn Ser Ser Arg Ala Leu Glu Asp Val Phe Met 370 375 380		
Arg Thr Gly Val Pro Tyr Lys Val Val Gly Gly Thr Lys Phe Tyr Glu 385 390 395 400		
Arg Lys Glu Ile Arg Asp Ile Ile Ala Tyr Leu Arg Val Leu Glu Asn 405 410 415		
Pro Asp Asp Thr Val Asn Leu Arg Arg Ile Ile Asn Thr Pro Lys Arg 420 425 430		
Gly Ile Gly Asp Arg Ala Gln Ala Phe Ile Ala Leu His Ser Glu Asn 435 440 445		
Asn Gln Ile Ser Phe Gly Gln Ala Leu Leu Asp Ala Ala Leu Gly Lys 450 455 460		
Val Asp Leu Leu Gly Ala Arg Gly Lys Asn Ala Ala Ile Lys Phe Asn 465 470 475 480		
Glu Leu Phe Asp Ala Leu Arg Ser Glu Leu Pro Thr Met Val Asn Glu 485 490 495		
Val Thr Gly Leu Pro Asp Ile Gly Gln Val Ile Ser Arg Ile Leu Asp 500 505 510		
Ile Thr Gly Tyr Lys Ala Glu Leu Glu Ala Ser Asn Asp Pro Gln Asp 515 520 525		
Gly Ala Arg Leu Asp Asn Leu Asn Glu Leu Val Ser Val Ala Arg Glu 530 535 540		
Phe Ser Ser Asp Ala Ala Asn Arg Met Val Asn Glu Val Pro Glu Gly 545 550 555 560		
Glu Ala Gln Pro Gly Ser Leu Gln Ala Phe Leu Glu Arg Val Ser Leu 565 570 575		
Val Ala Asp Ala Asp Gln Ile Pro Asp Ser Asp Asn Gly Val Val Thr 580 585 590		
Leu Met Thr Leu His Thr Ala Lys Gly Leu Glu Phe Pro Ile Val Phe 595 600 605		

Leu Thr Gly Trp Glu Asp Gly Gln Phe Pro His Leu Arg Ser Leu Gly  
610 615 620

Asp Ala Lys Glu Leu Ala Glu Glu Arg Arg Leu Ala Tyr Val Gly Ile  
625 630 635 640

Thr Arg Ala Arg Lys Arg Leu Tyr Met Thr Arg Ala Met Leu Arg Ser  
645 650 655

Ser Trp Gly Asn Pro Val Thr Asn Pro Pro Ser Arg Phe Leu Gln Glu  
660 665 670

Val Pro Ala Glu Leu Ile Asp Trp Arg Arg Glu Glu Pro Gln Met Ser  
675 680 685

Ser Ala Trp Ala Pro Arg Pro Thr Arg Ser Ile Pro Thr Lys Thr Arg  
690 695 700

Thr Asn Asn Lys Gln Leu Asp Leu Ser Val Gly Asp Arg Val Asn His  
705 710 715 720

Asp Lys Tyr Gly Leu Gly Thr Val Leu Ser Ser Asp Gly Ser Gly Pro  
725 730 735

Arg Ala Thr Val Thr Ile Asp Phe Gly Ser Ser Gly Lys Val Arg Leu  
740 745 750

Met Leu Leu Gly Gly Val Pro Met Glu Lys Leu  
755 760

<210> 57

<211> 1070

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(1047)

<223> RXN02819

<400> 57

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Lys Leu Gln Ile Gly Asp Val Ile Ala Met Pro Gly Arg Lys Arg Pro  
1 5 10 15

gtt ctc gca gta gtg atg acg cct gct aat cag agc aga gat ccc cgc 96  
Val Leu Ala Val Val Met Thr Pro Ala Asn Gln Ser Arg Asp Pro Arg  
20 25 30

cca tgg gtg acc acc gaa tct ggt tgg tca ggt cgt gtg gat gcg gaa 144  
Pro Trp Val Thr Thr Glu Ser Gly Trp Ser Gly Arg Val Asp Ala Glu  
35 40 45

tcc ttt act aat ccg ccg atc acc att ggg cat atg cgt ctg cct cgc 192  
Ser Phe Thr Asn Pro Pro Ile Thr Ile Gly His Met Arg Leu Pro Arg  
50 55 60

caa gct att gaa gag cct cgc cgc aat gcc cgg cgc gtc cag gaa ctg 240  
Gln Ala Ile Glu Glu Pro Arg Arg Asn Ala Arg Arg Val Gln Glu Leu

65	70	75	80	
ttt agg cgt gag cac	ttc aag cga ccc aac aag atg	cgg gag ttt gct	288	
Phe Arg Arg Glu His	Phe Lys Arg Pro Asn Lys Met Arg Glu Phe Ala	95		
85	90			
cgg gtt cgt ccc aat gag gca gtg acc aaa ctg cgt aat gct att cgg	336			
Arg Val Arg Pro Asn Glu Ala Val Thr Lys Leu Arg Asn Ala Ile Arg	100	105	110	
gat cat gag cgc cat cat tgg cct gat cgg gag cac	384			
Asp His Glu Ala His His Trp Pro Asp Arg Glu His Leu Ala Arg Thr	115	120	125	
gcg gag cgt atg atc cgt aaa gaa cgt gat ctg gct aag ttg acc ggc	432			
Ala Glu Arg Met Ile Arg Lys Glu Arg Asp Leu Ala Lys Leu Thr Gly	130	135	140	
aat gtg gat aaa gcc agg gaa acc ctg ggt agg acg ttt gag cgc att	480			
Asn Val Asp Lys Ala Arg Glu Thr Leu Gly Arg Thr Phe Glu Arg Ile	145	150	155	
			160	
ttg tgc ctg ctg agt gaa atg gac tat gtg gat tac tct aat cca gat	528			
Leu Ser Leu Leu Ser Glu Met Asp Tyr Val Asp Tyr Ser Asn Pro Asp	165	170	175	
aat cca gtg atc act gat gaa ggt gag cgt ttg gcg aaa atc cac agt	576			
Asn Pro Val Ile Thr Asp Glu Gly Glu Arg Leu Ala Lys Ile His Ser	180	185	190	
gag gca gac ctg ttg gtt gct cag tgc ctg aag cgt ggc att tgg gac	624			
Glu Ala Asp Leu Leu Val Ala Gln Cys Leu Lys Arg Gly Ile Trp Asp	195	200	205	
aac ctt gat ccc gca gag ctg gcc ggt gtg gtg agt atg tgc acg ttt	672			
Asn Leu Asp Pro Ala Glu Leu Ala Gly Val Val Ser Met Cys Thr Phe	210	215	220	
gaa aat cgt cgc gaa acc ggt ggt gag gct caa gct gtc aca gag gcc	720			
Glu Asn Arg Arg Glu Thr Gly Gly Glu Ala Gln Ala Val Thr Glu Ala	225	230	235	
			240	
atg gct gat tcc atg aat agc gtg gaa cgt att tgg ggt gag ctg gtt	768			
Met Ala Asp Ser Met Asn Ser Val Glu Arg Ile Trp Gly Glu Leu Val	245	250	255	
gaa gat gag cgc cgt cac cgt ctg cca att act cgc cag ccg gaa gca	816			
Glu Asp Glu Arg Arg His Arg Leu Pro Ile Thr Arg Gln Pro Glu Ala	260	265	270	
ggt ttt gcc acc cgc atc cac cag tgg gct tca ggt gct ccg ctg gga	864			
Gly Phe Ala Thr Ala Ile His Gln Trp Ala Ser Gly Ala Pro Leu Gly	275	280	285	
tat tgc atg gct gcg gca gcg gaa aac ggc gcg gag ttg acc cct ggt	912			
Tyr Cys Met Ala Ala Ala Ala Glu Asn Gly Ala Glu Leu Thr Pro Gly	290	295	300	
gac ttc gtg cgc tgg tgc cgt caa gtc atc gat ctt cta gag cag gtt	960			
Asp Phe Val Arg Trp Cys Arg Gln Val Ile Asp Leu Leu Glu Gln Val	305	310	315	
			320	

gct aag act gcc tac ttt gat gag acc aca cgg aat gct cgt cag gct 1008  
 Ala Lys Thr Ala Tyr Phe Asp Glu Thr Thr Arg Asn Ala Arg Gln Ala  
                   325                  330                  335

att gat gcg att agg cgt gga gtt gtg gcg atc ggt tcc tagcgagcta 1057  
 Ile Asp Ala Ile Arg Arg Gly Val Val Ala Ile Gly Ser  
                   340                  345

gctatgttcg agc 1070

<210> 58  
 <211> 349  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 58  
 Lys Leu Gln Ile Gly Asp Val Ile Ala Met Pro Gly Arg Lys Arg Pro  
   1                  5                  10                  15  
 Val Leu Ala Val Val Met Thr Pro Ala Asn Gln Ser Arg Asp Pro Arg  
                   20                  25                  30  
 Pro Trp Val Thr Thr Glu Ser Gly Trp Ser Gly Arg Val Asp Ala Glu  
                   35                  40                  45  
 Ser Phe Thr Asn Pro Pro Ile Thr Ile Gly His Met Arg Leu Pro Arg  
                   50                  55                  60  
 Gln Ala Ile Glu Glu Pro Arg Arg Asn Ala Arg Arg Val Gln Glu Leu  
                   65                  70                  75                  80  
 Phe Arg Arg Glu His Phe Lys Arg Pro Asn Lys Met Arg Glu Phe Ala  
                   85                  90                  95  
 Arg Val Arg Pro Asn Glu Ala Val Thr Lys Leu Arg Asn Ala Ile Arg  
                   100                  105                  110  
 Asp His Glu Ala His His Trp Pro Asp Arg Glu His Leu Ala Arg Thr  
                   115                  120                  125  
 Ala Glu Arg Met Ile Arg Lys Glu Arg Asp Leu Ala Lys Leu Thr Gly  
                   130                  135                  140  
 Asn Val Asp Lys Ala Arg Glu Thr Leu Gly Arg Thr Phe Glu Arg Ile  
                   145                  150                  155                  160  
 Leu Ser Leu Leu Ser Glu Met Asp Tyr Val Asp Tyr Ser Asn Pro Asp  
                   165                  170                  175  
 Asn Pro Val Ile Thr Asp Glu Gly Glu Arg Leu Ala Lys Ile His Ser  
                   180                  185                  190  
 Glu Ala Asp Leu Leu Val Ala Gln Cys Leu Lys Arg Gly Ile Trp Asp  
                   195                  200                  205  
 Asn Leu Asp Pro Ala Glu Leu Ala Gly Val Val Ser Met Cys Thr Phe  
                   210                  215                  220  
 Glu Asn Arg Arg Glu Thr Gly Gly Glu Ala Gln Ala Val Thr Glu Ala

225	230	235	240
Met Ala Asp Ser	Met Asn Ser Val	Glu Arg Ile Trp Gly	Glu Leu Val
245		250	255
Glu Asp Glu Arg	His Arg Leu Pro	Ile Thr Arg Gln	Pro Glu Ala
260		265	270
Gly Phe Ala Thr	Ala Ile His Gln	Trp Ala Ser Gly	Ala Pro Leu Gly
275		280	285
Tyr Cys Met Ala	Ala Ala Ala Glu	Asn Gly Ala Glu	Leu Thr Pro Gly
290		295	300
Asp Phe Val Arg	Trp Cys Arg Gln	Val Ile Asp Leu	Leu Glu Gln Val
305		310	315
Ala Lys Thr Ala	Tyr Phe Asp Glu	Thr Thr Arg Asn	Ala Arg Gln Ala
	325		330
			335
Ile Asp Ala Ile	Arg Arg Gly Val	Val Ala Ile Gly	Ser
	340		345

<210> 59  
 <211> 612  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (1) .. (612)  
 <223> FRXA02819

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Lys Leu Gln Ile Gly Asp Val Ile Ala Met Pro Gly Arg Lys Arg Pro	
1 5 10 15	
ggt ctc gca gta gtg atg acg cct gct aat cag agc aga gat ccc cgc	96
Val Leu Ala Val Val Met Thr Pro Ala Asn Gln Ser Arg Asp Pro Arg	
20 25 30	
cca tgg gtg acc acc gaa tct ggt tgg tca ggt cgt gtg gat gcg gaa	144
Pro Trp Val Thr Thr Glu Ser Gly Trp Ser Gly Arg Val Asp Ala Glu	
35 40 45	
tcc ttt act aat ccg ccg atc acc att ggg cat atg cgt ctg cct cgc	192
Ser Phe Thr Asn Pro Pro Ile Thr Ile Gly His Met Arg Leu Pro Arg	
50 55 60	
caa gct att gaa gag cct cgc cgc aat gcc cgg cgc gtc cag gaa ctg	240
Gln Ala Ile Glu Glu Pro Arg Arg Asn Ala Arg Arg Val Gln Glu Leu	
65 70 75 80	
ttt agg cgt gag cac ttc aag cga ccc aac aag atg cgg gag ttt gct	288
Phe Arg Arg Glu His Phe Lys Arg Pro Asn Lys Met Arg Glu Phe Ala	
85 90 95	
cgg gtt cgt ccc aat gag gca gtg acc aaa ctg cgt aat gct att cgg	336
Arg Val Arg Pro Asn Glu Ala Val Thr Lys Leu Arg Asn Ala Ile Arg	



100	105	110	
gat cat gag gcg cat cat tgg cct gat	cgg gag cac ttg gct cgc acc		384
Asp His Glu Ala His His Trp Pro Asp Arg	Glu His Leu Ala Arg Thr		
115	120	125	
gcg gag cgt atg atc cgt aaa gaa cgt	gat ctg gct aag ttg acc ggc		432
Ala Glu Arg Met Ile Arg Lys Glu Arg Asp	Leu Ala Lys Leu Thr Gly		
130	135	140	
aat gtg gat aaa gcc agg gaa acc ctc	ggt agg acg ttt gag cgc att		480
Asn Val Asp Lys Ala Arg Glu Thr Leu Gly	Arg Thr Phe Glu Arg Ile		
145	150	155	160
ttg tgg ctg ctc agt gaa atg gac tat	gtg gat tac tct aat cca gat		528
Leu Ser Leu Leu Ser Glu Met Asp Tyr	Val Asp Tyr Ser Asn Pro Asp		
165	170	175	
aat cca gtg atc act gat gaa ggt gag	cgt ttg gcg aaa atc cac agt		576
Asn Pro Val Ile Thr Asp Glu Gly Glu Arg	Leu Ala Lys Ile His Ser		
180	185	190	
gag gca gac ctg ttg gtt gct cag tgc	ctc aag cgt		612
Glu Ala Asp Leu Leu Val Ala Gln Cys	Leu Lys Arg		
195	200		
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<211> 204			
<212> PRT			
<213> Corynebacterium glutamicum			
 <400> 60			
Lys Leu Gln Ile Gly Asp Val Ile Ala Met	Pro Gly Arg Lys Arg Pro		
1	5	10	15
Val Leu Ala Val Val Met Thr Pro Ala Asn	Gln Ser Arg Asp Pro Arg		
20	25	30	
Pro Trp Val Thr Thr Glu Ser Gly Trp Ser	Gly Arg Val Asp Ala Glu		
35	40	45	
Ser Phe Thr Asn Pro Pro Ile Thr Ile Gly	His Met Arg Leu Pro Arg		
50	55	60	
Gln Ala Ile Glu Glu Pro Arg Arg Asn Ala	Arg Arg Val Gln Glu Leu		
65	70	75	80
Phe Arg Arg Glu His Phe Lys Arg Pro Asn	Lys Met Arg Glu Phe Ala		
85	90	95	
Arg Val Arg Pro Asn Glu Ala Val Thr Lys	Leu Arg Asn Ala Ile Arg		
100	105	110	
Asp His Glu Ala His His Trp Pro Asp Arg	Glu His Leu Ala Arg Thr		
115	120	125	
Ala Glu Arg Met Ile Arg Lys Glu Arg Asp	Leu Ala Lys Leu Thr Gly		
130	135	140	
Asn Val Asp Lys Ala Arg Glu Thr Leu Gly	Arg Thr Phe Glu Arg Ile		

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145              150              155              160
Leu Ser Leu Leu Ser Glu Met Asp Tyr Val Asp Tyr Ser Asn Pro Asp
      165              170              175
Asn Pro Val Ile Thr Asp Glu Gly Glu Arg Leu Ala Lys Ile His Ser
      180              185              190
Glu Ala Asp Leu Leu Val Ala Gln Cys Leu Lys Arg
      195              200

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<210> 61
<211> 1705
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (101)..(1705)  
<223> RXA01157
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400> 61	cggatgctga acccaagtgg ggaggcgctcg ataagctata aacccgggcg cgccgacttc	60
ggtgacgtgc tctagggcgct agccagggtac ccttagaggc	atg agt ttt tct gcc Met Ser Phe Ser Ala 1 5	115
gaa aag ggc acc cac ctt tca gag ttc ata gca gac ctg ggc ttt gat	Ile Ala Asp Leu Gly Phe Asp 15 20	165
Glu Lys Gly Thr His Leu Ser Glu Phe		
ctg gac gag ttc caa atc aaa ggc tgc cac gct gtg gaa gaa gac cac	Cys His Ala Val Glu Glu Asp His 30 35	211
Leu Asp Glu Phe Gln Ile Lys Gly		
ggt gtt tta gta tgt gcg ccc acc ggc gcg ggc aaa aca att gtt ggt	Gly Val Leu Val Cys Ala Pro Thr Gly Ala Gly Lys Thr Ile Val Gly 40 45 50	259
gaa ttc gca gtg tcc ctc gca tta tgc cgg ggg aca aag tgt ttc tac	Thr Lys Cys Phe Tyr 60 65	307
Glu Phe Ala Val Ser Leu Ala Leu Ser Arg Gly		
acc acc ccc atc aaa gcg ctg agc aac cag aag tac cac gat ttg gtg	Thr Thr Pro Ile Lys Ala Leu Ser Asn Gln Lys Tyr His Asp Leu Val 70 75 80 85	355
gct aaa cac ggc tcc gat gcc gtt ggt ctg ctc acc ggt gat gtt tcc	Ala Lys His Gly Ser Asp Ala Val Gly Leu Leu Thr Gly Asp Val Ser 90 95 100	403
att aac cat gat gct gac atc gtg gtc atg acc acc gaa gtg ctg cgc	Ile Asn His Asp Ala Asp Ile Val Val Met Thr Thr Glu Val Leu Arg 105 110 115	451
aac atg att tac gcg ggc tct ttt gcg ctt gag cgc tta agc cac gtg	Asn Met Ile Tyr Ala Gly Ser Phe Ala Leu Glu Arg Leu Ser His Val 120 125 130	495

gtc atg gat gag atc cac ttc ctt gct gat gcc tcc cgt ggc gcg gtg 547  
 Val Met Asp Glu Ile His Phe Leu Ala Asp Ala Ser Arg Gly Ala Val  
 135 140 145

tgg gaa gaa gtg atc ctc aac ttg gat gat tcc gtc aac atc atc ggt 595  
 Trp Glu Glu Val Ile Leu Asn Leu Asp Asp Val Val Asn Ile Ile Gly  
 150 155 160 165

cta tct gcc acg gtg tcc aac tca gag gag ttt ggt gag tgg ctg acc 643  
 Leu Ser Ala Thr Val Ser Asn Ser Glu Glu Phe Gly Glu Trp Leu Thr  
 170 175 180

act gtt cgc ggc gat acc cgt gtg att gtt act gat cac cgc ccc gtt 691  
 Thr Val Arg Gly Asp Thr Arg Val Ile Val Thr Asp His Arg Pro Val  
 185 190 195

ccg ctt gat cag tac atg atg gtg cag cgc aaa gtg atg cca ctg ttt 739  
 Pro Leu Asp Gln Tyr Met Met Val Gln Arg Lys Val Met Pro Leu Phe  
 200 205 210

gag cct ggc acc gat gga cgc gtg aac aag gag tta gag gca acg att 787  
 Glu Pro Gly Thr Asp Gly Arg Val Asn Lys Glu Leu Glu Ala Thr Ile  
 215 220 225

gat cgc ctc aac agc aag caa agc gaa caa ggc cgt gcg gca tac cgc 835  
 Asp Arg Leu Asn Ser Lys Gln Ser Glu Gln Gly Arg Ala Ala Tyr Arg  
 230 235 240 245

tct ggt gaa ggc ttc cgt gca cgc agc aaa ggc gat aag cag gat tct 883  
 Ser Gly Glu Gly Phe Arg Ala Arg Ser Lys Gly Asp Lys Gln Asp Ser  
 250 255 260

cgc act ggt aag cca cgg gaa caa gac cgc cac agg cca ctg ggt cgg 931  
 Arg Thr Gly Lys Pro Arg Glu Gln Asp Arg His Arg Pro Leu Gly Arg  
 265 270 275

cct gaa gtg ctc agc atc ctc aag ggc atc aac atg ctg cca gcg att 979  
 Pro Glu Val Leu Ser Ile Leu Lys Gly Ile Asn Met Leu Pro Ala Ile  
 280 285 290

acg ttt atc ttc tcc cgc gcg ggc tgt gat ggt gcg ctg tac caa tgc 1027  
 Thr Phe Ile Phe Ser Arg Ala Gly Cys Asp Gly Ala Leu Tyr Gln Cys  
 295 300 305

ttg cgt tct aag ttg gtc ttg acg gat caa gca gaa tca gaa gag att 1075  
 Leu Arg Ser Lys Leu Val Leu Thr Asp Gln Ala Glu Ser Glu Glu Ile  
 310 315 320 325

gca cgc att gtc gac gcc ggc gtg gtg ggg atc ccc gag gaa gac ctt 1123  
 Ala Arg Ile Val Asp Ala Gly Val Val Gly Ile Pro Glu Glu Asp Leu  
 330 335 340

caa gta ctg aac ttt aag cag tgg cgt gct gca ctg atg cgc ggt ttc 1171  
 Gln Val Leu Asn Phe Lys Gln Trp Arg Ala Ala Leu Met Arg Gly Phe  
 345 350 355

gca gcc cac cac gcg ggt atg ctt cca gcg ttt agg cac atc gtg gaa 1219  
 Ala Ala His His Ala Gly Met Leu Pro Ala Phe Arg His Ile Val Glu  
 360 365 370

gag ctc ttt gtt aaa ggt ctt gtc cgc gcg gtg ttt gcc acg gaa acc 1267

Glu Leu Phe Val Lys Gly Leu Val Arg Ala Val Phe Ala Thr Glu Thr  
 375 380 385  
 ctg gca ttg gga atc aac atg cca gcg cgc acc gtg gtg ttg gaa aag 1315  
 Leu Ala Leu Gly Ile Asn Met Pro Ala Arg Thr Val Val Leu Glu Lys  
 390 395 400 405  
 atg gtc aaa ttt gac ggc gaa ggc cac gtt gat ctc acc cct ggc caa 1363  
 Met Val Lys Phe Asp Gly Glu Gly His Val Asp Leu Thr Pro Gly Gln  
 410 415 420  
 tac acg cag ctg acc ggt cgt gct ggt cga cgt ggc atc gat gtg ttg 1411  
 Tyr Thr Gln Leu Thr Gly Arg Ala Gly Arg Arg Gly Ile Asp Val Leu  
 425 430 435  
 ggt aat gct gtg gtg cag tgg tca cca gca ctt gat cca cga tgg gtg 1459  
 Gly Asn Ala Val Val Gln Trp Ser Pro Ala Leu Asp Pro Arg Trp Val  
 440 445 450  
 gca ggt ctt gcc tct acg cgt acc tac ccg ctg atc tct acg ttc cag 1507  
 Ala Gly Leu Ala Ser Thr Arg Thr Tyr Pro Leu Ile Ser Thr Phe Gln  
 455 460 465  
 ccg ggc tac aac atg tcg gtt aac ctg ctg aaa acc att ggt tat gag 1555  
 Pro Gly Tyr Asn Met Ser Val Asn Leu Leu Lys Thr Ile Gly Tyr Glu  
 470 475 480 485  
 cct tcg ctg cgc ctt ttg gaa aaa tct ttt gca cag ttc caa gcc gat 1603  
 Pro Ser Leu Arg Leu Leu Glu Lys Ser Phe Ala Gln Phe Gln Ala Asp  
 490 495 500  
 ggt tcc gtc gtg ggc gat gtg cgt gaa att gaa cgt gca gaa gcc aag 1651  
 Gly Ser Val Val Gly Asp Val Arg Glu Ile Glu Arg Ala Glu Ala Lys  
 505 510 515  
 gtg gca gaa ttg cgt gcc cag ctg aac aaa gag att gct gcc acc aac 1699  
 Val Ala Glu Leu Arg Ala Gln Leu Asn Lys Glu Ile Ala Ala Thr Asn  
 520 525 530  
 cct gcg 1705  
 Pro Ala  
 535  
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 <211> 535  
 <212> PRT  
 <213> Corynebacterium glutamicum  
 <400> 62  
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 Asp Leu Gly Phe Asp Leu Asp Glu Phe Gln Ile Lys Gly Cys His Ala  
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 Val Glu Glu Asp His Gly Val Leu Val Cys Ala Pro Thr Gly Ala Gly  
 35 40 45  
 Lys Thr Ile Val Gly Glu Phe Ala Val Ser Leu Ala Leu Ser Arg Gly  
 50 55 60

Thr Lys Cys Phe Tyr Thr Thr Pro Ile Lys Ala Leu Ser Asn Gln Lys  
 65 70 75 80  
 Tyr His Asp Leu Val Ala Lys His Gly Ser Asp Ala Val Gly Leu Leu  
 85 90 95  
 Thr Gly Asp Val Ser Ile Asn His Asp Ala Asp Ile Val Val Met Thr  
 100 105 110  
 Thr Glu Val Leu Arg Asn Met Ile Tyr Ala Gly Ser Phe Ala Leu Glu  
 115 120 125  
 Arg Leu Ser His Val Val Met Asp Glu Ile His Phe Leu Ala Asp Ala  
 130 135 140  
 Ser Arg Gly Ala Val Trp Glu Glu Val Ile Leu Asn Leu Asp Asp Ser  
 145 150 155 160  
 Val Asn Ile Ile Gly Leu Ser Ala Thr Val Ser Asn Ser Glu Glu Phe  
 165 170 175  
 Gly Glu Trp Leu Thr Thr Val Arg Gly Asp Thr Arg Val Ile Val Thr  
 180 185 190  
 Asp His Arg Pro Val Pro Leu Asp Gln Tyr Met Met Val Gln Arg Lys  
 195 200 205  
 Val Met Pro Leu Phe Glu Pro Gly Thr Asp Gly Arg Val Asn Lys Glu  
 210 215 220  
 Leu Glu Ala Thr Ile Asp Arg Leu Asn Ser Lys Gln Ser Glu Gln Gly  
 225 230 235 240  
 Arg Ala Ala Tyr Arg Ser Gly Glu Gly Phe Arg Ala Arg Ser Lys Gly  
 245 250 255  
 Asp Lys Gln Asp Ser Arg Thr Gly Lys Pro Arg Glu Gln Asp Arg His  
 260 265 270  
 Arg Pro Leu Gly Arg Pro Glu Val Leu Ser Ile Leu Lys Gly Ile Asn  
 275 280 285  
 Met Leu Pro Ala Ile Thr Phe Ile Phe Ser Arg Ala Gly Cys Asp Gly  
 290 295 300  
 Ala Leu Tyr Gln Cys Leu Arg Ser Lys Leu Val Leu Thr Asp Gln Ala  
 305 310 315 320  
 Glu Ser Glu Glu Ile Ala Arg Ile Val Asp Ala Gly Val Val Gly Ile  
 325 330 335  
 Pro Glu Glu Asp Leu Gln Val Leu Asn Phe Lys Gln Trp Arg Ala Ala  
 340 345 350  
 Leu Met Arg Gly Phe Ala Ala His His Ala Gly Met Leu Pro Ala Phe  
 355 360 365  
 Arg His Ile Val Glu Glu Leu Phe Val Lys Gly Leu Val Arg Ala Val  
 370 375 380

Phe Ala Thr Glu Thr Leu Ala Leu Gly Ile Asn Met Pro Ala Arg Thr  
385 390 395 400

Val Val Leu Glu Lys Met Val Lys Phe Asp Gly Glu Gly His Val Asp  
405 410 415

Leu Thr Pro Gly Gln Tyr Thr Gln Leu Thr Gly Arg Ala Gly Arg Arg  
420 425 430

Gly Ile Asp Val Leu Gly Asn Ala Val Val Gln Trp Ser Pro Ala Leu  
435 440 445

Asp Pro Arg Trp Val Ala Gly Leu Ala Ser Thr Arg Thr Tyr Pro Leu  
450 455 460

Ile Ser Thr Phe Gln Pro Gly Tyr Asn Met Ser Val Asn Leu Leu Lys  
465 470 475 480

Thr Ile Gly Tyr Glu Pro Ser Leu Arg Leu Leu Glu Lys Ser Phe Ala  
485 490 495

Gln Phe Gln Ala Asp Gly Ser Val Val Gly Asp Val Arg Glu Ile Glu  
500 505 510

Arg Ala Glu Ala Lys Val Ala Glu Leu Arg Ala Gln Leu Asn Lys Glu  
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Ile Ala Ala Thr Asn Pro Ala  
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<210> 63

<211> 1974

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1951)

<223> RXN01876

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Met Ala Arg Pro Phe  
1 5

tat ctg gcc acc acc gtt tca ccg gag ggc gtg cat atc cgc cgg cac 163  
Tyr Leu Ala Thr Thr Val Ser Pro Glu Gly Val His Ile Arg Arg His  
10 15 20

att cgc acc cgt ggg cgc gtt gtc acg ggt gtt gat gat gag gta ttg 211  
Ile Arg Thr Arg Gly Arg Val Val Thr Gly Val Asp Asp Glu Val Leu  
25 30 35

acc ggt gag atg gcc gat gtt atc gag cag ggt ggt gtc gcc tct gaa 259  
Thr Gly Glu Met Ala Asp Val Ile Glu Gln Gly Gly Val Gly Ser Glu  
40 45 50

tct gtg ctg cac cag gcg ttg gaa cag gcc cgc agc ggc cac atg cgc 307

Ser Val Leu His Gln Ala Leu Glu Gln Ala Arg Ser Gly His Met Arg	
55 60 65	
aac atc gtt gaa aca att cag cgc gag cag gat gag atc atc cgc gat	355
Asn Ile Val Glu Thr Ile Gln Arg Glu Gln Asp Glu Ile Ile Arg Asp	
70 75 80	
acc acc cgc ggt gtc atg gtt gtt caa ggt ggc cct gga aca ggt aaa	403
Thr Thr Arg Gly Val Met Val Val Gln Gly Gly Pro Gly Thr Gly Lys	
90 95 100	
act gcg gtc cgc ttg cac cgt gtg gct tat ctg ctt tat acc tgg cgc	451
Thr Ala Val Ala Leu His Arg Val Ala Tyr Leu Leu Tyr Thr Trp Arg	
105 110 115	
gat cag ctg gct aag tct ggc gtg ttg atc att ggc cgc aac aag aca	499
Asp Gln Leu Ala Lys Ser Gly Val Leu Ile Ile Gly Pro Asn Lys Thr	
120 125 130	
ttt ttg gag tat att tct cac gtt ttg cct gaa ctc ggc gag act ggc	547
Phe Leu Glu Tyr Ile Ser His Val Leu Pro Glu Gly Gly Thr Gly	
135 140 145	
gtg gtg ttg tcc acc gtc ggt gag ctg ttc ccc ggt atc gtc cca acg	595
Val Val Leu Ser Thr Val Gly Glu Leu Phe Pro Gly Ile Val Pro Thr	
150 155 160 165	
ggt tcc gag gac act ttg acc agg gaa att aag ggc agc gag gaa atg	643
Gly Ser Glu Asp Thr Leu Thr Arg Glu Ile Lys Gly Ser Glu Glu Met	
170 175 180	
gcc agc att ttg gcc gag gca gtc aag gcg tat caa gtg ctg cca gag	691
Ala Ser Ile Leu Ala Glu Ala Val Lys Ala Tyr Gln Val Leu Pro Glu	
185 190 195	
aag acc atc gtg gtc tct gtt gat ggc atc gag att tcc att gat gag	739
Lys Thr Ile Val Val Ser Val Asp Gly Ile Glu Ile Ser Ile Asp Glu	
200 205 210	
aaa acg gtg gca aaa tcc cgc acc cga gct cgt cgt gcc agg cag tgc	787
Lys Thr Val Ala Lys Ser Arg Thr Arg Ala Arg Ala Arg Gln Ser	
215 220 225	
cac aat tcc gca cgc cca att ttc cgc gag cat tta gtc gaa caa ctc	835
His Asn Ser Ala Arg Pro Ile Phe Arg Glu His Leu Val Glu Gln Leu	
230 235 240 245	
gcg cac caa atg gct caa acg atc ggc gcg gat ccg ctg ggc ggc aaa	883
Ala His Gln Met Ala Gln Thr Ile Gly Ala Asp Pro Leu Gly Gly Lys	
250 255 260	
aac ctg ctg tca gcc gcc gac atc gat cag ctg cac gat gat ttg ctt	931
Asn Leu Leu Ser Ala Ala Asp Ile Asp Gln Leu His Asp Asp Leu Leu	
265 270 275	
gac gac gcg gcc ctc cag tcc gtc atc gac gat ttc tgg ccg gag ctc	979
Asp Asp Ala Ala Leu Gln Ser Phe Val Ile Asp Asp Phe Trp Pro Glu Leu	
280 285 290	
cgg cct cag gac gtc ctg cat gat ctg ttg att tcc gaa gag cgc att	1027
Arg Pro Gln Asp Val Leu His Asp Leu Leu Ile Ser Glu Glu Arg Ile	

295	300	305	
aat gtt gct gcc gcg ggg tat gac gag gaa act aag tct gct ttg ctg			1075
Asn Val Ala Ala Ala Gly Tyr Asp Glu Glu Thr Lys Ser Ala Leu Leu			
310	315	320	325
cgt ggt gaa ctc gat ccg tgg gca cca tcg gac gct gca ttg ctt gat			1123
Arg Gly Glu Leu Asp Pro Trp Ala Pro Ser Asp Ala Ala Leu Leu Asp			
	330	335	340
gag tta gcc ctg ctc atc ggt ctt ccc gat cca gag gag gca cgg gag			1171
Glu Leu Ala Leu Leu Ile Gly Leu Pro Asp Pro Glu Glu Ala Arg Glu			
	345	350	355
aag gct gag gcc aaa tgg cgc gag cag atc gat gac gct cag gaa gtc			1219
Lys Ala Glu Ala Lys Trp Arg Glu Gln Ile Asp Asp Ala Gln Glu Val			
	360	365	370
ctg gac gtt ctt agt tca tca cag tca tcg gat att gat gat gtc acg			1267
Leu Asp Val Leu Ser Ser Gln Ser Ser Asp Ile Asp Asp Val Thr			
	375	380	385
gaa gct gaa gtt ctc tcc gct ttc gac gtc atc gat gcg gaa act ttg			1315
Glu Ala Glu Val Leu Ser Ser Ala Phe Asp Val Ile Asp Ala Glu Thr Leu			
	390	395	400
gca caa cgc caa act gtc acg gat aat cgc acc act gcg gaa cgt gca			1363
Ala Gln Arg Gln Thr Val Thr Asp Asn Arg Thr Thr Ala Glu Arg Ala			
	410	415	420
cag gcg gat cat aag tgg gca tat ggt cac gtg att gta gat gaa gct			1411
Gln Ala Asp His Lys Trp Ala Tyr Gly His Val Ile Val Asp Glu Ala			
	425	430	435
cag gag ctc agt ccg atg gaa tgg cgc atg gtg ttt cgc cgt agc cct			1459
Gln Glu Leu Ser Pro Met Glu Trp Arg Met Val Phe Arg Arg Ser Pro			
	440	445	450
tcg cga tgg atg acc ctt gtg ggc gat att gca caa act ggt tgg cct			1507
Ser Arg Trp Met Thr Leu Val Gly Asp Ile Ala Gln Thr Gly Trp Pro			
	455	460	465
gcc ggc gtt gac gat tgg gca gaa tca ctg tgg ccc ttc gtc gaa aag			1555
Ala Gly Val Asp Asp Trp Ala Glu Ser Leu Trp Pro Phe Val Glu Lys			
	470	475	480
cgt ttc agg cac cac gag ctc acc gtt aac tac cgc acc ccg gcc gag			1603
Arg Phe Arg His His Glu Leu Thr Val Asn Tyr Arg Thr Pro Ala Glu			
	490	495	500
atc atg tcg gtg gcc aat gag ctt ttg acg cag atc aat cct gat att			1651
Ile Met Ser Val Ala Asn Glu Leu Leu Thr Gln Ile Asn Pro Asp Ile			
	505	510	515
gcg ccg gca atg gcg atc cgc gaa tct ggt cga gag gta gtg aac ttg			1699
Ala Pro Ala Met Ala Ile Arg Glu Ser Gly Arg Glu Val Val Asn Leu			
	520	525	530
ccg ctt gat gcc gat ttg tcg gca gtg atg gat agt ttg cgt gag gag			1747
Pro Leu Asp Ala Asp Leu Ser Ala Val Met Asp Ser Leu Arg Glu Glu			
	535	540	545



gat tca cag cgc acc atc gcg gtg att tct tcg cgc cgc cac cac gaa 1795  
 Asp Ser Gln Arg Thr Ile Ala Val Ile Ser Ser Arg Arg His His Glu  
 550 555 560 565

agc gat ttc tac ctg gtc gat gac atc aag gcc tta gag ttt gac cac 1843  
 Ser Asp Phe Tyr Leu Val Asp Asp Ile Lys Gly Leu Glu Phe Asp His  
 570 575 580

gtc atc gtg gtg gat cct gcg gga atc gtt gaa gaa tcc ccc cag gga 1891  
 Val Ile Val Val Asp Pro Ala Gly Ile Val Glu Glu Ser Pro Gln Gly  
 585 590 595

ttg caa gac ctc tac gtt gcg gtc act cgt gca acg cag agc ctc acc 1939  
 Leu Gln Asp Leu Tyr Val Ala Val Thr Arg Ala Thr Gln Ser Leu Thr  
 600 605 610

att tta ggt gag tagcaggtta tgagctcagg gcc 1974  
 Ile Leu Gly Glu  
 615

&lt;210&gt; 64

&lt;211&gt; 617

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 64

Met Ala Arg Pro Phe Tyr Leu Ala Thr Thr Val Ser Pro Glu Gly Val  
 1 5 10 15

His Ile Arg Arg His Ile Arg Thr Arg Gly Arg Val Val Thr Gly Val  
 20 25 30

Asp Asp Glu Val Leu Thr Gly Glu Met Ala Asp Val Ile Glu Gln Gly  
 35 40 45

Gly Val Gly Ser Glu Ser Val Leu His Gln Ala Leu Glu Gln Ala Arg  
 50 55 60

Ser Gly His Met Arg Asn Ile Val Glu Thr Ile Gln Arg Glu Gln Asp  
 65 70 75 80

Glu Ile Ile Arg Asp Thr Thr Arg Gly Val Met Val Val Gln Gly Gly  
 85 90 95

Pro Gly Thr Gly Lys Thr Ala Val Ala Leu His Arg Val Ala Tyr Leu  
 100 105 110

Leu Tyr Thr Trp Arg Asp Gln Leu Ala Lys Ser Gly Val Leu Ile Ile  
 115 120 125

Gly Pro Asn Lys Thr Phe Leu Glu Tyr Ile Ser His Val Leu Pro Glu  
 130 135 140

Leu Gly Glu Thr Gly Val Val Leu Ser Thr Val Gly Glu Leu Phe Pro  
 145 150 155 160

Gly Ile Val Pro Thr Gly Ser Glu Asp Thr Leu Thr Arg Glu Ile Lys  
 165 170 175

Gly Ser Glu Glu Met Ala Ser Ile Leu Ala Glu Ala Val Lys Ala Tyr  
 180 185 190  
 Gln Val Leu Pro Glu Lys Thr Ile Val Val Ser Val Asp Gly Ile Glu  
 195 200 205  
 Ile Ser Ile Asp Glu Lys Thr Val Ala Lys Ser Arg Thr Arg Ala Arg  
 210 215 220  
 Arg Ala Arg Gln Ser His Asn Ser Ala Arg Pro Ile Phe Arg Glu His  
 225 230 235 240  
 Leu Val Glu Gln Leu Ala His Gln Met Ala Gln Thr Ile Gly Ala Asp  
 245 250 255  
 Pro Leu Gly Gly Lys Asn Leu Leu Ser Ala Ala Asp Ile Asp Gln Leu  
 260 265 270  
 His Asp Asp Leu Leu Asp Asp Ala Ala Leu Gln Ser Val Ile Asp Asp  
 275 280 285  
 Phe Trp Pro Glu Leu Arg Pro Gln Asp Val Leu His Asp Leu Leu Ile  
 290 295 300  
 Ser Glu Glu Arg Ile Asn Val Ala Ala Ala Gly Tyr Asp Glu Glu Thr  
 305 310 315 320  
 Lys Ser Ala Leu Leu Arg Gly Glu Leu Asp Pro Trp Ala Pro Ser Asp  
 325 330 335  
 Ala Ala Leu Leu Asp Glu Leu Ala Leu Leu Ile Gly Leu Pro Asp Pro  
 340 345 350  
 Glu Glu Ala Arg Glu Lys Ala Glu Ala Lys Trp Arg Glu Gln Ile Asp  
 355 360 365  
 Asp Ala Gln Glu Val Leu Asp Val Leu Ser Ser Ser Gln Ser Ser Asp  
 370 375 380  
 Ile Asp Asp Val Thr Glu Ala Glu Val Leu Ser Ala Phe Asp Val Ile  
 385 390 395 400  
 Asp Ala Glu Thr Leu Ala Gln Arg Gln Thr Val Thr Asp Asn Arg Thr  
 405 410 415  
 Thr Ala Glu Arg Ala Gln Ala Asp His Lys Trp Ala Tyr Gly His Val  
 420 425 430  
 Ile Val Asp Glu Ala Gln Glu Leu Ser Pro Met Glu Trp Arg Met Val  
 435 440 445  
 Phe Arg Arg Ser Pro Ser Arg Trp Met Thr Leu Val Gly Asp Ile Ala  
 450 455 460  
 Gln Thr Gly Trp Pro Ala Gly Val Asp Asp Trp Ala Glu Ser Leu Trp  
 465 470 475 480  
 Pro Phe Val Glu Lys Arg Phe Arg His His Glu Leu Thr Val Asn Tyr  
 485 490 495  
 Arg Thr Pro Ala Glu Ile Met Ser Val Ala Asn Glu Leu Leu Thr Gln

500	505	510	
Ile Asn Pro Asp Ile Ala Pro	Ala Met Ala Ile Arg Glu Ser Gly Arg		
515	520	525	
Glu Val Val Asn Leu Pro Leu Asp Ala Asp Leu Ser Ala Val Met Asp			
530	535	540	
Ser Leu Arg Glu Glu Asp Ser Gln Arg Thr Ile Ala Val Ile Ser Ser			
545	550	555	560
Arg Arg His His Glu Ser Asp Phe Tyr Leu Val Asp Asp Ile Lys Gly			
565	570	575	
Leu Glu Phe Asp His Val Ile Val Val Asp Pro Ala Gly Ile Val Glu			
580	585	590	
Glu Ser Pro Gln Gly Leu Gln Asp Leu Tyr Val Ala Val Thr Arg Ala			
595	600	605	
Thr Gln Ser Leu Thr Ile Leu Gly Glu			
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1 5 10 15			
cct gaa ctc ggc gag act ggc gtg gtg ttg tcc acc gtc ggt gag ctg	96		
Pro Glu Leu Gly Glu Thr Gly Val Val Leu Ser Thr Val Gly Glu Leu			
20 25 30			
ttc ccc ggt atc gtc cca acg ggt tcc gag gac act ttg acc agg gaa	144		
Phe Pro Gly Ile Val Pro Thr Gly Ser Glu Asp Thr Leu Thr Arg Glu			
35 40 45			
att aag ggc agc gag gaa atg gcc agc att ttg gcc gag gca gtc aag	192		
Ile Lys Gly Ser Glu Glu Met Ala Ser Ile Leu Ala Glu Ala Val Lys			
50 55 60			
gcg tat caa gtg ctg cca gag aag acc atc gtg gtc tct gtt gat ggc	240		
Ala Tyr Gln Val Leu Pro Glu Lys Thr Ile Val Val Ser Val Asp Gly			
65 70 75 80			
atc gag att tcc att gat gag aaa acg gtg gca aaa tcc cgc acc cga	288		
Ile Glu Ile Ser Ile Asp Glu Lys Thr Val Ala Lys Ser Arg Thr Arg			
85 90 95			
gct cgt cgt gcc agg cag tcg cac aat tcc gca cgc cca att ttc cgc	336		
Ala Arg Arg Ala Arg Gln Ser His Asn Ser Ala Arg Pro Ile Phe Arg			

100	105	110	
gag cat tta gtc gaa caa ctc gcg cac caa atg gct caa acg atc ggc Glu His Leu Val Glu Gln Leu Ala His Gln Met Ala Gln Thr Ile Gly 115 120 125			384
gcg gat ccg ctg ggc ggc aaa aac ctg ctg tca gcc gcc gac atc gat Ala Asp Pro Leu Gly Gly Lys Asn Leu Leu Ser Ala Ala Asp Ile Asp 130 135 140			432
cag ctg cac gat gat ttg ctt gac gac gcg gcc ctc cag tcc gtc atc Gln Leu His Asp Asp Leu Leu Asp Asp Ala Ala Leu Gln Ser Val Ile 145 150 155 160			480
gac gat ttc tgg ccg gag ctc cgg cct cag gac gtc ctg cat gat ctg Asp Asp Phe Trp Pro Glu Leu Arg Pro Gln Asp Val Leu His Asp Leu 165 170 175			528
ttg att tcc gaa gag cgc att aat gtt gct gcc gcg ggg tat gac gag Leu Ile Ser Glu Glu Arg Ile Asn Val Ala Ala Ala Gly Tyr Asp Glu 180 185 190			576
gaa act aag tct gct ttg ctg cgt ggt gaa ctc gat ccg tgg gca cca Glu Thr Lys Ser Ala Leu Leu Arg Gly Glu Leu Asp Pro Trp Ala Pro 195 200 205			624
tcg gac gct gca ttg ctt gat gag tta gcc ctg ctc atc ggt ctt ccc Ser Asp Ala Ala Leu Leu Asp Glu Leu Ala Leu Ile Gly Leu Pro 210 215 220			672
gat cca gag gag gca ccg gag aag gct gag gcc aaa tgg cgc gag cag Asp Pro Glu Glu Ala Arg Glu Lys Ala Glu Ala Lys Trp Arg Glu Gln 225 230 235 240			720
atc gat gac gct cag gaa gtc ctg gac gtt ctt agt tca tca cag tca Ile Asp Asp Ala Gln Glu Val Leu Asp Val Leu Ser Ser Ser Gln Ser 245 250 255			768
tcg gat att gat gat gtc acg gaa gct gaa gtt ctc tcc gct ttc gac Ser Asp Ile Asp Asp Val Thr Glu Ala Glu Val Leu Ser Ala Phe Asp 260 265 270			816
gtc atc gat gcg gaa act ttg gca caa cgc caa act gtc acg gat aat Val Ile Asp Ala Glu Thr Leu Ala Gln Arg Gln Thr Val Thr Asp Asn 275 280 285			864
cgc acc act gcg gaa cgt gca cag gcg gat cat aag tgg gca tat ggt Arg Thr Thr Ala Glu Arg Ala Gln Ala Asp His Lys Trp Ala Tyr Gly 290 295 300			912
cac gtg att gta gat gaa gct cag gag ctc agt ccg atg gaa tgg cgc His Val Ile Val Asp Glu Ala Gln Glu Leu Ser Pro Met Glu Trp Arg 305 310 315 320			960
atg gtg ttt cgc cgt agc cct tcg cga tgg atg acc ctt gtg ggc gat Met Val Phe Arg Arg Ser Pro Ser Arg Trp Met Thr Leu Val Gly Asp 325 330 335			1008
att gca caa act ggt tgg cct gcc ggc gtt gac gat tgg gca gaa tca Ile Ala Gln Thr Gly Trp Pro Ala Gly Val Asp Asp Trp Ala Glu Ser 340 345 350			1056

ctg tgg ccc ttc gtc gaa aag cgt ttc agg cac cac gag ctc acc gtt 1104  
 Leu Trp Pro Phe Val Glu Lys Arg Phe Arg His His Glu Leu Thr Val  
 355 360 365

aac tac cgc acc ccg gcc gag atc atg tcg gtg gcc aat gag ctt ttg 1152  
 Asn Tyr Arg Thr Pro Ala Glu Ile Met Ser Val Ala Asn Glu Leu Leu  
 370 375 380

acg cag atc aat cct gat att gcg ccg gca atg gcg atc cgc gaa tct 1200  
 Thr Gln Ile Asn Pro Asp Ile Ala Pro Ala Met Ala Ile Arg Glu Ser  
 385 390 395 400

ggt cga gag gta gtg aac ttg ccg ctt gat gcc gat ttg tcg gca gtg 1248  
 Gly Arg Glu Val Val Asn Leu Pro Leu Asp Ala Asp Leu Ser Ala Val  
 405 410 415

atg gat agt ttg cgt gag gag gat tca cag cgc acc atc gcg gtg att 1296  
 Met Asp Ser Leu Arg Glu Glu Asp Ser Gln Arg Thr Ile Ala Val Ile  
 420 425 430

tct tcg cgc cgc cac cac gaa agc gat ttc tac ctg gtc gat gac atc 1344  
 Ser Ser Arg Arg His His Glu Ser Asp Phe Tyr Leu Val Asp Asp Ile  
 435 440 445

aag gcc tta gag ttt gac cac gtc atc gtg gtg gat cct gcg gga atc 1392  
 Lys Gly Leu Glu Phe Asp His Val Ile Val Val Asp Pro Ala Gly Ile  
 450 455 460

gtt gaa gaa tcc ccc cag gga ttg caa gac ctc tac gtt gcg gtc act 1440  
 Val Glu Glu Ser Pro Gln Gly Leu Gln Asp Leu Tyr Val Ala Val Thr  
 465 470 475 480

cgt gca acg cag agc ctc acc att tta ggt gag tagcaggta tgagctcagg 1493  
 Arg Ala Thr Gln Ser Leu Thr Ile Leu Gly Glu  
 485 490

gcc 1496

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 <211> 491  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 66  
 Ile Ile Gly Pro Asn Lys Thr Phe Leu Glu Tyr Ile Ser His Val Leu  
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Pro Glu Leu Gly Glu Thr Gly Val Val Leu Ser Thr Val Gly Glu Leu  
 20 25 30

Phe Pro Gly Ile Val Pro Thr Gly Ser Glu Asp Thr Leu Thr Arg Glu  
 35 40 45

Ile Lys Gly Ser Glu Glu Met Ala Ser Ile Leu Ala Glu Ala Val Lys  
 50 55 60

Ala Tyr Gln Val Leu Pro Glu Lys Thr Ile Val Val Ser Val Asp Gly  
 65 70 75 80

Ile Glu Ile Ser Ile Asp Glu Lys Thr Val Ala Lys Ser Arg Thr Arg  
 85 90 95  
 Ala Arg Arg Ala Arg Gln Ser His Asn Ser Ala Arg Pro Ile Phe Arg  
 100 105 110  
 Glu His Leu Val Glu Gln Leu Ala His Gln Met Ala Gln Thr Ile Gly  
 115 120 125  
 Ala Asp Pro Leu Gly Gly Lys Asn Leu Leu Ser Ala Ala Asp Ile Asp  
 130 135 140  
 Gln Leu His Asp Asp Leu Leu Asp Asp Ala Ala Leu Gln Ser Val Ile  
 145 150 155 160  
 Asp Asp Phe Trp Pro Glu Leu Arg Pro Gln Asp Val Leu His Asp Leu  
 165 170 175  
 Leu Ile Ser Glu Glu Arg Ile Asn Val Ala Ala Ala Gly Tyr Asp Glu  
 180 185 190  
 Glu Thr Lys Ser Ala Leu Leu Arg Gly Glu Leu Asp Pro Trp Ala Pro  
 195 200 205  
 Ser Asp Ala Ala Leu Leu Asp Glu Leu Ala Leu Leu Ile Gly Leu Pro  
 210 215 220  
 Asp Pro Glu Glu Ala Arg Glu Lys Ala Glu Ala Lys Trp Arg Glu Gln  
 225 230 235 240  
 Ile Asp Asp Ala Gln Glu Val Leu Asp Val Leu Ser Ser Ser Gln Ser  
 245 250 255  
 Ser Asp Ile Asp Asp Val Thr Glu Ala Glu Val Leu Ser Ala Phe Asp  
 260 265 270  
 Val Ile Asp Ala Glu Thr Leu Ala Gln Arg Gln Thr Val Thr Asp Asn  
 275 280 285  
 Arg Thr Thr Ala Glu Arg Ala Gln Ala Asp His Lys Trp Ala Tyr Gly  
 290 295 300  
 His Val Ile Val Asp Glu Ala Gln Glu Leu Ser Pro Met Glu Trp Arg  
 305 310 315 320  
 Met Val Phe Arg Arg Ser Pro Ser Arg Trp Met Thr Leu Val Gly Asp  
 325 330 335  
 Ile Ala Gln Thr Gly Trp Pro Ala Gly Val Asp Asp Trp Ala Glu Ser  
 340 345 350  
 Leu Trp Pro Phe Val Glu Lys Arg Phe Arg His His Glu Leu Thr Val  
 355 360 365  
 Asn Tyr Arg Thr Pro Ala Glu Ile Met Ser Val Ala Asn Glu Leu Leu  
 370 375 380  
 Thr Gln Ile Asn Pro Asp Ile Ala Pro Ala Met Ala Ile Arg Glu Ser  
 385 390 395 400  
 Gly Arg Glu Val Val Asn Leu Pro Leu Asp Ala Asp Leu Ser Ala Val

	405		410		415
Met Asp Ser	Leu Arg Glu Glu Asp	Ser Gln Arg Thr Ile Ala Val Ile			
	420	425		430	
Ser Ser Arg Arg	His His Glu Ser Asp Phe Tyr	Leu Val Asp Asp Ile			
	435	440		445	
Lys Gly Leu Glu Phe Asp His Val Ile Val Val Asp Pro Ala Gly Ile					
	450	455		460	
Val Glu Glu Ser Pro Gln Gly Leu Gln Asp Leu Tyr Val Ala Val Thr					
	465	470		475	480
Arg Ala Thr Gln Ser Leu Thr Ile Leu Gly Glu					
	485	490			

&lt;210&gt; 67

&lt;211&gt; 1653

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1630)

&lt;223&gt; RXA00544

&lt;400&gt; 67

agttggaaat cacaagcct cggggtgggg gctttcgtgc cttctggaaa ggcctatgca 60

ggggctagag tgaacttaga atcagattgg ggaagaaaa	atg gct aca gat aca	115
	Met Ala Thr Asp Thr	
	1 5	

cac gcc gca agt ttt gat gat gac tac gta cct cca cag gag cca agc	163
His Ala Ala Ser Phe Asp Asp Asp Tyr Val Pro Pro Gln Glu Pro Ser	
10 15 20	

gat tcc ttc gcg gat gac gca cac gta gat gtc cct gct ccg gcg ttt	211
Asp Ser Phe Ala Asp Asp Ala His Val Asp Val Pro Ala Pro Ala Phe	
25 30 35	

gaa gat ttc tcc ccg gcc cag gcc ttt ggt cag gga act agg gga gga	259
Glu Asp Phe Ser Pro Ala Gln Ala Phe Gly Gln Gly Thr Arg Gly Gly	
40 45 50	

gac tct cag ggc ttc aag aag agg ggt cgc aag gac gag tcc cgt gaa	307
Asp Ser Gln Gly Phe Lys Lys Arg Gly Arg Lys Asp Glu Ser Arg Glu	
55 60 65	

tac cga gac ttc cgc caa cct ccc tat gac aat gac gct gag atg ggc	355
Tyr Arg Asp Phe Arg Gln Pro Pro Tyr Asp Asn Asp Ala Glu Met Gly	
70 75 80 85	

gtg ctg ggc gcg atg ctg ctc agt ccg acc acg gtc atc gac att ctg	403
Val Leu Gly Ala Met Leu Leu Ser Pro Thr Val Ile Asp Ile Leu	
90 95 100	

gat atc ctc acc cca gaa gac ttc tac agg ccg tcc cac cag ctg att	451
Asp Ile Leu Thr Pro Glu Asp Phe Tyr Arg Pro Ser His Gln Leu Ile	

105						110						115						
ttc	cag	gcg	atc	att	gac	ctg	ttc	agt	gac	aac	cgt	gat	att	gac	ccc	499		
Phe	Gln	Ala	Ile	Ile	Asp	Leu	Phe	Ser	Asp	Asn	Arg	Ile	Asp	Pro				
120						125						130						
gtg	att	gtc	tcc	ggt	cgc	ctc	gat	cga	acc	aac	gat	ctg	gac	cgc	gtc	547		
Val	Ile	Val	Ser	Gly	Arg	Leu	Asp	Arg	Thr	Asn	Asp	Leu	Asp	Arg	Val			
135						140						145						
ggc	ggt	ggc	gcg	tac	ctc	cac	gac	ctc	atc	cag	tcc	gtt	ccc	acc	gca	595		
Gly	Gly	Gly	Ala	Tyr	Leu	His	Asp	Leu	Ile	Gln	Ser	Val	Pro	Thr	Ala			
150						155						160						165
gcc	aac	gcg	cgc	tac	tat	gcg	gaa	atc	gtt	tcc	gaa	aag	gca	gtg	ctt	643		
Ala	Asn	Ala	Arg	Tyr	Tyr	Ala	Glu	Ile	Val	Ser	Glu	Lys	Ala	Val	Leu			
170						175						180						
cgc	agg	ctt	gtc	gac	gcc	ggc	acc	cgc	gtc	gtc	cag	ctc	ggc	tac	gag	691		
Arg	Arg	Leu	Val	Asp	Ala	Gly	Thr	Arg	Val	Val	Gln	Leu	Gly	Tyr	Glu			
185						190						195						
ggc	gat	gaa	ggc	gcc	gaa	att	gac	gcg	gtg	att	gac	cgc	gcg	cag	caa	739		
Gly	Asp	Glu	Gly	Ala	Glu	Ile	Asp	Ala	Val	Ile	Asp	Arg	Ala	Gln	Gln			
200						205						210						
gaa	gtc	ttc	gcc	gtt	tcc	caa	aag	aat	cag	agc	gaa	gac	tat	gca	gtc	787		
Glu	Val	Phe	Ala	Val	Ser	Gln	Lys	Asn	Gln	Ser	Glu	Asp	Tyr	Ala	Val			
215						220						225						
cta	gcc	gat	att	ctg	gat	gaa	acc	atg	gct	gag	ctg	gaa	atg	ctc	aac	835		
Leu	Ala	Asp	Ile	Leu	Asp	Glu	Thr	Met	Ala	Glu	Leu	Glu	Met	Leu	Asn			
230						235						240						245
gac	ggc	ggc	atc	gcc	acc	ggt	att	cca	acc	ggc	ttc	aaa	gat	ctc	gat	883		
Asp	Gly	Gly	Ile	Ala	Thr	Gly	Ile	Pro	Thr	Gly	Phe	Lys	Asp	Leu	Asp			
250						255						260						
gac	ctc	acc	aac	ggt	ctg	cgc	ggt	ggc	cag	atg	atc	atc	gtt	gca	gct	931		
Asp	Leu	Thr	Asn	Gly	Leu	Arg	Gly	Gly	Gln	Met	Ile	Ile	Val	Ala	Ala			
265						270						275						
cgt	cct	ggt	gtg	ggt	aaa	tcc	acc	atc	gcc	ttg	gac	ttc	atg	cgt	tcg	979		
Arg	Pro	Gly	Val	Gly	Lys	Ser	Thr	Ile	Ala	Leu	Asp	Phe	Met	Arg	Ser			
280						285						290						
gca	tcc	atc	aag	aac	aac	atg	gcg	tct	gtc	att	ttc	ttc	ttg	gaa	atg	1027		
Ala	Ser	Ile	Lys	Asn	Asn	Met	Ala	Ser	Val	Ile	Phe	Ser	Leu	Glu	Met			
295						300						305						
tcc	aag	tca	gag	atc	gtg	atg	cgt	ttg	ctc	tct	gca	gaa	aca	gaa	atc	1075		
Ser	Lys	Ser	Glu	Ile	Val	Met	Arg	Leu	Leu	Ser	Ala	Glu	Thr	Glu	Ile			
310						315						320						325
cgc	ctg	gct	gat	atg	cgt	ggt	gga	aag	atg	gat	gaa	acc	gca	tgg	gaa	1123		
Arg	Leu	Ala	Asp	Met	Arg	Gly	Gly	Lys	Met	Asp	Glu	Thr	Ala	Trp	Glu			
330						335						340						
aag	atg	gtg	cag	aag	tta	gac	aag	gta	gcc	cag	gca	cct	ttg	ttc	atc	1171		
Lys	Met	Val	Gln	Lys	Leu	Asp	Lys	Val	Ala	Gln	Ala	Pro	Leu	Phe	Ile			
345						350						355						



gat gac tcc gcg aac ctc acc atg atg gaa atc cgc tcc aag gcc aga 1219  
Asp Asp Ser Ala Asn Leu Thr Met Met Glu Ile Arg Ser Lys Ala Arg  
360 365 370  
aag ctg aag cag aag cat gat ctg aaa atg atc gtg gtg gac tac ctc 1267  
Lys Leu Lys Gln Lys His Asp Leu Lys Met Ile Val Val Asp Tyr Leu  
375 380 385  
cag ctg atg agc tcc ggt aaa cgc gtg gaa tcc cgt cag cag gaa gtc 1315  
Gln Leu Met Ser Ser Gly Lys Arg Val Glu Ser Arg Gln Gln Glu Val  
390 395 400 405  
tcc gag ttc tcc cgt cag ctc aag ctg ctg gcc aaa gaa ctc gat gtg 1363  
Ser Glu Phe Ser Arg Gln Leu Lys Leu Ala Lys Glu Leu Asp Val  
410 415 420  
ccg ttg atc gcg att tcc cag ctg aac cgt gga cct gaa tcc cgt acc 1411  
Pro Leu Ile Ala Ile Ser Gln Leu Asn Arg Gly Pro Glu Ser Arg Thr  
425 430 435  
gat aag cga cca cag ctt gct gac ctt cgt gaa tcc gcc tgc ctg gag 1459  
Asp Lys Arg Pro Gln Leu Ala Asp Leu Arg Glu Ser Gly Ser Leu Glu  
440 445 450  
cag gac gcc gat atc gtt atg ctg cta tac cgc cca gac tcc cag gat 1507  
Gln Asp Ala Asp Ile Val Met Leu Leu Tyr Arg Pro Asp Ser Gln Asp  
455 460 465  
aag gac gac gag cgc gcg gcc gag gcc gac atc att ttg gct aag cac 1555  
Lys Asp Asp Glu Arg Ala Gly Glu Ala Asp Ile Ile Leu Ala Lys His  
470 475 480 485  
cgt ggt gcc cgc atc gat acc gtc cag gtg gcg cac cag ctg cac tat 1603  
Arg Gly Gly Pro Ile Asp Thr Val Gln Val Ala His Gln Leu His Tyr  
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505 510  
aaa 1653  
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<211> 510  
<212> PRT  
<213> Corynebacterium glutamicum  
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20 25 30  
Pro Ala Pro Ala Phe Glu Asp Phe Ser Pro Ala Gln Ala Phe Gly Gln  
35 40 45  
Gly Thr Arg Gly Gly Asp Ser Gln Gly Phe Lys Lys Arg Gly Arg Lys  
50 55 60

Asp Glu Ser Arg Glu Tyr Arg Asp Phe Arg Gln Pro Pro Tyr Asp Asn  
 65 70 75 80  
 Asp Ala Glu Met Gly Val Leu Gly Ala Met Leu Leu Ser Pro Thr Thr  
 85 90  
 Val Ile Asp Ile Leu Asp Ile Leu Thr Pro Glu Asp Phe Tyr Arg Pro  
 100 105 110  
 Ser His Gln Leu Ile Phe Gln Ala Ile Ile Asp Leu Phe Ser Asp Asn  
 115 120 125  
 Arg Asp Ile Asp Pro Val Ile Val Ser Gly Arg Leu Asp Arg Thr Asn  
 130 135 140  
 Asp Leu Asp Arg Val Gly Gly Ala Tyr Leu His Asp Leu Ile Gln  
 145 150 155 160  
 Ser Val Pro Thr Ala Ala Asn Ala Arg Tyr Tyr Ala Glu Ile Val Ser  
 165 170 175  
 Glu Lys Ala Val Leu Arg Arg Leu Val Asp Ala Gly Thr Arg Val Val  
 180 185 190  
 Gln Leu Gly Tyr Glu Gly Asp Glu Gly Ala Glu Ile Asp Ala Val Ile  
 195 200 205  
 Asp Arg Ala Gln Gln Glu Val Phe Ala Val Ser Gln Lys Asn Gln Ser  
 210 215 220  
 Glu Asp Tyr Ala Val Leu Ala Asp Ile Leu Asp Glu Thr Met Ala Glu  
 225 230 235 240  
 Leu Glu Met Leu Asn Asp Gly Gly Ile Ala Thr Gly Ile Pro Thr Gly  
 245 250 255  
 Phe Lys Asp Leu Asp Asp Leu Thr Asn Gly Leu Arg Gly Gly Gln Met  
 260 265 270  
 Ile Ile Val Ala Ala Arg Pro Gly Val Gly Lys Ser Thr Ile Ala Leu  
 275 280 285  
 Asp Phe Met Arg Ser Ala Ser Ile Lys Asn Asn Met Ala Ser Val Ile  
 290 295 300  
 Phe Ser Leu Glu Met Ser Lys Ser Glu Ile Val Met Arg Leu Leu Ser  
 305 310 315 320  
 Ala Glu Thr Glu Ile Arg Leu Ala Asp Met Arg Gly Gly Lys Met Asp  
 325 330 335  
 Glu Thr Ala Trp Glu Lys Met Val Gln Lys Leu Asp Lys Val Ala Gln  
 340 345 350  
 Ala Pro Leu Phe Ile Asp Asp Ser Ala Asn Leu Thr Met Met Glu Ile  
 355 360 365  
 Arg Ser Lys Ala Arg Lys Leu Lys Gln Lys His Asp Leu Lys Met Ile  
 370 375 380

Val Val Asp Tyr Leu Gln Leu Met Ser Ser Gly Lys Arg Val Glu Ser  
385 390 395 400

Arg Gln Gln Glu Val Ser Glu Phe Ser Arg Gln Leu Lys Leu Ala  
405 410 415

Lys Glu Leu Asp Val Pro Leu Ile Ala Ile Ser Gln Leu Asn Arg Gly  
420 425 430

Pro Glu Ser Arg Thr Asp Lys Arg Pro Gln Leu Ala Asp Leu Arg Glu  
435 440 445

Ser Gly Ser Leu Glu Gln Asp Ala Asp Ile Val Met Leu Leu Tyr Arg  
450 455 460

Pro Asp Ser Gln Asp Lys Asp Asp Glu Arg Ala Gly Glu Ala Asp Ile  
465 470 475 480

Ile Leu Ala Lys His Arg Gly Gly Pro Ile Asp Thr Val Gln Val Ala  
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His Gln Leu His Tyr Ser Arg Phe Val Asp Met Ala Arg Gly  
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<213> *Corynebacterium glutamicum*

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<223> RXA01866

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tggattaag ccagcctgat tcttcgatct cagctaccac ttg aaa ccc ggc cac 115  
Leu Lys Pro Gly His  
1 5

cgc gat gac ggc gtc aca gtc ctc atc ccc att cca gtg ctg ggt gga 163  
Arg Asp Asp Gly Val Thr Val Leu Ile Pro Ile Pro Val Leu Gly Gly  
10 15 20

ctt gat acc gaa ggc ttc gat tgg cta gtt cca ggc tta agg ctt gat 211  
Leu Asp Thr Glu Gly Phe Asp Trp Leu Val Pro Gly Leu Arg Leu Asp  
25 30 35

ttg gtg acc gag tta atc cgc acc atg cct aag gct tta cga cgc acc 259  
Leu Val Thr Glu Leu Ile Arg Thr Met Pro Lys Ala Leu Arg Arg Thr  
40 45 50

gtt gtc cct gcc ccg gat ttc gcc gag cgg gtc ttg ccg tta ctg cgt 307  
Val Val Pro Ala Pro Asp Phe Ala Glu Arg Val Leu Pro Leu Leu Arg  
55 60 65

ccc tac atg aca cca ctg acc acc caa ctt gcc gat gca ctc cat acc 355  
Pro Tyr Met Thr Pro Leu Thr Thr Gln Leu Ala Asp Ala Leu His Thr  
70 75 80 85

ctg ggc ggc caa gga atc aac gcc tct gat ttc gat cct gcc aaa ctg 403  
 Leu Gly Gly Gln Gly Ile Asn Ala Ser Asp Phe Asp Pro Ala Lys Leu  
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                   20                  25                  30

Gly Leu Arg Leu Asp Leu Val Thr Glu Leu Ile Arg Thr Met Pro Lys  
                   35                  40                  45

Ala Leu Arg Arg Thr Val Val Pro Ala Pro Asp Phe Ala Glu Arg Val  
           50                  55                  60

Leu Pro Leu Leu Arg Pro Tyr Met Thr Pro Leu Thr Thr Gln Leu Ala  
           65                  70                  75                  80

Asp Ala Leu His Thr Leu Gly Gly Gln Gly Ile Asn Ala Ser Asp Phe  
                   85                  90                  95

Asp Pro Ala Lys Leu Pro Asp His Leu Arg Ile  
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<213> *Corynebacterium glutamicum*

<220>

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<222> (1)..(492)

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 Ser Glu Pro Tyr Trp Ser Ser Lys Arg Gly Ala Ala Met Val His Arg  
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aaa tca acg ctc ttc ggt gtg aca att gtt gcc gtc aag gta gtt ccc 144  
 Lys Ser Thr Leu Phe Gly Val Thr Ile Val Ala Val Lys Val Val Pro  
           35                  40                  45

tac cac acg gtt gat ccc gtg gct gcg cgc gat atg ttc atc cgc cat 192  
 Tyr His Thr Val Asp Pro Val Ala Ala Arg Asp Met Phe Ile Arg His  
 50 55 60

gcc ctc atc gaa ggc gat tgg tcc act cac cac cgc ttc tac cac gac 240  
 Ala Leu Ile Glu Gly Asp Trp Ser Thr His His Arg Phe Tyr His Asp  
 65 70 75 80

aac gtg gcc aaa ttg gag gca atc gga gaa ctt gaa gcc aag gcg cgt 288  
 Asn Val Ala Lys Leu Glu Ala Ile Gly Glu Leu Glu Ala Lys Ala Arg  
 85 90 95

cgc cgc gac atc gtc gta gat gaa gac acc ctg ttt gat ttc tac gat 336  
 Arg Arg Asp Ile Val Val Asp Glu Asp Thr Leu Phe Asp Phe Tyr Asp  
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gcc aag ctt cca agc aac gcc acc acc acc cgc aat ttc gat tcc tgg 384  
 Ala Lys Leu Pro Ser Asn Ala Thr Thr Arg Asn Phe Asp Ser Trp  
 115 120 125

tgg aag aaa aca tca cgc gtc aca cca gat ctt ctc gat ttc gac cca 432  
 Trp Lys Lys Thr Ser Arg Val Thr Pro Asp Leu Leu Asp Phe Asp Pro  
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 Asp Ser Leu Ile Lys Glu Asp Ala Gly Ala Leu Arg Arg Ser Leu Ser  
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 Arg Gln Val Asp

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 35 40 45

Tyr His Thr Val Asp Pro Val Ala Ala Arg Asp Met Phe Ile Arg His  
 50 55 60

Ala Leu Ile Glu Gly Asp Trp Ser Thr His His Arg Phe Tyr His Asp  
 65 70 75 80

Asn Val Ala Lys Leu Glu Ala Ile Gly Glu Leu Glu Ala Lys Ala Arg  
 85 90 95

Arg Arg Asp Ile Val Val Asp Glu Asp Thr Leu Phe Asp Phe Tyr Asp  
 100 105 110

Ala Lys Leu Pro Ser Asn Ala Thr Thr Thr Arg Asn Phe Asp Ser Trp

115 120 125

Trp Lys Lys Thr Ser Arg Val Thr Pro Asp Leu Leu Asp Phe Asp Pro  
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Met Thr Thr Ser Glu  
1 5

act gcc cca tca aag gct tcc ctg tat gaa ctt tta gag ggc gta tcc 163  
Thr Ala Pro Ser Lys Ala Ser Leu Tyr Glu Leu Leu Glu Gly Val Ser  
10 15 20

ctc tcc gac gag cgc acg ttt agg cgc cga ctg tcc aaa gcc cgc gcg 211  
Leu Ser Asp Glu Arg Thr Phe Arg Arg Arg Leu Ser Lys Ala Arg Ala  
25 30 35

ccc aag gcg ctt ggt gcg att aag gct gat atc gat aag gca cgc ttg 259  
Pro Lys Ala Leu Gly Ala Ile Lys Ala Asp Ile Asp Lys Ala Arg Leu  
40 45 50

ctt atc gac gaa aag agc cag tta att ccg tct atc acc tac cca gaa 307  
Leu Ile Asp Glu Lys Ser Gln Leu Ile Pro Ser Ile Thr Tyr Pro Glu  
55 60 65

aac ctt ccg gtg agt tcc cgg cgc gat gat atc gcc gag gct atc cgt 355  
Asn Leu Pro Val Ser Ser Arg Arg Asp Asp Ile Ala Glu Ala Ile Arg  
70 75 80 85

gat aat cag gtg gtt att atc gcc ggt gag act ggt tgg ggt aag acg 403  
Asp Asn Gln Val Val Ile Ile Ala Gly Glu Thr Gly Ser Gly Lys Thr  
90 95 100

act cag att cct aag att tgt ttg gac cta ggc cgt ggc cgg cgt ggg 451  
Thr Gln Ile Pro Lys Ile Cys Leu Asp Leu Gly Arg Gly Arg Arg Gly  
105 110 115

ctc att ggc cac aca cag cca cgt cga tta gca gct agg acc gtc gcc 499  
Leu Ile Gly His Thr Gln Pro Arg Arg Leu Ala Ala Arg Thr Val Ala  
120 125 130

gag cgc atc gcc gat gaa ttg ggg caa gac atc ggc gaa tcg gtg ggt 547  
 Glu Arg Ile Ala Asp Glu Leu Gly Gln Asp Ile Gly Glu Ser Val Gly  
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tat gcg att cgt ttt gat gat cga gtt tcc tcg cat aca tcc gtg aag 595  
 Tyr Ala Ile Arg Phe Asp Asp Arg Val Ser Ser His Thr Ser Val Lys  
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 Leu Met Thr Asp Gly Ile Leu Leu Ala Glu Met Gln Arg Asp Arg Phe  
 170 175 180

ctc aat gcg tat gac acc atc atc atc gat gag gcg cat gaa cgt tcc 691  
 Leu Asn Ala Tyr Asp Thr Ile Ile Ile Asp Glu Ala His Glu Arg Ser  
 185 190 195

ctc aac att gac ttc att ctg ggt tat ttg cgc cag ttg ttc cct aag 739  
 Leu Asn Ile Asp Phe Ile Leu Gly Tyr Leu Arg Gln Leu Leu Pro Lys  
 200 205 210

cgc cct gat ctt aaa gtc att att acc tcc gca acg att gac cct gag 787  
 Arg Pro Asp Leu Lys Val Ile Ile Thr Ser Ala Thr Ile Asp Pro Glu  
 215 220 225

cgt ttc gcg gag cac ttt gct gat gct tct gga aaa cca gca cca att 835  
 Arg Phe Ala Glu His Phe Ala Asp Ala Ser Gly Lys Pro Ala Pro Ile  
 230 235 240 245

atc gag gtc tcc ggc cgc acc ttc ccg gta gag atc cgt tat cgc cca 883  
 Ile Glu Val Ser Gly Arg Thr Phe Pro Val Glu Ile Arg Tyr Arg Pro  
 250 255 260

ctt gag gta tta gac ggc gat aaa att atc gat acc gat ccc ctt gac 931  
 Leu Glu Val Leu Asp Gly Asp Lys Ile Ile Asp Thr Asp Pro Leu Asp  
 265 270 275

ggc ttg tgt tct gct ttg gaa gag ctc atg gct gaa ggc gac ggc gat 979  
 Gly Leu Cys Ser Ala Leu Glu Glu Leu Met Ala Glu Gly Asp Gly Asp  
 280 285 290

atc ctc tgc ttc ttt gcc ggt gag cgt gat atc cgc gat gcc atg gag 1027  
 Ile Leu Cys Phe Phe Ala Gly Glu Arg Asp Ile Arg Asp Ala Met Glu  
 295 300 305

gca atc gag gcc cga cgc tgg aaa ggt gtg gaa gtc act ccc ctg ttt 1075  
 Ala Ile Glu Ala Arg Arg Trp Lys Gly Val Glu Val Thr Pro Leu Phe  
 310 315 320 325

ggc cgc ctg tcc aac cag gag cag cac cgt gta ttt agc ccg cac tct 1123  
 Gly Arg Leu Ser Asn Gln Glu Gln His Arg Val Phe Ser Pro His Ser  
 330 335 340

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 Gly Arg Arg Ile Val Leu Ser Thr Asn Ile Ala Glu Thr Ser Leu Thr  
 345 350 355

gtt ccg ggc att cac tac gtg gtt gat acc ggt acg gcg cgt atc tct 1219  
 Val Pro Gly Ile His Tyr Val Val Asp Thr Gly Thr Ala Arg Ile Ser  
 360 365 370

cgt tat tca gtg cgc acc aag gtg cag cgc ctt ccg att gag aac att 1267

Arg Tyr Ser Val Arg Thr Lys Val Gln Arg Leu Pro Ile Glu Asn Ile	
375 380 385	
tcc cag gcc agc gca aac cag cgt tct ggt cgt tgt ggt cgt gtc gca	1315
Ser Gln Ala Ser Ala Asn Gln Arg Ser Gly Arg Cys Gly Arg Val Ala	
390 395 400 405	
gac ggt att gcg att cgt ttg tat tcc gaa gat gat ttc aac tct cgc	1363
Asp Gly Ile Ala Ile Arg Leu Tyr Ser Glu Asp Asp Phe Asn Ser Arg	
410 415 420	
cca gag ttc acc gat ccg gaa att ctg cgc acc aac ttg gcg agc gtt	1411
Pro Glu Phe Thr Asp Pro Glu Ile Leu Arg Thr Asn Leu Ala Ser Val	
425 430 435	
att ttg cgc atg gcg tcg ctg cgt ctt ggc gat att aat gat ttc ccc	1459
Ile Leu Arg Met Ala Ser Leu Arg Leu Gly Asp Ile Asn Asp Phe Pro	
440 445 450	
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Phe Val Gln Ala Pro Glu Gln Arg Ser Ile Arg Asp Gly Ile Leu Leu	
455 460 465	
ctc cac gag ttg ggc gca ctc acc gac gac acc caa gcc gat ggt tca	1555
Leu His Glu Leu Gly Ala Leu Thr Asp Asp Thr Gln Ala Asp Gly Ser	
470 475 480 485	
ccg cag ctc acc cag atc ggt aaa gac tta gcc aac atc cca gtc gat	1603
Pro Gln Leu Thr Gln Ile Gly Lys Asp Leu Ala Asn Ile Pro Val Asp	
490 495 500	
ccc cgc atg gcc cgc atg ctc gta gaa gcc aac act cta ggc tgc ctg	1651
Pro Arg Met Ala Arg Met Leu Val Glu Ala Asn Thr Leu Gly Cys Leu	
505 510 515	
cat tct gtc atg gtc att gtg tcc gct ctg acg att caa gat gtt cgc	1699
His Ser Val Met Val Ile Val Ser Ala Leu Thr Ile Gln Asp Val Arg	
520 525 530	
gaa cgc ccc ctg gaa ttc caa gcc caa gct gat caa gcc cac gct agg	1747
Glu Arg Pro Leu Glu Phe Gln Ala Gln Ala Asp Gln Ala His Ala Arg	
535 540 545	
ttc aag gac acc acc tca gat ttc tta ggc ttt ttg aaa ctg tgg gag	1795
Phe Lys Asp Thr Thr Ser Asp Phe Leu Gly Phe Leu Lys Leu Trp Glu	
550 555 560 565	
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Tyr Ile Ala Asp Gln Arg Asn Gln Ser Ser Gly Asn Ser Phe Arg Lys	
570 575 580	
cag atg aaa aaa gaa ttc ctc cac tac atg cgt atc cgc gag tgg tgg	1891
Gln Met Lys Lys Glu Phe Leu His Tyr Met Arg Ile Arg Glu Trp Trp	
585 590 595	
gat ttg gtg cgc caa tta gag cag att ggc cag caa ctt ggt tgg gca	1939
Asp Leu Val Arg Gln Leu Glu Gln Ile Gly Gln Gln Leu Gly Trp Ala	
600 605 610	
aag aag gag cag gtt gca ggc acc gcc agc cct gac atc att cac caa	1987
Lys Lys Glu Gln Val Ala Gly Thr Ala Ser Pro Asp Ile Ile His Gln	



615	620	625	
tcc ttg ctc acc ggt ctg ttc tgc caa atc ggt tcc cgt gat ggt gag			2035
Ser Leu Leu Thr Gly Leu Phe Ser Gln Ile Gly Ser Arg Asp Gly Glu			
630	635	640	645
agc aaa gaa ttc act gga gcc aga ggt acc aaa ttc ttg gtc ttt cct			2083
Ser Lys Glu Phe Thr Gly Ala Arg Gly Thr Lys Phe Leu Val Phe Pro			
650	655		660
ggg tct gcg cta acc aag aag ccg cca cag ttc atc atg gct ggc caa			2131
Gly Ser Ala Leu Thr Lys Lys Pro Pro Gln Phe Ile Met Ala Gly Gln			
665	670		675
ttg gta gaa acc tca cgt ttg tgg gct cgc gat gta gcc aag att gaa			2179
Leu Val Glu Thr Ser Arg Leu Trp Ala Arg Asp Val Ala Lys Ile Glu			
680	685		690
cca gag tgg gtg gaa aaa gca gcc ggc cca ttg ctc aag cac caa tac			2227
Pro Glu Trp Val Glu Lys Ala Ala Gly Pro Leu Leu Lys His Gln Tyr			
695	700		705
tct gaa ccg tat tgg tcc tca aag cgt ggc ggc tgc cat ggt gca ccg			2275
Ser Glu Pro Tyr Trp Ser Ser Lys Arg Gly Gly Cys His Gly Ala Pro			
710	715		720
caa atc aac gct ctt cgg tgt gac aat tgt tgc cgt caa ggt agt tcc			2323
Gln Ile Asn Ala Leu Arg Cys Asp Asn Cys Cys Arg Gln Gly Ser Ser			
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Leu Pro His Gly			
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Ser Lys Ala Arg Ala Pro Lys Ala Leu Gly Ala Ile Lys Ala Asp Ile			
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Asp Lys Ala Arg Leu Leu Ile Asp Glu Lys Ser Gln Leu Ile Pro Ser			
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Ile Thr Tyr Pro Glu Asn Leu Pro Val Ser Ser Arg Arg Asp Asp Ile			
65	70	75	80
Ala Glu Ala Ile Arg Asp Asn Gln Val Val Ile Ile Ala Gly Glu Thr			
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Gly Ser Gly Lys Thr Thr Gln Ile Pro Lys Ile Cys Leu Asp Leu Gly			
100	105		110

Arg Gly Arg Arg Gly Leu Ile Gly His Thr Gln Pro Arg Arg Leu Ala  
 115 120 125  
 Ala Arg Thr Val Ala Glu Arg Ile Ala Asp Glu Leu Gly Gln Asp Ile  
 130 135 140  
 Gly Glu Ser Val Gly Tyr Ala Ile Arg Phe Asp Arg Val Ser Ser  
 145 150 155 160  
 His Thr Ser Val Lys Leu Met Thr Asp Gly Ile Leu Leu Ala Glu Met  
 165 170 175  
 Gln Arg Asp Arg Phe Leu Asn Ala Tyr Asp Thr Ile Ile Ile Asp Glu  
 180 185 190  
 Ala His Glu Arg Ser Leu Asn Ile Asp Phe Ile Leu Gly Tyr Leu Arg  
 195 200 205  
 Gln Leu Leu Pro Lys Arg Pro Asp Leu Lys Val Ile Ile Thr Ser Ala  
 210 215 220  
 Thr Ile Asp Pro Glu Arg Phe Ala Glu His Phe Ala Asp Ala Ser Gly  
 225 230 235 240  
 Lys Pro Ala Pro Ile Ile Glu Val Ser Gly Arg Thr Phe Pro Val Glu  
 245 250 255  
 Ile Arg Tyr Arg Pro Leu Glu Val Leu Asp Gly Asp Lys Ile Ile Asp  
 260 265 270  
 Thr Asp Pro Leu Asp Gly Leu Cys Ser Ala Leu Glu Glu Leu Met Ala  
 275 280 285  
 Glu Gly Asp Gly Asp Ile Leu Cys Phe Phe Ala Gly Glu Arg Asp Ile  
 290 295 300  
 Arg Asp Ala Met Glu Ala Ile Glu Ala Arg Arg Trp Lys Gly Val Glu  
 305 310 315 320  
 Val Thr Pro Leu Phe Gly Arg Leu Ser Asn Gln Glu Gln His Arg Val  
 325 330 335  
 Phe Ser Pro His Ser Gly Arg Arg Ile Val Leu Ser Thr Asn Ile Ala  
 340 345 350  
 Glu Thr Ser Leu Thr Val Pro Gly Ile His Tyr Val Val Asp Thr Gly  
 355 360 365  
 Thr Ala Arg Ile Ser Arg Tyr Ser Val Arg Thr Lys Val Gln Arg Leu  
 370 375 380  
 Pro Ile Glu Asn Ile Ser Gln Ala Ser Ala Asn Gln Arg Ser Gly Arg  
 385 390 395 400  
 Cys Gly Arg Val Ala Asp Gly Ile Ala Ile Arg Leu Tyr Ser Glu Asp  
 405 410 415  
 Asp Phe Asn Ser Arg Pro Glu Phe Thr Asp Pro Glu Ile Leu Arg Thr  
 420 425 430

Asn Leu Ala Ser Val Ile Leu Arg Met Ala Ser Leu Arg Leu Gly Asp  
 435 440 445  
 Ile Asn Asp Phe Pro Phe Val Gln Ala Pro Glu Gln Arg Ser Ile Arg  
 450 455 460  
 Asp Gly Ile Leu Leu Leu His Glu Leu Gly Ala Leu Thr Asp Asp Thr  
 465 470 475 480  
 Gln Ala Asp Gly Ser Pro Gln Leu Thr Gln Ile Gly Lys Asp Leu Ala  
 485 490 495  
 Asn Ile Pro Val Asp Pro Arg Met Ala Arg Met Leu Val Glu Ala Asn  
 500 505 510  
 Thr Leu Gly Cys Leu His Ser Val Met Val Ile Val Ser Ala Leu Thr  
 515 520 525  
 Ile Gln Asp Val Arg Glu Arg Pro Leu Glu Phe Gln Ala Gln Ala Asp  
 530 535 540  
 Gln Ala His Ala Arg Phe Lys Asp Thr Thr Ser Asp Phe Leu Gly Phe  
 545 550 555 560  
 Leu Lys Leu Trp Glu Tyr Ile Ala Asp Gln Arg Asn Gln Ser Ser Gly  
 565 570 575  
 Asn Ser Phe Arg Lys Gln Met Lys Lys Glu Phe Leu His Tyr Met Arg  
 580 585 590  
 Ile Arg Glu Trp Trp Asp Leu Val Arg Gln Leu Glu Gln Ile Gly Gln  
 595 600 605  
 Gln Leu Gly Trp Ala Lys Lys Glu Gln Val Ala Gly Thr Ala Ser Pro  
 610 615 620  
 Asp Ile Ile His Gln Ser Leu Leu Thr Gly Leu Phe Ser Gln Ile Gly  
 625 630 635 640  
 Ser Arg Asp Gly Glu Ser Lys Glu Phe Thr Gly Ala Arg Gly Thr Lys  
 645 650 655  
 Phe Leu Val Phe Pro Gly Ser Ala Leu Thr Lys Lys Pro Pro Gln Phe  
 660 665 670  
 Ile Met Ala Gly Gln Leu Val Glu Thr Ser Arg Leu Trp Ala Arg Asp  
 675 680 685  
 Val Ala Lys Ile Glu Pro Glu Trp Val Glu Lys Ala Ala Gly Pro Leu  
 690 695 700  
 Leu Lys His Gln Tyr Ser Glu Pro Tyr Trp Ser Ser Lys Arg Gly Gly  
 705 710 715 720  
 Cys His Gly Ala Pro Gln Ile Asn Ala Leu Arg Cys Asp Asn Cys Cys  
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 Arg Gln Gly Ser Ser Leu Pro His Gly  
 740 745

gat ggt att ttg ctt gct gaa atg cag cgg gat cgt ttc ctc aat gcg 643  
Asp Gly Ile Leu Leu Ala Glu Met Gln Arg Asp Arg Phe Leu Asn Ala  
170 175 180

tat gac acc atc atc atc gat gag gcg cat gaa cgt tcc etc aac att 691  
 Tyr Asp Thr Ile Ile Ile Asp Glu Ala His Glu Arg Ser Leu Asn Ile 200  
 185 190 195

gac ttc att ctg ggt tat ttg cgc cag ttg ttg cct aag cgc cct gat 739  
 Asp Phe Ile Leu Gly Tyr Leu Arg Gln Leu Leu Pro Lys Arg Pro Asp 215  
 205 210

ctt aaa gtc att att acc tcc gca acg att gac cct gag cgt ttc gcg 787  
 Leu Lys Val Ile Ile Thr Ser Ala Thr Ile Asp Pro Glu Arg Phe Ala 230  
 220 225

gag cac ttt gct gat gct tct gga aaa cca gca cca att atc gag gtc 835  
 Glu His Phe Ala Asp Ala Ser Gly Lys Pro Ala Pro Ile Ile Glu Val 245  
 235 240

tcc ggc cgc acc ttc ccg gta gag atc cgt tat cgc cca ctt gag gta 883  
 Ser Gly Arg Thr Phe Pro Val Glu Ile Arg Tyr Arg Pro Leu Glu Val 260  
 250 255

tta gac ggc gat aaa att atc gat acc gat ccc ctt gac ggc ttg tgt 931  
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 265 270 275

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 Phe Phe Ala Glu Gly Glu Arg Asp Ile Arg Asp Ala Met Glu Ala Ile Glu 310  
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gcc cga cgc tgg aaa ggt gtg gaa gtc act ccc ctg ttt ggc cgc ctg 1075  
 Ala Arg Arg Trp Lys Gly Val Glu Val Thr Pro Leu Phe Gly Arg Leu 325  
 315 320

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 Ile Val Leu Ser Thr Asn Ile Ala Glu Thr Ser Leu Thr Val Pro Gly 360  
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 Ile His Tyr Val Val Asp Thr Gly Thr Ala Arg Ile Ser Arg Tyr Ser 375  
 365 370

gtg cgc acc aag gtg cag cgc ctt ccg att gag aac att tcc cag gcc 1267  
 Val Arg Thr Lys Val Gln Arg Leu Pro Ile Glu Asn Ile Ser Gln Ala 390  
 380 385

agc gca aac cag cgt tct ggt cgt tgt ggt cgt gtc gca gac ggt att 1315  
 Ser Ala Asn Gln Arg Ser Gly Arg Cys Gly Arg Val Ala Asp Gly Ile 405  
 395 400

gcg att cgt ttg tat tcc gaa gat gat ttc aac tct cgc cca gag ttc 1363  
 Ala Ile Arg Leu Tyr Ser Glu Asp Asp Phe Asn Ser Arg Pro Glu Phe 420  
 410 415

acc gat ccg gaa att ctg cgc acc aac ttg gcg agc gtt att ttg cgc 1411

Thr Asp Pro Glu Ile Leu Arg Thr Asn Leu Ala Ser Val Ile Leu Arg 1459  
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 Met Ala Ser Leu Arg Leu Gly Asp Ile Asn Asp Phe Pro Phe Val Gln  
 445 450 455  
 gcc cca gag caa cgc tcc atc agg gat ggt att ttg ctg ctc cac gag 1507  
 Ala Pro Glu Gln Arg Ser Ile Arg Asp Gly Ile Leu Leu Leu His Glu  
 460 465 470  
 ttg ggc gca ctc acc gac gac acc caa gcc gat ggt tca ccg cag ctc 1555  
 Leu Gly Ala Leu Thr Asp Asp Thr Gln Ala Asp Gly Ser Pro Gln Leu  
 475 480 485  
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 Thr Gln Ile Gly Lys Asp Leu Ala Asn Ile Pro Val Asp Pro Arg Met  
 490 495 500  
 gcc cgc atg ctc gta gaa gcc aac act cta gcc tgc ctg cat tct gtc 1651  
 Ala Arg Met Leu Val Glu Ala Asn Thr Leu Gly Cys Leu His Ser Val  
 505 510 515 520  
 atg gtc att gtg tcc gct ctg acg att caa gat gtt cgc gaa cgc ccc 1699  
 Met Val Ile Val Ser Ala Leu Thr Ile Gln Asp Val Arg Glu Arg Pro  
 525 530 535  
 ctg gaa ttc caa gcc caa gct gat caa gcc cac gct agg ttc aag gac 1747  
 Leu Glu Phe Gln Ala Gln Ala Asp Gln Ala His Ala Arg Phe Lys Asp  
 540 545 550  
 acc acc tca gat ttc tta ggc ttt ttg aaa ctg tgg gag tac atc gcc 1795  
 Thr Thr Ser Asp Phe Leu Gly Phe Leu Lys Leu Trp Glu Tyr Ile Ala  
 555 560 565  
 gat cag cgc aat caa agc agc gcc aat tcc ttc cgc aag cag atg aaa 1843  
 Asp Gln Arg Asn Gln Ser Ser Gly Asn Ser Phe Arg Lys Leu Met Lys  
 570 575 580  
 aaa gaa ttc ctc cac tac atg cgt atc cgc gag tgg tgg gat ttg gtg 1891  
 Lys Glu Phe Leu His Tyr Met Arg Ile Arg Glu Trp Trp Asp Leu Val  
 585 590 595 600  
 cgc caa tta gag cag att ggc cag caa ctt ggt tgg gca aag aag gag 1939  
 Arg Gln Leu Glu Gln Ile Gly Gln Gln Leu Gly Trp Ala Lys Lys Glu  
 605 610 615

&lt;210&gt; 76

&lt;211&gt; 616

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 76

Met Thr Thr Ser Glu Thr Ala Pro Ser Lys Ala Ser Leu Tyr Glu Leu  
 1 5 10 15

Leu Glu Gly Val Ser Leu Ser Asp Glu Arg Thr Phe Arg Arg Arg Leu  
 20 25 30

Ser Lys Ala Arg Ala Pro Lys Ala Leu Gly Ala Ile Lys Ala Asp Ile

35

40

45

Asp Lys Ala Arg Leu Leu Ile Asp Glu Lys Ser Gln Leu Ile Pro Ser  
50 55 60

Ile Thr Tyr Pro Glu Asn Leu Pro Val Ser Ser Arg Arg Asp Ile  
65 70 75 80

Ala Glu Ala Ile Arg Asp Asn Gln Val Val Ile Ile Ala Gly Glu Thr  
85 90 95

Gly Ser Gly Lys Thr Thr Gln Ile Pro Lys Ile Cys Leu Asp Leu Gly  
100 105 110

Arg Gly Arg Arg Gly Leu Ile Gly His Thr Gln Pro Arg Arg Leu Ala  
115 120 125

Ala Arg Thr Val Ala Glu Arg Ile Ala Asp Glu Leu Gly Gln Asp Ile  
130 135 140

Gly Glu Ser Val Gly Tyr Ala Ile Arg Phe Asp Asp Arg Val Ser Ser  
145 150 155 160

His Thr Ser Val Lys Leu Met Thr Asp Gly Ile Leu Leu Ala Glu Met  
165 170 175

Gln Arg Asp Arg Phe Leu Asn Ala Tyr Asp Thr Ile Ile Ile Asp Glu  
180 185 190

Ala His Glu Arg Ser Leu Asn Ile Asp Phe Ile Leu Gly Tyr Leu Arg  
195 200 205

Gln Leu Leu Pro Lys Arg Pro Asp Leu Lys Val Ile Ile Thr Ser Ala  
210 215 220

Thr Ile Asp Pro Glu Arg Phe Ala Glu His Phe Ala Asp Ala Ser Gly  
225 230 235 240

Lys Pro Ala Pro Ile Ile Glu Val Ser Gly Arg Thr Phe Pro Val Glu  
245 250 255

Ile Arg Tyr Arg Pro Leu Glu Val Leu Asp Gly Asp Lys Ile Ile Asp  
260 265 270

Thr Asp Pro Leu Asp Gly Leu Cys Ser Ala Leu Glu Glu Leu Met Ala  
275 280 285

Glu Gly Asp Gly Asp Ile Leu Cys Phe Phe Ala Gly Glu Arg Asp Ile  
290 295 300

Arg Asp Ala Met Glu Ala Ile Glu Ala Arg Arg Trp Lys Gly Val Glu  
305 310 315 320

Val Thr Pro Leu Phe Gly Arg Leu Ser Asn Gln Glu Gln His Arg Val  
325 330 335

Phe Ser Pro His Ser Gly Arg Arg Ile Val Leu Ser Thr Asn Ile Ala  
340 345 350

Glu Thr Ser Leu Thr Val Pro Gly Ile His Tyr Val Val Asp Thr Gly  
355 360 365

Thr Ala Arg Ile Ser Arg Tyr Ser Val Arg Thr Lys Val Gln Arg Leu  
 370 375 380  
 Pro Ile Glu Asn Ile Ser Gln Ala Ser Ala Asn Gln Arg Ser Gly Arg  
 385 390 395 400  
 Cys Gly Arg Val Ala Asp Gly Ile Ala Ile Arg Leu Tyr Ser Glu Asp  
 405 410 415  
 Asp Phe Asn Ser Arg Pro Glu Phe Thr Asp Pro Glu Ile Leu Arg Thr  
 420 425 430  
 Asn Leu Ala Ser Val Ile Leu Arg Met Ala Ser Leu Arg Leu Gly Asp  
 435 440 445  
 Ile Asn Asp Phe Pro Phe Val Gln Ala Pro Glu Gln Arg Ser Ile Arg  
 450 455 460  
 Asp Gly Ile Leu Leu Leu His Glu Leu Gly Ala Leu Thr Asp Asp Thr  
 465 470 475 480  
 Gln Ala Asp Gly Ser Pro Gln Leu Thr Gln Ile Gly Lys Asp Leu Ala  
 485 490 495  
 Asn Ile Pro Val Asp Pro Arg Met Ala Arg Met Leu Val Glu Ala Asn  
 500 505 510  
 Thr Leu Gly Cys Leu His Ser Val Met Val Ile Val Ser Ala Leu Thr  
 515 520 525  
 Ile Gln Asp Val Arg Glu Arg Pro Leu Glu Phe Gln Ala Gln Ala Asp  
 530 535 540  
 Gln Ala His Ala Arg Phe Lys Asp Thr Thr Ser Asp Phe Leu Gly Phe  
 545 550 555 560  
 Leu Lys Leu Trp Glu Tyr Ile Ala Asp Gln Arg Asn Gln Ser Ser Gly  
 565 570 575  
 Asn Ser Phe Arg Lys Gln Met Lys Lys Glu Phe Leu His Tyr Met Arg  
 580 585 590  
 Ile Arg Glu Trp Trp Asp Leu Val Arg Gln Leu Glu Gln Ile Gly Gln  
 595 600 605  
 Gln Leu Gly Trp Ala Lys Lys Glu  
 610 615

&lt;210&gt; 77

&lt;211&gt; 2511

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101) .. (2488)

&lt;223&gt; RXN02293

&lt;400&gt; 77



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gatgtgt	ctca	ctcagcaa	at	tcttaatg	ta	caggcaattg	atg agt tca aga att	115	
							Met Ser Ser Arg Ile		
							1 5		
ggc aat ttt ctt ata aat cgc att tcc acg ggc ctg ccc gta gaa aat	163								
Gly Asn Phe Leu Ile Asn Arg Ile Ser Thr Gly Leu Pro Val Glu Asn									
	10 15 20								
att atc cct cac ctg caa gaa gct ttt tct ggc gga cct aaa aac ctt	211								
Ile Ile Pro His Leu Gln Glu Ala Phe Ser Ala Gly Pro Lys Asn Leu									
	25 30 35								
gtc att cag gcc cct ccc ggc aca gga aaa acg aca ctt ctc ccc cca	259								
Val Ile Gln Ala Pro Pro Gly Thr Gly Lys Thr Thr Leu Leu Pro Pro									
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tta gta gct aac atc tta tgt aat gaa gga gcg gga aat gcc acc cca	307								
Leu Val Ala Asn Ile Leu Cys Asn Glu Gly Ala Gly Asn Ala Thr Pro									
	55 60 65								
acc aag gtt tta gta acg gca cct cgt cgt gtg gcc gtc cga gca gca	355								
Thr Lys Val Leu Val Thr Ala Pro Arg Arg Val Ala Val Arg Ala Ala									
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Ala Arg Arg Leu Ala Gln Leu Asp Asp Ser Gln Leu Gly Thr Lys Val									
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gga ttc agc gtg cgt ggt gaa cat att tca ggc tcc cac gtg caa ttt	451								
Gly Phe Ser Val Arg Gly Glu His Ile Ser Gly Ser His Val Gln Phe									
	105 110 115								
atg acc ccc ggt gtg tta atc cgc cag ctc tta aac aac cca gaa tta	499								
Met Thr Pro Gly Val Leu Ile Arg Gln Leu Leu Asn Asn Pro Glu Leu									
	120 125 130								
ccc ggc atc ggc gct gtg att atc gat gaa gtc cac gaa cgt caa ctc	547								
Pro Gly Ile Gly Ala Val Ile Ile Asp Glu Val His Glu Arg Gln Leu									
	135 140 145								
gat tcc gat cta ctg cta gga atg ctt gct gaa gtc ctc agt caa ctg cgc	595								
Asp Ser Asp Leu Leu Leu Gly Met Leu Ala Glu Leu Ser Gln Leu Arg									
	150 155 160 165								
gac gat ttc tcc ctc atc gcc atg tcc gca acc tta gat tca gat aaa	643								
Asp Asp Phe Ser Leu Ile Ala Met Ser Ala Thr Leu Asp Ser Asp Lys									
	170 175 180								
ttc gca aac tta tta gac gct cag gtc ctt agt gtt gaa gca ccg att	691								
Phe Ala Asn Leu Leu Asp Ala Gln Val Leu Ser Val Glu Ala Pro Ile									
	185 190 195								
ttc ccc tta gac att tct tat gct cca gcc cgc gcg cct cgc ctc aat	739								
Phe Pro Leu Asp Ile Ser Tyr Ala Pro Ala Arg Ala Pro Arg Leu Asn									
	200 205 210								
gca aaa ggt gtc gac tgg gat ttc ctc gac cac atg gcg cag aaa act	787								
Ala Lys Lys Gly Val Asp Trp Asp Phe Leu Asp His Met Ala Gln Lys Thr									
	215 220 225								

cac gat gcg gtg aca cat tca gag cac tct gca ctc att ttc gtc cca 835  
 His Asp Ala Val Thr His Ser Glu His Ser Ala Leu Ile Phe Val Pro  
 230 235 240 245

ggt gtg cgt gaa att gat cga gta atg agc acg ctc aaa tcg ctc ggc 883  
 Gly Val Arg Glu Ile Asp Arg Val Met Ser Thr Leu Lys Ser Leu Gly  
 250 255 260

cat aat aat gtt ttc cca ctt cat ggc caa ctc agc ccg acc gaa caa 931  
 His Asn Asn Val Phe Pro Leu His Gly Gln Leu Ser Pro Thr Glu Gln  
 265 270 275

gac cgc gcc ctc gca ccg tca caa cag cag cgc atc att gtc tcc act 979  
 Asp Arg Ala Leu Ala Pro Ser Gln Gln Arg Ile Val Ser Thr  
 280 285 290

ccc gtt gcg gaa agc tcc cta act gtg cct gga gtt cgc atc ggg gtg 1027  
 Pro Val Ala Glu Ser Ser Leu Thr Val Pro Gly Val Arg Ile Gly Val  
 295 300 305

gat tcc ggc ctc tca cga agc ccc aaa cga gac tct gcc cgc ggc atg 1075  
 Asp Ser Gly Leu Ser Arg Ser Pro Lys Arg Asp Ser Ala Arg Gly Met  
 310 315 320 325

aca gga ctg atc acc agc agt tgc gcg cag gct tca gca ggc caa cgc 1123  
 Thr Gly Leu Ile Thr Ser Ser Cys Ala Gln Ala Ser Ala Gly Gln Arg  
 330 335 340

gca ggt cgc gct ggc cgt gaa gga cca gga caa ata atc aga tgc tat 1171  
 Ala Gly Arg Ala Gly Arg Glu Gly Pro Gly Gln Ile Ile Arg Cys Tyr  
 345 350 355

tcc gaa gaa gac ttc tcc cac ttc cca cga ttt gtg aca cca gaa atc 1219  
 Ser Glu Glu Asp Phe Ser His Phe Pro Arg Phe Val Thr Pro Glu Ile  
 360 365 370

agc tcc gct gac ctc acc caa gca gcc ctc tgg ctc gcc caa tgg gga 1267  
 Ser Ser Ala Asp Leu Thr Gln Ala Ala Leu Trp Leu Ala Gln Trp Gly  
 375 380 385

acg tca cct gcg gat tta ccg ctt ctt gat caa ccc cct cac gca gcc 1315  
 Thr Ser Pro Ala Asp Leu Pro Leu Leu Asp Gln Pro Pro His Ala Ala  
 390 395 400 405

tgg acg gct gca caa cag atc ctg cgc ctc atc ggc gcg ctt gaa ggt 1363  
 Trp Thr Ala Ala Gln Gln Ile Leu Arg Leu Ile Gly Ala Leu Glu Gly  
 410 415 420

gac gct atc acg agc ctg gga cat cgc tta tcg acg ctt ccc ctc tgc 1411  
 Asp Ala Ile Thr Ser Leu Gly His Arg Leu Ser Thr Leu Pro Leu Cys  
 425 430 435

cct caa ctc agc gct tct ctc ctc cgc ttc ggt gaa caa tcc gca aaa 1459  
 Pro Gln Leu Ser Ala Ser Leu Leu Arg Phe Gly Glu Gln Ser Ala Lys  
 440 445 450

atc ttg gcg gtg gtg tcc gaa aac ccg cag ggg gac gtc gaa aag caa 1507  
 Ile Leu Ala Val Val Ser Glu Asn Pro Gln Gly Asp Val Glu Lys Gln  
 455 460 465

caa ccc gac aag cgt gaa gtg gaa cgc ctt cgc cgt ttg gca cct gcg 1555  
 Gln Pro Asp Lys Arg Glu Val Glu Arg Leu Arg Ala Pro Ala  
 470 475 480 485

tcg gtt gga aaa gcg agt gcg ggg caa atc gta ggc gct gca ttc ccg 1603  
 Ser Val Gly Lys Ala Ser Ala Gly Gln Ile Val Gly Ala Ala Phe Pro  
 490 495 500

cag ctc atc ggc cga aaa ata gac aat gga gaa tac ctt tta gcc agt 1651  
 Gln Leu Ile Gly Arg Lys Ile Asp Asn Gly Glu Tyr Leu Leu Ala Ser  
 505 510 515

gga acc cgc gca cgc ctc atg gat tca gat ctc aaa gat gcc gaa tgg 1699  
 Gly Thr Arg Ala Arg Leu Met Asp Ser Ser Asp Leu Lys Asp Ala Glu Trp  
 520 525 530

atc tcc gtt gct gca att aac cgc tca caa aat tct gcc atc atc cgc 1747  
 Ile Ser Val Ala Ala Ile Asn Arg Ser Gln Asn Ser Ala Ile Ile Arg  
 535 540 545

gcc gcc gcc cgc att tca gag gac gat gcc ata gac atc atc gga gtc 1795  
 Ala Ala Ala Arg Ile Ser Glu Asp Asp Ala Ile Asp Ile Ile Gly Val  
 550 555 560 565

gtg gaa gaa acc cgc gcg att ttt gtc aac gga aaa gtc caa gcc cgg 1843  
 Val Glu Glu Thr Arg Ala Ile Phe Val Asn Gly Lys Val Gln Ala Arg  
 570 575 580

aag gtc aaa gca gca ggc gcg atc gaa tta agt tcc act ccg aca aaa 1891  
 Lys Val Lys Ala Ala Gly Ala Ile Glu Leu Ser Ser Thr Pro Thr Lys  
 585 590 595

cca aca ccc gcc gaa gcc tcg gaa aca atc gcc aca gcc ctt gcc aaa 1939  
 Pro Thr Pro Ala Glu Ala Ser Glu Thr Ile Ala Thr Ala Leu Ala Lys  
 600 605 610

ggc gga atc gac cta ttc cac ttc tcc gac aaa gcg gca tcc ttg cgt 1987  
 Gly Gly Ile Asp Leu Phe His Phe Ser Asp Lys Ala Ala Ser Leu Arg  
 615 620 625

gac cga ctg aaa ttc atc cac gaa cac cgt ggc gaa ccc tgg cca gat 2035  
 Asp Arg Leu Lys Phe Ile His Glu His Arg Gly Glu Pro Trp Pro Asp  
 630 635 640 645

att gaa act gcg gac ccg cac ctg tgg tta tct cca gaa att gag gcg 2083  
 Ile Glu Thr Ala Asp Pro His Leu Trp Leu Ser Pro Glu Ile Glu Ala  
 650 655 660

ctc agc cac gga aca cga cta aac aat atc gat atg tat ccc gca ctc 2131  
 Leu Ser His Gly Thr Arg Leu Asn Asn Ile Asp Met Tyr Pro Ala Leu  
 665 670 675

cag cga ctt ctc ccc tgg cct gaa gca acc aac ttt gaa gaa ttc gct 2179  
 Gln Arg Leu Leu Pro Trp Pro Glu Ala Thr Asn Phe Glu Glu Phe Ala  
 680 685 690

cct tcc cac cta tcc gta ccc agc ggg aat cag cac cga cta gat tat 2227  
 Pro Ser His Leu Ser Val Pro Ser Gly Asn Gln His Arg Leu Asp Tyr  
 695 700 705

tca tca ggc agg cca gtt ata cga gtg aaa tta caa gaa tgc ttc gga 2275

Ser Ser Gly Arg Pro Val Ile Arg Val Lys Leu Gln Glu Cys Phe Gly  
 710 715 720 725

tta gaa gaa tcc ccg cag ctc tgc gga atc ccg gtg caa ttt cat ctc 2323  
 Leu Glu Glu Ser Pro Gln Leu Cys Gly Ile Pro Val Gln Phe His Leu  
 730 735 740

ctg tca cct gcg gga aga cct ctt gca gtt acc gat gac ctg cgt agt 2371  
 Leu Ser Pro Ala Gly Arg Pro Leu Ala Val Thr Asp Asp Leu Arg Ser  
 745 750 755

ttc tgg tct gcc ccg tac agc caa gtc cgt gca gaa atg cgg ggc cgg 2419  
 Phe Trp Ser Gly Pro Tyr Ser Gln Val Arg Ala Glu Met Arg Gly Arg  
 760 765 770

tac ccc aaa cac ccg tgg ccg gag gat cca tgg acc gct cct gcc act 2467  
 Tyr Pro Lys His Pro Trp Pro Glu Asp Pro Trp Thr Ala Pro Ala Thr  
 775 780 785

gcg cgc acc aag aat cgc atg tagttttggc acgacttgat gtg 2511  
 Ala Arg Thr Lys Asn Arg Met  
 790 795

&lt;210&gt; 78

&lt;211&gt; 796

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 78

Met Ser Ser Arg Ile Gly Asn Phe Leu Ile Asn Arg Ile Ser Thr Gly  
 1 5 10 15

Leu Pro Val Glu Asn Ile Ile Pro His Leu Gln Glu Ala Phe Ser Ala  
 20 25 30

Gly Pro Lys Asn Leu Val Ile Gln Ala Pro Pro Gly Thr Gly Lys Thr  
 35 40 45

Thr Leu Leu Pro Pro Leu Val Ala Asn Ile Leu Cys Asn Glu Gly Ala  
 50 55 60

Gly Asn Ala Thr Pro Thr Lys Val Leu Val Thr Ala Pro Arg Arg Val  
 65 70 75 80

Ala Val Arg Ala Ala Ala Arg Arg Leu Ala Gln Leu Asp Asp Ser Gly  
 85 90 95

Leu Gly Thr Lys Val Gly Phe Ser Val Arg Gly Glu His Ile Ser Gly  
 100 105 110

Ser His Val Gln Phe Met Thr Pro Gly Val Leu Ile Arg Gln Leu Leu  
 115 120 125

Asn Asn Pro Glu Leu Pro Gly Ile Gly Ala Val Ile Ile Asp Glu Val  
 130 135 140

His Glu Arg Gln Leu Asp Ser Asp Leu Leu Leu Gly Met Leu Ala Glu  
 145 150 155 160

Leu Ser Gln Leu Arg Asp Asp Phe Ser Leu Ile Ala Met Ser Ala Thr

165										170										175																																			
Leu	Asp	Ser	Asp	Lys	Phe	Ala	Asn	Leu	Leu	Asp	Ala	Gln	Val	Leu	Ser					Leu	Asp	Ser	Asp	Lys	Phe	Ala	Asn	Leu	Leu	Asp	Ala	Gln	Val	Leu	Ser			Leu	Asp	Ser	Asp	Lys	Phe	Ala	Asn	Leu	Leu	Asp	Ala	Gln	Val	Leu	Ser		
180										185										190																																			
Val	Glu	Ala	Pro	Ile	Phe	Pro	Leu	Asp	Ile	Ser	Tyr	Ala	Pro	Ala	Arg					Val	Glu	Ala	Pro	Ile	Phe	Pro	Leu	Asp	Ile	Ser	Tyr	Ala	Pro	Ala	Arg			Val	Glu	Ala	Pro	Ile	Phe	Pro	Leu	Asp	Ile	Ser	Tyr	Ala	Pro	Ala	Arg		
195										200										205																																			
Ala	Pro	Arg	Leu	Asn	Ala	Lys	Gly	Val	Asp	Trp	Asp	Phe	Leu	Asp	His					Ala	Pro	Arg	Leu	Asn	Ala	Lys	Gly	Val	Asp	Trp	Asp	Phe	Leu	Asp	His			Ala	Pro	Arg	Leu	Asn	Ala	Lys	Gly	Val	Asp	Trp	Asp	Phe	Leu	Asp	His		
210										215										220																																			
Met	Ala	Gln	Lys	Thr	His	Asp	Ala	Val	Thr	His	Ser	Glu	His	Ser	Ala					Met	Ala	Gln	Lys	Thr	His	Asp	Ala	Val	Thr	His	Ser	Glu	His	Ser	Ala			Met	Ala	Gln	Lys	Thr	His	Asp	Ala	Val	Thr	His	Ser	Glu	His	Ser	Ala		
225										230										235																																			
Leu	Ile	Phe	Val	Pro	Gly	Val	Arg	Glu	Ile	Asp	Arg	Val	Met	Ser	Thr					Leu	Ile	Phe	Val	Pro	Gly	Val	Arg	Glu	Ile	Asp	Arg	Val	Met	Ser	Thr			Leu	Ile	Phe	Val	Pro	Gly	Val	Arg	Glu	Ile	Asp	Arg	Val	Met	Ser	Thr		
245										250										255																																			
Leu	Lys	Ser	Leu	Gly	His	Asn	Asn	Val	Phe	Pro	Leu	His	Gly	Gln	Leu					Leu	Lys	Ser	Leu	Gly	His	Asn	Asn	Val	Phe	Pro	Leu	His	Gly	Gln	Leu			Leu	Lys	Ser	Leu	Gly	His	Asn	Asn	Val	Phe	Pro	Leu	His	Gly	Gln	Leu		
260										265										270																																			
Ser	Pro	Thr	Glu	Gln	Asp	Arg	Ala	Leu	Ala	Pro	Ser	Gln	Gln	Gln	Arg					Ser	Pro	Thr	Glu	Gln	Asp	Arg	Ala	Leu	Ala	Pro	Ser	Gln	Gln	Gln	Arg			Ser	Pro	Thr	Glu	Gln	Asp	Arg	Ala	Leu	Ala	Pro	Ser	Gln	Gln	Gln	Arg		
275										280										285																																			
Ile	Ile	Val	Ser	Thr	Pro	Val	Ala	Glu	Ser	Ser	Leu	Thr	Val	Pro	Gly					Ile	Ile	Val	Ser	Thr	Pro	Val	Ala	Glu	Ser	Ser	Leu	Thr	Val	Pro	Gly			Ile	Ile	Val	Ser	Thr	Pro	Val	Ala	Glu	Ser	Ser	Leu	Thr	Val	Pro	Gly		
290										295										300																																			
Val	Arg	Ile	Gly	Val	Asp	Ser	Gly	Leu	Ser	Arg	Ser	Pro	Lys	Arg	Asp					Val	Arg	Ile	Gly	Val	Asp	Ser	Gly	Leu	Ser	Arg	Ser	Pro	Lys	Arg	Asp			Val	Arg	Ile	Gly	Val	Asp	Ser	Gly	Leu	Ser	Arg	Ser	Pro	Lys	Arg	Asp		
305										310										315																																			
Ser	Ala	Arg	Gly	Met	Thr	Gly	Leu	Ile	Thr	Ser	Ser	Cys	Ala	Gln	Ala					Ser	Ala	Arg	Gly	Met	Thr	Gly	Leu	Ile	Thr	Ser	Ser	Cys	Ala	Gln	Ala			Ser	Ala	Arg	Gly	Met	Thr	Gly	Leu	Ile	Thr	Ser	Ser	Cys	Ala	Gln	Ala		
325										330										335																																			
Ser	Ala	Gly	Gln	Arg	Ala	Gly	Arg	Ala	Gly	Arg	Glu	Gly	Pro	Gly	Gln					Ser	Ala	Gly																																	

Gly Ala Ala Phe Pro Gln Leu Ile Gly Arg Lys Ile Asp Asn Gly Glu  
 500 505 510  
 Tyr Leu Leu Ala Ser Gly Thr Arg Ala Arg Leu Met Asp Ser Asp Leu  
 515 520 525  
 Lys Asp Ala Glu Trp Ile Ser Val Ala Ala Ile Asn Arg Ser Gln Asn  
 530 535 540  
 Ser Ala Ile Ile Arg Ala Ala Ala Arg Ile Ser Glu Asp Asp Ala Ile  
 545 550 555 560  
 Asp Ile Ile Gly Val Val Glu Glu Thr Arg Ala Ile Phe Val Asn Gly  
 565 570 575  
 Lys Val Gln Ala Arg Lys Val Lys Ala Ala Gly Ala Ile Glu Leu Ser  
 580 585 590  
 Ser Thr Pro Thr Lys Pro Thr Pro Ala Glu Ala Ser Glu Thr Ile Ala  
 595 600 605  
 Thr Ala Leu Ala Lys Gly Gly Ile Asp Leu Phe His Phe Ser Asp Lys  
 610 615 620  
 Ala Ala Ser Leu Arg Asp Arg Leu Lys Phe Ile His Glu His Arg Gly  
 625 630 635 640  
 Glu Pro Trp Pro Asp Ile Glu Thr Ala Asp Pro His Leu Trp Leu Ser  
 645 650 655  
 Pro Glu Ile Glu Ala Leu Ser His Gly Thr Arg Leu Asn Asn Ile Asp  
 660 665 670  
 Met Tyr Pro Ala Leu Gln Arg Leu Leu Pro Trp Pro Glu Ala Thr Asn  
 675 680 685  
 Phe Glu Glu Phe Ala Pro Ser His Leu Ser Val Pro Ser Gly Asn Gln  
 690 695 700  
 His Arg Leu Asp Tyr Ser Ser Gly Arg Pro Val Ile Arg Val Lys Leu  
 705 710 715 720  
 Gln Glu Cys Phe Gly Leu Glu Glu Ser Pro Gln Leu Cys Gly Ile Pro  
 725 730 735  
 Val Gln Phe His Leu Leu Ser Pro Ala Gly Arg Pro Leu Ala Val Thr  
 740 745 750  
 Asp Asp Leu Arg Ser Phe Trp Ser Gly Pro Tyr Ser Gln Val Arg Ala  
 755 760 765  
 Glu Met Arg Gly Arg Tyr Pro Lys His Pro Trp Pro Glu Asp Pro Trp  
 770 775 780  
 Thr Ala Pro Ala Thr Ala Arg Thr Lys Asn Arg Met  
 785 790 795

<210> 79  
 <211> 2511

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	1 5	
ggc aat ttt ctt ata aat cgc att tcc acg ggc ctg ccc gta gaa aat	Gly Asn Phe Leu Ile Asn Arg Ile Ser Thr Gly Leu Pro Val Glu Asn	163
	10 15 20	
att atc cct cac ctg caa gaa gct ttt tcg gcc gga cct aaa aac ctt	Ile Ile Pro His Leu Gln Glu Ala Phe Ser Ala Gly Pro Lys Asn Leu	211
	25 30 35	
gtc att cag gcc cct ccc ggc aca gga aaa acg aca ctt ctc ccc cca	Val Ile Gln Ala Pro Pro Gly Thr Gly Lys Thr Thr Leu Leu Pro Pro	259
	40 45 50	
tta gta gct aac atc tta tgt aat gaa gga gcg gga aat gcc acc cca	Leu Val Ala Asn Ile Leu Cys Asn Glu Gly Ala Gly Asn Ala Thr Pro	307
	55 60 65	
acc aag gtt tta gta acg gca cct cgt cgt gtg gcc gtc cga gca gca	Thr Lys Val Val Leu Val Thr Ala Pro Arg Arg Val Ala Val Arg Ala Ala	355
	70 75 80 85	
gct cgc aga ctc gcc caa cta gat gat agc cag ctc gga aca aaa gtg	Ala Arg Arg Leu Ala Gln Leu Asp Asp Ser Gln Leu Gly Thr Lys Val	403
	90 95 100	
gga ttc agc gtg cgt ggt gaa cat att tca ggc tcc cac gtg caa ttt	Gly Phe Ser Val Arg Gly Glu His Ile Ser Gly Ser His Val Gln Phe	451
	105 110 115	
atg acc ccc ggt gtg tta atc cgc cag ctc tta aac aac cca gaa tta	Met Thr Pro Gly Val Leu Ile Arg Gln Leu Leu Asn Asn Pro Glu Leu	499
	120 125 130	
ccc ggc atc ggc gct gtg att atc gat gaa gtc cac gaa cgt caa ctc	Pro Gly Ile Gly Ala Val Ile Ile Asp Glu Val His Glu Arg Gln Leu	547
	135 140 145	
gat tcc gat cta ctg cta gga atg ctt gct gaa ctc agt caa ctg cgc	Asp Ser Asp Leu Leu Leu Gly Met Leu Ala Glu Leu Ser Gln Leu Arg	595
	150 155 160 165	
gac gat ttc tcc ctc atc gcc atg tcc gca acc tta gat tca gat aaa	Asp Asp Phe Ser Leu Ile Ala Met Ser Ala Thr Leu Asp Ser Asp Lys	643
	170 175 180	
ttc gca aac tta tta gac gct cag gtc ctt agt gtt gaa gca cgc att	Phe Ala Asn Leu Leu Asp Ala Gln Val Leu Ser Val Glu Ala Pro Ile	691

185	190	195	
ttc ccc tta gac att tct tat gct cca gcc cgc gcg cct cgc ctc aat Phe Pro Leu Asp Ile Ser Tyr Ala Pro Ala Arg Ala Pro Arg Leu Asn 200 205 210			739
gca aaa ggt gtc gac tgg gat ttc ctc gac cac atg gcg cag aaa act Ala Lys Gly Val Asp Trp Asp Phe Leu Asp His Met Ala Gln Lys Thr 215 220 225			787
cac gat gcg gtg aca cat tca gag cac tct gca ctc att ttc gtc cca His Asp Ala Val Thr His Ser Glu His Ser Ala Leu Ile Phe Val Pro 230 235 240 245			835
ggt gtg cgt gaa att gat cga gta atg agc acg ctc aaa tgg ctc ggc Gly Val Arg Glu Ile Asp Arg Val Met Ser Thr Leu Lys Ser Leu Gly 250 255 260			883
cat aat aat gtt ttc cca ctt cat ggc caa ctc agc ccg acc gaa caa His Asn Asn Val Phe Pro Leu His Gly Gln Leu Ser Pro Thr Glu Gln 265 270 275			931
gac cgc gcc ctc gca ccg tca caa cag cag cgc atc att gtc tcc act Asp Arg Ala Leu Ala Pro Ser Gln Gln Gln Arg Ile Val Ser Thr 280 285 290			979
ccc gtt gcg gaa agc tcc cta act gtg cct gga gtt cgc atc ggg gtg Pro Val Ala Glu Ser Ser Leu Thr Val Pro Gly Val Arg Ile Gly Val 295 300 305			1027
gat tcc ggc ctc tca cga agc ccc aaa cga gac tct gcc cgc ggc atg Asp Ser Gly Leu Ser Arg Ser Pro Lys Arg Asp Ser Ala Arg Gly Met 310 315 320 325			1075
aca gga ctg atc acc agc agt tgc gcg cag gct tca gca ggc caa cgc Thr Gly Leu Ile Thr Ser Ser Cys Ala Gln Ala Ser Ala Gly Gln Arg 330 335 340			1123
gca ggt cgc gct ggc cgt gaa gga cca gga caa ata atc aga tgc tat Ala Gly Arg Ala Gly Arg Glu Gly Pro Gly Gln Ile Ile Arg Cys Tyr 345 350 355			1171
tcc gaa gaa gac ttc tcc cac ttc cca cga ttt gtg aca cca gaa atc Ser Glu Glu Asp Phe Ser His Phe Pro Arg Phe Val Thr Pro Glu Ile 360 365 370			1219
agc tcc gct gac ctc acc caa gca gcc ctc tgg ctc gcc caa tgg gga Ser Ser Ala Asp Leu Thr Gln Ala Ala Leu Trp Leu Ala Gln Trp Gly 375 380 385			1267
acg tca cct gcg gat tta cgg ctt ctt gat caa ccc cct cac gca gcc Thr Ser Pro Ala Asp Leu Pro Leu Leu Asp Gln Pro Pro His Ala Ala 390 395 400 405			1315
tgg acg gct gca caa cag atc ctg cgc ctc atc ggc gcg ctt gaa ggt Trp Thr Ala Ala Gln Gln Ile Leu Arg Leu Ile Gly Ala Leu Glu Gly 410 415 420			1363
gac gct atc acg agc ctg gga cat cgc tta tgg acg ctt ccc ctc tgc Asp Ala Ile Thr Ser Leu Gly His Arg Leu Ser Thr Leu Pro Leu Cys 425 430 435			1411

G0001503.000000



cct caa ctc agc gct tct ctc ctc cgc ttc ggt gaa caa tcc gca aaa 1459  
 Pro Gln Leu Ser Ala Ser Leu Leu Arg Phe Gly Glu Gln Ser Ala Lys  
 440 445 450

atc ttg gcg gtg gtg tcc gaa aac ccg cag ggg gac gtc gaa aag caa 1507  
 Ile Leu Ala Val Val Ser Glu Asn Pro Gln Gly Asp Val Glu Lys Gln  
 455 460 465

caa ccc gac aag cgt gaa gtg gaa cgc ctt cgc cgt ttg gca cct gcg 1555  
 Gln Pro Asp Lys Arg Glu Val Glu Arg Leu Arg Leu Ala Pro Ala  
 470 475 480 485

tcg gtt gga aaa gcg agt gcg ggg caa atc gta ggc gct gca ttc ccg 1603  
 Ser Val Gly Lys Ala Ser Ala Gly Gln Ile Val Gly Ala Ala Phe Pro  
 490 495 500

cag ctc atc ggc cga aaa ata gac aat gga gaa tac ctt tta gcc agt 1651  
 Gln Leu Ile Gly Arg Lys Ile Asp Asn Gly Glu Tyr Leu Leu Ala Ser  
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gga acc cgc gca cgc ctc atg gat tca gat ctc aaa gat gcc gaa tgg 1699  
 Gly Thr Arg Ala Arg Leu Met Asp Ser Asp Leu Lys Asp Ala Glu Trp  
 520 525 530

atc tcc gtt gct gca att aac cgc tca caa aat tct gcc atc atc cgc 1747  
 Ile Ser Val Ala Ala Ile Asn Arg Ser Gln Asn Ser Ala Ile Ile Arg  
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gcc gcc gcc cgc att tca gag gac gat gcc ata gac atc atc gga gtc 1795  
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 550 555 560 565

gtg gaa gaa acc cgc gcg att ttt gtc aac gga aaa gtc caa gcc ccg 1843  
 Val Glu Glu Thr Arg Ala Ile Phe Val Asn Gly Lys Val Gln Ala Arg  
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aag gtc aaa gca gca ggc gcg atc gaa tta agt tcc act ccg aca aaa 1891  
 Lys Val Lys Ala Ala Gly Ala Ile Glu Leu Ser Ser Thr Pro Thr Lys  
 585 590 595

cca aca ccc gcc gaa gcc tcg gaa aca atc gcc aca gcc ctt gcc aaa 1939  
 Pro Thr Pro Ala Glu Ala Ser Glu Thr Ile Ala Thr Ala Leu Ala Lys  
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ggc gga atc gac cta ttc cac ttc tcc gac aaa gcg gca tcc ttg cgt 1987  
 Gly Gly Ile Asp Leu Phe His Phe Ser Asp Lys Ala Ala Ser Leu Arg  
 615 620 625

gac cga ctg aaa ttc atc cac gaa cac cgt ggc gaa ccc tgg cca gat 2035  
 Asp Arg Leu Lys Phe Ile His Glu His Arg Gly Glu Pro Trp Pro Asp  
 630 635 640 645

att gaa act gcg gac ccg cac ctg tgg tta tct cca gaa att gag gcg 2083  
 Ile Glu Thr Ala Asp Pro His Leu Trp Leu Ser Pro Glu Ile Glu Ala  
 650 655 660

ctc agc cac gga aca cga cta aac aat atc gat atg tat ccc gca ctc 2131  
 Leu Ser His Gly Thr Arg Leu Asn Asn Ile Asp Met Tyr Pro Ala Leu  
 665 670 675

cag cga ctt ctc ccc tgg cct gaa gca acc aac ttt gaa gaa ttc gct 2179  
Gln Arg Leu Leu Pro Trp Pro Glu Ala Thr Asn Phe Glu Glu Phe Ala  
680 685 690

cct tcc cac cta tcc gta ccc agc ggg aat cag cac cga cta gat tat 2227  
Pro Ser His Leu Ser Val Pro Ser Gly Asn Gln His Arg Leu Asp Tyr  
695 700 705

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Ser Ser Gly Arg Pro Val Ile Arg Val Lys Leu Gln Glu Cys Phe Gly  
710 715 720 725

tta gaa gaa tcc ccg cag ctc tgc gga atc ccg gtg caa ttt cat ctc 2323  
Leu Glu Glu Ser Pro Gln Leu Cys Gly Ile Pro Val Gln Phe His Leu  
730 735 740

ctg tca cct gcg gga aga cct ctt gca gtt acc gat gac ctg cgt agt 2371  
Leu Ser Pro Ala Gly Arg Pro Leu Ala Val Thr Asp Asp Leu Arg Ser  
745 750 755

ttc tgg tct ggc ccg tac agc caa gtc cgt gca gaa atg cgg ggc ccg 2419  
Phe Trp Ser Gly Pro Tyr Ser Gln Val Arg Ala Glu Met Arg Gly Arg  
760 765 770

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Tyr Pro Lys His Pro Trp Pro Glu Asp Pro Trp Thr Ala Pro Ala Thr  
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790 795

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<212> PRT

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Gly Pro Lys Asn Leu Val Ile Gln Ala Pro Pro Gly Thr Gly Lys Thr  
35 40 45

Thr Leu Leu Pro Pro Leu Val Ala Asn Ile Leu Cys Asn Glu Gly Ala  
50 55 60

Gly Asn Ala Thr Pro Thr Lys Val Leu Val Thr Ala Pro Arg Arg Val  
65 70 75 80

Ala Val Arg Ala Ala Ala Arg Arg Leu Ala Gln Leu Asp Asp Ser Gln  
85 90 95

Leu Gly Thr Lys Val Gly Phe Ser Val Arg Gly Glu His Ile Ser Gly  
100 105 110

Ser His Val Gln Phe Met Thr Pro Gly Val Leu Ile Arg Gln Leu Leu

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130					135					140					
His	Glu	Arg	Gln	Leu	Asp	Ser	Asp	Leu	Leu	Leu	Gly	Met	Leu	Ala	Glu
145					150					155					
Leu	Ser	Gln	Leu	Arg	Asp	Asp	Phe	Ser	Leu	Ile	Ala	Met	Ser	Ala	Thr
165					170					175					
Leu	Asp	Ser	Asp	Lys	Phe	Ala	Asn	Leu	Leu	Asp	Ala	Gln	Val	Leu	Ser
180					185					190					
Val	Glu	Ala	Pro	Ile	Phe	Pro	Leu	Asp	Ile	Ser	Tyr	Ala	Pro	Ala	Arg
195					200					205					
Ala	Pro	Arg	Leu	Asn	Ala	Lys	Gly	Val	Asp	Trp	Asp	Phe	Leu	Asp	His
210					215					220					
Met	Ala	Gln	Lys	Thr	His	Asp	Ala	Val	Thr	His	Ser	Glu	His	Ser	Ala
225					230					235					
Leu	Ile	Phe	Val	Pro	Gly	Val	Arg	Glu	Ile	Asp	Arg	Val	Met	Ser	Thr
245					250					255					
Leu	Lys	Ser	Leu	Gly	His	Asn	Asn	Val	Phe	Pro	Leu	His	Gly	Gln	Leu
260					265					270					
Ser	Pro	Thr	Glu	Gln	Asp	Arg	Ala	Leu	Ala	Pro	Ser	Gln	Gln	Gln	Arg
275					280					285					
Ile	Ile	Val	Ser	Thr	Pro	Val	Ala	Glu	Ser	Ser	Leu	Thr	Val	Pro	Gly
290					295					300					
Val	Arg	Ile	Gly	Val	Asp	Ser	Gly	Leu	Ser	Arg	Ser	Pro	Lys	Arg	Asp
305					310					315					
Ser	Ala	Arg	Gly	Met	Thr	Gly	Leu	Ile	Thr	Ser	Ser	Cys	Ala	Gln	Ala
325					330					335					
Ser	Ala	Gly	Gln	Arg	Ala	Gly	Arg	Ala	Gly	Arg	Glu	Gly	Pro	Gly	Gln
340					345					350					
Ile	Ile	Arg	Cys	Tyr	Ser	Glu	Glu	Asp	Phe	Ser	His	Phe	Pro	Arg	Phe
355					360					365					
Val	Thr	Pro	Glu	Ile	Ser	Ser	Ala	Asp	Leu	Thr	Gln	Ala	Ala	Leu	Trp
370					375					380					
Leu	Ala	Gln	Trp	Gly	Thr	Ser	Pro	Ala	Asp	Leu	Pro	Leu	Leu	Asp	Gln
385					390					395					
Pro	Pro	His	Ala	Ala	Trp	Thr	Ala	Ala	Gln	Gln	Ile	Leu	Arg	Leu	Ile
405					410					415					
Gly	Ala	Leu	Glu	Gly	Asp	Ala	Ile	Thr	Ser	Leu	Gly	His	Arg	Leu	Ser
420					425					430					
Thr	Leu	Pro	Leu	Cys	Pro	Gln	Leu	Ser	Ala	Ser	Leu	Leu	Arg	Phe	Gly
435					440					445					

Glu Gln Ser Ala Lys Ile Leu Ala Val Val Ser Glu Asn Pro Gln Gly  
 450 455 460  
 Asp Val Glu Lys Gln Gln Pro Asp Lys Arg Glu Val Glu Arg Leu Arg  
 465 470 475 480  
 Arg Leu Ala Pro Ala Ser Val Gly Lys Ala Ser Ala Gly Gln Ile Val  
 485 490 495  
 Gly Ala Ala Phe Pro Gln Leu Ile Gly Arg Lys Ile Asp Asn Gly Glu  
 500 505 510  
 Tyr Leu Leu Ala Ser Gly Thr Arg Ala Arg Leu Met Asp Ser Asp Leu  
 515 520 525  
 Lys Asp Ala Glu Trp Ile Ser Val Ala Ala Ile Asn Arg Ser Gln Asn  
 530 535 540  
 Ser Ala Ile Ile Arg Ala Ala Ala Arg Ile Ser Glu Asp Asp Ala Ile  
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 Asp Ile Ile Gly Val Val Glu Glu Thr Arg Ala Ile Phe Val Asn Gly  
 565 570 575  
 Lys Val Gln Ala Arg Lys Val Lys Ala Ala Gly Ala Ile Glu Leu Ser  
 580 585 590  
 Ser Thr Pro Thr Lys Pro Thr Pro Ala Glu Ala Ser Glu Thr Ile Ala  
 595 600 605  
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 610 615 620  
 Ala Ala Ser Leu Arg Asp Arg Leu Lys Phe Ile His Glu His Arg Gly  
 625 630 635 640  
 Glu Pro Trp Pro Asp Ile Glu Thr Ala Asp Pro His Leu Trp Leu Ser  
 645 650 655  
 Pro Glu Ile Glu Ala Leu Ser His Gly Thr Arg Leu Asn Asn Ile Asp  
 660 665 670  
 Met Tyr Pro Ala Leu Gln Arg Leu Leu Pro Trp Pro Glu Ala Thr Asn  
 675 680 685  
 Phe Glu Glu Phe Ala Pro Ser His Leu Ser Val Pro Ser Gly Asn Gln  
 690 695 700  
 His Arg Leu Asp Tyr Ser Ser Gly Arg Pro Val Ile Arg Val Lys Leu  
 705 710 715 720  
 Gln Glu Cys Phe Gly Leu Glu Glu Ser Pro Gln Leu Cys Gly Ile Pro  
 725 730 735  
 Val Gln Phe His Leu Leu Ser Pro Ala Gly Arg Pro Leu Ala Val Thr  
 740 745 750  
 Asp Asp Leu Arg Ser Phe Trp Ser Gly Pro Tyr Ser Gln Val Arg Ala  
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Met Ser Ala Pro Glu  
1 5  
tca ccc aca aat acc acc cca gat ccg ctc aat gct tcc acg gaa gag 163  
Ser Pro Thr Asn Thr Thr Pro Asp Pro Leu Asn Ala Ser Thr Glu Glu  
10 15 20  
ttg ctt act gct gcc gtt gaa gcg ttg ggc ggt gcc cgt cgt gct gga 211  
Leu Leu Thr Ala Ala Val Glu Ala Leu Gly Gly Ala Arg Arg Ala Gly  
25 30 35  
cag gaa gca atg gct aag gct gtg acc aag gct ttt gat aca gag cgt 259  
Gln Glu Ala Met Ala Lys Ala Val Thr Lys Ala Phe Asp Thr Glu Arg  
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cac ttg gcg gtg cag gcg ggt acg ggt acg ggt aag tct ttg gct tat 307  
His Leu Ala Val Gln Ala Gly Thr Gly Thr Gly Lys Ser Leu Ala Tyr  
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ctt gtt ccg tcg att cgt cat gcg cag aag tct gat tcc acg gtc att 355  
Leu Val Pro Ser Ile Arg His Ala Gln Lys Ser Asp Ser Thr Val Ile  
70 75 80 85  
gtg tct act gcg acg atc gcg ttg cag cgc cag ttg gtc aat agg gat 403  
Val Ser Thr Ala Thr Ile Ala Leu Gln Arg Gln Leu Val Asn Arg Asp  
90 95 100  
etc ccc cgc ttg gtg gat gcg ttg gaa ccc ttg atg gaa cgt cgc ccg 451  
Leu Pro Arg Leu Val Asp Ala Leu Glu Pro Leu Met Glu Arg Arg Pro  
105 110 115  
act ttt gcg att atg aag ggc cgt tcc aat tat ttg tgc atg aat aag 499  
Thr Phe Ala Ile Met Lys Gly Arg Ser Asn Tyr Leu Cys Met Asn Lys  
120 125 130  
gtt gcc cgc cag gaa gag ctg aat cag gaa gat gcc ctg att gag cag 547  
Val Ala Arg Gln Glu Glu Leu Asn Gln Glu Asp Ala Leu Ile Glu Gln  
135 140 145  
gag gat atc tcg tgg tta ggt aag cac att gtg cgc ctt aat gag tgg 595

Glu Asp Ile Ser Trp Leu Gly Lys His Ile Val Arg Leu Asn Glu Trp  
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 gcc aat gag act gag act ggc gat cgt gat gat ttg gat ccg ggt gtt 643  
 Ala Asn Glu Thr Glu Thr Gly Asp Arg Asp Asp Leu Asp Pro Gly Val  
 170 175 180  
 cct gat ctt gcg tgg aag cag gta agt gtt act gcc cgt gag tgc att 691  
 Pro Asp Leu Ala Trp Lys Gln Val Ser Val Thr Ala Arg Glu Cys Ile  
 185 190 195  
 ggc gcg tca agg tgc ccg cat ggc gag gat tgt ttc gct gag att gcc 739  
 Gly Ala Ser Arg Cys Pro His Gly Glu Asp Cys Phe Ala Glu Ile Ala  
 200 205 210  
 cgc ggg aag gca aag gag gct gat gtg gtg gtc acc aac cat gcg tta 787  
 Arg Gly Lys Ala Lys Glu Ala Asp Val Val Thr Asn His Ala Leu  
 215 220 225  
 ctt gct att gat gcg ttg tgc gat gtt tct gtg ctt cct gaa cat gat 835  
 Leu Ala Ile Asp Ala Leu Ser Asp Val Ser Val Leu Pro Glu His Asp  
 230 235 240 245  
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 Val Val Val Ile Asp Glu Ala His Glu Leu Asp Gly Arg Ile Thr Ala  
 250 255 260  
 gtg gcg tgc gct gag atc acg gtg aat tgc ctc aat tta gct gct cgc 931  
 Val Ala Ser Ala Glu Ile Thr Val Asn Ser Leu Asn Leu Ala Ala Arg  
 265 270 275  
 cgt gcg tcc aag ttg gat tcc gat aag cgg gaa gaa cgc gtc cag gaa 979  
 Arg Ala Ser Lys Leu Asp Ser Asp Lys Arg Glu Glu Arg Val Gln Glu  
 280 285 290  
 atc gct ggc gat ttg gaa acc ttg ttg caa acc atg cag ccg ggc cgg 1027  
 Ile Ala Gly Asp Leu Glu Thr Leu Leu Gln Thr Met Gln Pro Gly Arg  
 295 300 305  
 tgg aat gac atg gat gag ggt tcc aaa ggc aca ctg gtg gca ttg aag 1075  
 Trp Asn Asp Met Asp Glu Gly Ser Lys Gly Thr Leu Val Ala Leu Lys  
 310 315 320 325  
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 Asp Ala Leu Trp Ala Leu Arg Ala Gln Ile Ala Gly Ala Pro Glu Gly  
 330 335 340  
 gag gct gcg aat gat ccg gag cgt ttc gcc gag cga cag aat tta agc 1171  
 Glu Ala Ala Asn Asp Pro Glu Arg Phe Ala Glu Arg Gln Asn Leu Ser  
 345 350 355  
 aat cac ttg atg gaa atc cat gat gcc aac gtg cgc att ttg gag gtc 1219  
 Asn His Leu Met Glu Ile His Asp Ala Asn Val Arg Ile Leu Glu Val  
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 Phe Ala Glu Glu Asp Pro Ser Lys Gln Tyr Asp Val Val Trp His Asn  
 375 380 385  
 cac gat gat cgt cgc ggg gat tcc ctc aat gtg gcg ccg ctg tgc gtt 1315  
 His Asp Asp Arg Arg Gly Asp Ser Leu Asn Val Ala Pro Leu Ser Val

390	395	400	405	
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gcc agt gcg acg ctg acc att ggt ggc aat ttc aac gca atg gct gcc Ala Ser Ala Thr Leu Thr Ile Gly Gly Asn Phe Asn Ala Met Ala Ala 425 430 435				1411
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ccg ttt gat cca gcg aag tcg ggt att ttg tac acc gct cga cac ctt Pro Phe Asp Pro Ala Lys Ser Gly Ile Leu Tyr Thr Ala Arg His Leu 455 460 465				1507
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tac gag ttg atc act gcg gcg ggt ggc cga act ttg ggg ctc ttt tcg Tyr Glu Leu Ile Thr Ala Ala Gly Gly Arg Thr Leu Gly Leu Phe Ser 490 495 500				1603
tcg aaa cgc gct gcg gaa caa gcc acc aag gcg atg cgt ctg cgc ctg Ser Lys Arg Ala Ala Glu Gln Ala Thr Lys Ala Met Arg Ser Leu Arg Leu 505 510 515				1651
cct ttt gat gtg ctc tgc cag gga gat gac aat act gcc gcg ctg gtg Pro Phe Asp Val Leu Cys Gln Gly Asp Asp Asn Thr Ala Ala Leu Val 520 525 530				1699
aag aag ttt tcc gac agc gaa aac acg tgc ctt ttt ggc act etc acg Lys Lys Phe Ser Asp Ser Glu Asn Thr Cys Leu Phe Gly Thr Leu Thr 535 540 545				1747
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att gac cgc atc ccg ttc ccc cgc ccc gac gac ccg ctg ctg cag gcc Ile Asp Arg Ile Pro Phe Pro Arg Pro Asp Asp Pro Leu Leu Gln Ala 570 575 580				1843
cgc aag gag gcc gcc gat gcc gaa ggc cgc aac ggt ttc atg gag gtc Arg Lys Glu Ala Ala Asp Ala Glu Gly Arg Asn Gly Phe Met Glu Val 585 590 595				1891
gca gcc acc cac gcg gcg ttg ttg atg gcg cag ggc gcg ggc cgg ttg Ala Ala Thr His Ala Ala Leu Met Ala Gln Gly Ala Gly Arg Leu 600 605 610				1939
ttg cgg cac gtc ggc gac cgc ggc gtg gta gca gtg cta gac cac cgc Leu Arg His Val Gly Asp Arg Gly Val Val Ala Val Leu Asp His Arg 615 620 625				1987
tta tcg acg aaa cgt tac ggc ggt ttc ctg cgc ttc tcc atg ccc aga Leu Ser Thr Lys Arg Tyr Gly Gly Phe Leu Arg Phe Ser Met Pro Arg 630 635 640 645				2035

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 Phe Trp Glu Thr Thr Asn Pro Glu Thr Val Arg Ala Ala Leu Lys Arg  
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           20                  25                  30

Ala Arg Arg Ala Gly Gln Glu Ala Met Ala Lys Ala Val Thr Lys Ala  
           35                  40                  45

Phe Asp Thr Glu Arg His Leu Ala Val Gln Ala Gly Thr Gly Thr Gly  
           50                  55                  60

Lys Ser Leu Ala Tyr Leu Val Pro Ser Ile Arg His Ala Gln Lys Ser  
           65                  70                  75                  80

Asp Ser Thr Val Ile Val Ser Thr Ala Thr Ile Ala Leu Gln Arg Gln  
           85                  90                  95

Leu Val Asn Arg Asp Leu Pro Arg Leu Val Asp Ala Leu Glu Pro Leu  
           100                  105                  110

Met Glu Arg Arg Pro Thr Phe Ala Ile Met Lys Gly Arg Ser Asn Tyr  
           115                  120                  125

Leu Cys Met Asn Lys Val Ala Arg Gln Glu Glu Leu Asn Gln Glu Asp  
           130                  135                  140

Ala Leu Ile Glu Gln Glu Asp Ile Ser Trp Leu Gly Lys His Ile Val  
           145                  150                  155                  160

Arg Leu Asn Glu Trp Ala Asn Glu Thr Glu Thr Gly Asp Arg Asp Asp  
           165                  170                  175

Leu Asp Pro Gly Val Pro Asp Leu Ala Trp Lys Gln Val Ser Val Thr  
           180                  185                  190

Ala Arg Glu Cys Ile Gly Ala Ser Arg Cys Pro His Gly Glu Asp Cys  
           195                  200                  205

Phe Ala Glu Ile Ala Arg Gly Lys Ala Lys Glu Ala Asp Val Val Val  
           210                  215                  220

Thr Asn His Ala Leu Leu Ala Ile Asp Ala Leu Ser Asp Val Ser Val  
           225                  230                  235                  240



Leu Pro Glu His Asp Val Val Val Ile Asp Glu Ala His Glu Leu Asp  
 245 250 255  
 Gly Arg Ile Thr Ala Val Ala Ser Ala Glu Ile Thr Val Asn Ser Leu  
 260 265 270  
 Asn Leu Ala Ala Arg Arg Ala Ser Lys Leu Asp Ser Asp Lys Arg Glu  
 275 280 285  
 Glu Arg Val Gln Glu Ile Ala Gly Asp Leu Glu Thr Leu Leu Gln Thr  
 290 295 300  
 Met Gln Pro Gly Arg Trp Asn Asp Met Asp Glu Gly Ser Lys Gly Thr  
 305 310 315 320  
 Leu Val Ala Leu Lys Asp Ala Leu Trp Ala Leu Arg Ala Gln Ile Ala  
 325 330 335  
 Gly Ala Pro Glu Gly Glu Ala Ala Asn Asp Pro Glu Arg Phe Ala Glu  
 340 345 350  
 Arg Gln Asn Leu Ser Asn His Leu Met Glu Ile His Asp Ala Asn Val  
 355 360 365  
 Arg Ile Leu Glu Val Phe Ala Glu Glu Asp Pro Ser Lys Gln Tyr Asp  
 370 375 380  
 Val Val Trp His Asn His Asp Asp Arg Arg Gly Asp Ser Leu Asn Val  
 385 390 395 400  
 Ala Pro Leu Ser Val Ala Gly Leu Leu His Glu Lys Leu Phe Ala Glu  
 405 410 415  
 Asn Thr Val Val Leu Ala Ser Ala Thr Leu Thr Ile Gly Gly Asn Phe  
 420 425 430  
 Asn Ala Met Ala Ala Ser Trp Gly Leu Pro Lys Gly Ser Trp Asp Ser  
 435 440 445  
 Met Asp Ala Gly Thr Pro Phe Asp Pro Ala Lys Ser Gly Ile Leu Tyr  
 450 455 460  
 Thr Ala Arg His Leu Pro Asp Pro Gly Arg Asp Gly Leu Pro Glu Glu  
 465 470 475 480  
 Thr Leu Asp Glu Ile Tyr Glu Leu Ile Thr Ala Ala Gly Gly Arg Thr  
 485 490 495  
 Leu Gly Leu Phe Ser Ser Lys Arg Ala Ala Glu Gln Ala Thr Lys Ala  
 500 505 510  
 Met Arg Leu Arg Leu Pro Phe Asp Val Leu Cys Gln Gly Asp Asp Asn  
 515 520 525  
 Thr Ala Ala Leu Val Lys Lys Phe Ser Asp Ser Glu Asn Thr Cys Leu  
 530 535 540  
 Phe Gly Thr Leu Thr Leu Trp Gln Gly Val Asp Val Pro Gly Arg Ser  
 545 550 555 560  
 Leu Ser Leu Val Leu Ile Asp Arg Ile Pro Phe Pro Arg Pro Asp Asp

565 570 575

Pro Leu Leu Gln Ala Arg Lys Glu Ala Ala Asp Ala Glu Gly Arg Asn  
580 585 590

Gly Phe Met Glu Val Ala Ala Thr His Ala Ala Leu Leu Met Ala Gln  
595 600 605

Gly Ala Gly Arg Leu Leu Arg His Val Gly Asp Arg Gly Val Val Ala  
610 615 620

Val Leu Asp His Arg Leu Ser Thr Lys Arg Tyr Gly Gly Phe Leu Arg  
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<223> RXN01374

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Met Ser Glu Ser Gly  
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gcg cta agt tct act gac tct cta tcc ccg ggt gtc acc att gaa gtc 163  
Ala Leu Ser Ser Thr Asp Ser Leu Ser Pro Gly Val Thr Ile Glu Val  
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cga gat gaa att tgg ctg gtt act cac gtt act cgc tcc aca gat ggt 211  
Arg Asp Glu Ile Trp Leu Val Thr His Val Thr Arg Ser Thr Asp Gly  
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Phe Arg Val Lys Ala Arg Gly Leu Ser Asp Tyr Val Arg Asp His Glu  
40 45 50

gct acg ttc ttc acc gca ctt gat aaa gat ttg aag gtc att gac cct 307  
Ala Thr Phe Phe Thr Ala Leu Asp Lys Asp Leu Lys Val Ile Asp Pro  
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acc cag gtc acc gtc agt ctt gat gat tcc tcc aat tac cgt cgc acc 355  
Thr Gln Val Thr Val Ser Leu Asp Asp Ser Ser Asn Tyr Arg Arg Thr  
70 75 80 85

cgc ctg tgg ttg gag gcc acc atg cgt aaa act ccg gta ccg ctc tat 403  
Arg Leu Trp Leu Glu Ala Thr Met Arg Lys Thr Pro Val Pro Leu Tyr  
90 95 100

caa gag tca ctt tcc gtg gca gat caa atg ctc gcc gat cca ctg gag 451  
 Gln Glu Ser Leu Ser Val Ala Asp Gln Met Leu Ala Asp Pro Leu Glu  
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 Tyr Gln Leu Ala Ala Val Arg Lys Thr Leu Ser Ser Ala Asn Leu Arg  
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ccc cgc gtg ctt att gct gat gcc gtg gga ctt ggc aaa acc cta gaa 547  
 Pro Arg Val Leu Ile Ala Asp Ala Val Gly Leu Gly Lys Thr Leu Glu  
 135 140 145

atg ggc atg atc ttg gcg gaa ctt atc cgc cgt ggc cgt ggt gag cgc 595  
 Met Gly Met Ile Leu Ala Glu Leu Ile Arg Arg Gly Arg Gly Glu Arg  
 150 155 160 165

att ttg gta gtc acc ccg cgc cac att atg gag cag ttc cag cag gaa 643  
 Ile Leu Val Val Thr Pro Arg His Ile Met Glu Gln Phe Gln Gln Glu  
 170 175 180

atg tgg acc cgt ttt gcc atc ccg ctc gtt cgt cta gat tcc gtg ggc 691  
 Met Trp Thr Arg Arg Phe Ala Ile Pro Leu Val Arg Leu Asp Ser Val Gly  
 185 190 195

atc cag caa gtg cgc caa aaa ttg cca gca tca cgc aac cct ttt act 739  
 Ile Gln Gln Val Arg Gln Lys Leu Pro Ala Ser Arg Asn Pro Phe Thr  
 200 205 210

tat ttc ccg cgc gtg att gtc tct atg gat act ttg aaa tct ccg aag 787  
 Tyr Phe Pro Arg Val Ile Val Ser Met Asp Thr Leu Lys Ser Pro Lys  
 215 220 225

tac cgc gcg caa cta gaa aag gtg cac tgg gat gcg gtg gtt ata gat 835  
 Tyr Arg Ala Gln Leu Glu Lys Val His Trp Asp Ala Val Val Ile Asp  
 230 235 240 245

gaa atc cac aat gca acc aat gct ggc acc caa aat aat gag cta gcc 883  
 Glu Ile His Asn Ala Thr Asn Ala Gly Thr Gln Asn Asn Glu Leu Ala  
 250 255 260

ggc aca ctt ggg cct act gcc gag gct ctt att ttg gcc tct gcc acc 931  
 Gly Thr Leu Gly Pro Thr Ala Glu Ala Leu Ile Leu Ala Ser Ala Thr  
 265 270 275

ccg cac aat ggt gat cca gaa tcc ttt aag gag atc ttg cgt ttg ctt 979  
 Pro His Asn Gly Asp Pro Glu Ser Phe Lys Glu Ile Leu Arg Leu Leu  
 280 285 290

gat ccc acc gct gtg atg cct gat ggc acc att gat gcc gaa gct gca 1027  
 Asp Pro Thr Ala Val Met Pro Asp Gly Thr Ile Asp Ala Glu Ala Ala  
 295 300 305

cag cgt ctg atc att cgt cgc cat cgc aat agc cct gag gtt tca ggt 1075  
 Gln Arg Leu Ile Ile Arg Arg His Arg Asn Ser Pro Glu Val Ser Gly  
 310 315 320 325

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 Phe Val Gly Glu Lys Trp Ala Pro Arg Asn Glu Pro Gln Asn Phe Leu  
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gtc gct gcg tca aaa gaa gaa aac ggc gtt gct gca gaa ctc aac cat 1171  
 Val Ala Ala Ser Lys Glu Glu Asn Gly Val Ala Ala Glu Leu Asn His  
 345 350 355

gtg tgg att tca cca ggt gcg agc aat ccg atc aag gat cgc ctc ttc 1219  
 Val Trp Ile Ser Pro Gly Ala Ser Asn Pro Ile Lys Asp Arg Leu Phe  
 360 365 370

ccc ctg gac att ggt gaa ggc ttt tct ctc ctc ccc tgc agc ctt ggg 1267  
 Pro Leu Asp Ile Gly Glu Gly Phe Ser Leu Leu Pro Cys Ser Leu Gly  
 375 380 385

cga aac agt gtc caa tgc cct caa aaa ggc ctc tgc acc aga aga aaa 1315  
 Arg Asn Ser Val Gln Ser Pro Gln Lys Gly Leu Cys Thr Arg Arg Lys  
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acg cgc cct aga aac cct ttc aca act taattctgcg atcaccccg 1362  
 Thr Arg Pro Arg Asn Pro Phe Thr Thr  
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aga 1365

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 <213> Corynebacterium glutamicum

<400> 84  
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 35 40 45

Val Arg Asp His Glu Ala Thr Phe Phe Thr Ala Leu Asp Lys Asp Leu  
 50 55 60

Lys Val Ile Asp Pro Thr Gln Val Thr Val Ser Leu Asp Asp Ser Ser  
 65 70 75 80

Asn Tyr Arg Arg Thr Arg Leu Trp Leu Glu Ala Thr Met Arg Lys Thr  
 85 90 95

Pro Val Pro Leu Tyr Gln Glu Ser Leu Ser Val Ala Asp Gln Met Leu  
 100 105 110

Ala Asp Pro Leu Glu Tyr Gln Leu Ala Ala Val Arg Lys Thr Leu Ser  
 115 120 125

Ser Ala Asn Leu Arg Pro Arg Val Leu Ile Ala Asp Ala Val Gly Leu  
 130 135 140

Gly Lys Thr Leu Glu Met Gly Met Ile Leu Ala Glu Leu Ile Arg Arg  
 145 150 155 160

Gly Arg Gly Glu Arg Ile Leu Val Val Thr Pro Arg His Ile Met Glu  
 165 170 175

Gln Phe Gln Gln Glu Met Trp Thr Arg Phe Ala Ile Pro Leu Val Arg  
 180 185 190  
 Leu Asp Ser Val Gly Ile Gln Gln Val Arg Gln Lys Leu Pro Ala Ser  
 195 200 205  
 Arg Asn Pro Phe Thr Tyr Phe Pro Arg Val Ile Val Ser Met Asp Thr  
 210 215 220  
 Leu Lys Ser Pro Lys Tyr Arg Ala Gln Leu Glu Lys Val His Trp Asp  
 225 230 235 240  
 Ala Val Val Ile Asp Glu Ile His Asn Ala Thr Asn Ala Gly Thr Gln  
 245 250 255  
 Asn Asn Glu Leu Ala Gly Thr Leu Gly Pro Thr Ala Glu Ala Leu Ile  
 260 265 270  
 Leu Ala Ser Ala Thr Pro His Asn Gly Asp Pro Glu Ser Phe Lys Glu  
 275 280 285  
 Ile Leu Arg Leu Leu Asp Pro Thr Ala Val Met Pro Asp Gly Thr Ile  
 290 295 300  
 Asp Ala Glu Ala Ala Gln Arg Leu Ile Ile Arg Arg His Arg Asn Ser  
 305 310 315 320  
 Pro Glu Val Ser Gly Phe Val Gly Glu Lys Trp Ala Pro Arg Asn Glu  
 325 330 335  
 Pro Gln Asn Phe Leu Val Ala Ala Ser Lys Glu Glu Asn Gly Val Ala  
 340 345 350  
 Ala Glu Leu Asn His Val Trp Ile Ser Pro Gly Ala Ser Asn Pro Ile  
 355 360 365  
 Lys Asp Arg Leu Phe Pro Leu Asp Ile Gly Glu Gly Phe Ser Leu Leu  
 370 375 380  
 Pro Cys Ser Leu Gly Arg Asn Ser Val Gln Ser Pro Gln Lys Gly Leu  
 385 390 395 400  
 Cys Thr Arg Arg Lys Thr Arg Pro Arg Asn Pro Phe Thr Thr  
 405 410

&lt;210&gt; 85

&lt;211&gt; 982

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(982)

&lt;223&gt; PRXA01374

&lt;400&gt; 85

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Ala Leu Ser Ser Thr Asp Ser Leu Ser His Val Thr Ile Glu Val						
	10			15	20	
cga gat gaa att tgg ctg gtt act cac gtt act cgc tcc aca gat ggt						211
Arg Asp Glu Ile Trp Leu Val Thr His Val Thr Arg Ser Thr Asp Gly						
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ttt agg gtt aaa gct cgt ggt ctc tct gat tat gtg cgg gac cac gaa						259
Phe Arg Val Lys Ala Arg Gly Leu Ser Asp Tyr Val Arg Asp His Glu						
	40		45		50	
gct acg ttc ttc acc gca ctt gat aaa gat ttg aag gtc att gac cct						307
Ala Thr Phe Phe Thr Ala Leu Asp Lys Asp Leu Lys Val Ile Asp Pro						
	55		60		65	
acc cag gtc acc gtc agt ctt gat gat tcc tcc aat tac cgt cgc acc						355
Thr Gln Val Thr Val Ser Leu Asp Asp Ser Ser Asn Tyr Arg Arg Thr						
	70		75		80	85
cgc ctg tgg ttg gag gcc acc atg cgt aaa act ccg gta ccg ctc tat						403
Arg Leu Trp Leu Glu Ala Thr Met Arg Lys Thr Pro Val Pro Leu Tyr						
		90		95		100
caa gag tca ctt tcc gtg gca gat caa atg ctc gcc gat cca ctg gag						451
Gln Glu Ser Leu Ser Val Ala Asp Gln Met Leu Ala Asp Pro Leu Glu						
		105		110		115
tac caa tta gca gcc gtg cgc aaa acc ctc tct agt gct aac ttg cgc						499
Tyr Gln Leu Ala Ala Val Arg Lys Thr Leu Ser Ser Ala Asn Leu Arg						
	120		125		130	
ccc cgc gtg ctt att gct gat gcc gtg gga ctt ggc aaa acc cta gaa						547
Pro Arg Val Leu Ile Ala Asp Ala Val Gly Leu Gly Lys Thr Leu Glu						
	135		140		145	
atg ggc atg atc ttg gcg gaa ctt atc cgc cgt ggc cgt ggt gag cgc						595
Met Gly Met Ile Leu Ala Glu Leu Ile Arg Arg Gly Arg Gly Glu Arg						
	150		155		160	165
att ttg gta gtc acc ccg cgc cac att atg gag cag ttc cag cag gaa						643
Ile Leu Val Val Thr Pro Arg His Ile Met Glu Gln Phe Gln Gln Glu						
		170		175		180
atg tgg acc cgt ttt gcc atc ccg ctc gtt cgt cta gat tcc gtg ggc						691
Met Trp Thr Arg Phe Ala Ile Pro Leu Val Arg Leu Asp Ser Val Gly						
	185		190		195	
atc cag caa gtg cgc caa aaa ttg cca gca tca cgc aac cct ttt act						739
Ile Gln Gln Val Arg Gln Lys Leu Pro Ala Ser Arg Asn Pro Phe Thr						
	200		205		210	
tat ttc ccg cgc gtg att gtc tct atg gat act ttg aaa tct ccg aag						787
Tyr Phe Pro Arg Val Ile Val Ser Met Asp Thr Leu Lys Ser Pro Lys						
	215		220		225	
tac cgc gcg caa cta gaa aag gtg cac tgg gat gcg gtg gtt ata gat						835
Tyr Arg Ala Gln Leu Glu Lys Val His Trp Asp Ala Val Ile Asp						

230	235	240	245	
gaa atc cac aat gca acc aat gct ggc acc caa aat aat gag cta gcc				883
Glu Ile His Asn Ala Thr Asn Ala Gly Thr Gln Asn Asn Glu Leu Ala				
250		255	260	
cgc aca ctt gcg cct act gcc gag gct ctt att ttg gcc tct gcc acc				931
Arg Thr Leu Ala Pro Thr Ala Glu Ala Leu Ile Leu Ala Ser Ala Thr				
265		270	275	
ccg cac aat ggt gat cca gaa tcc ttt aag gag atc ttg cgt ttg ctt				979
Pro His Asn Gly Asp Pro Glu Ser Phe Lys Glu Ile Leu Arg Leu Leu				
280		285	290	
gat				982
Asp				

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 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 86  
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 35 40 45  
 Val Arg Asp His Glu Ala Thr Phe Phe Thr Ala Leu Asp Lys Asp Leu  
 50 55 60  
 Lys Val Ile Asp Pro Thr Gln Val Thr Val Ser Leu Asp Asp Ser Ser  
 65 70 75 80  
 Asn Tyr Arg Arg Thr Arg Leu Trp Leu Glu Ala Thr Met Arg Lys Thr  
 85 90 95  
 Pro Val Pro Leu Tyr Gln Glu Ser Leu Ser Val Ala Asp Gln Met Leu  
 100 105 110  
 Ala Asp Pro Leu Glu Tyr Gln Leu Ala Ala Val Arg Lys Thr Leu Ser  
 115 120 125  
 Ser Ala Asn Leu Arg Pro Arg Val Leu Ile Ala Asp Ala Val Gly Leu  
 130 135 140  
 Gly Lys Thr Leu Glu Met Gly Met Ile Leu Ala Glu Leu Ile Arg Arg  
 145 150 155 160  
 Gly Arg Gly Glu Arg Ile Leu Val Val Thr Pro Arg His Ile Met Glu  
 165 170 175  
 Gln Phe Gln Gln Glu Met Trp Thr Arg Phe Ala Ile Pro Leu Val Arg  
 180 185 190

Leu Asp Ser Val Gly Ile Gln Gln Val Arg Gln Lys Leu Pro Ala Ser  
 195 200 205  
 Arg Asn Pro Phe Thr Tyr Phe Pro Arg Val Ile Val Ser Met Asp Thr  
 210 215 220  
 Leu Lys Ser Pro Lys Tyr Arg Ala Gln Leu Glu Lys Val His Trp Asp  
 225 230 235 240  
 Ala Val Val Ile Asp Glu Ile His Asn Ala Thr Asn Ala Gly Thr Gln  
 245 250 255  
 Asn Asn Glu Leu Ala Arg Thr Leu Ala Pro Thr Ala Glu Ala Leu Ile  
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 Ile Leu Arg Leu Leu Asp  
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 <212> DNA  
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 <223> RXN00817

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 Leu Thr Thr Pro Asp  
 1 5

ttt gag agt gaa aag act caa gct atg agg ccc agc ttt ggt gaa gag 163  
 Phe Glu Ser Glu Lys Thr Gln Ala Met Arg Pro Ser Phe Gly Glu Glu  
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ctg gcc gca atc gtt tcc aaa cgt tac tcc gaa tcg acg ctc act cat 211  
 Leu Ala Ala Ile Val Ser Lys Arg Tyr Ser Glu Ser Thr Leu Thr His  
 25 30 35

atg gtg acg ttg ccc gca tcg aaa gct aaa tac gtc gat tgg ccg agt 259  
 Met Val Thr Leu Pro Ala Ser Lys Ala Lys Tyr Val Asp Trp Pro Ser  
 40 45 50

tgg gta cct gct agc ctg cgc gat gcg ttg gtg aat cgt ggt atc aat 307  
 Trp Val Pro Ala Ser Leu Arg Asp Ala Leu Val Asn Arg Gly Ile Asn  
 55 60 65

aag ctc ttt tcc cac cag gag cag acc gca cat ctg gcg tgg aat ggc 355  
 Lys Leu Phe Ser His Gln Glu Gln Thr Ala His Leu Ala Trp Asn Gly  
 70 75 80 85

cag cat gtg gtg gtt gcc acc ggt aca tct tcg gga aaa tct ttg ggt 403  
 Gln His Val Val Val Ala Thr Gly Thr Ser Ser Gly Lys Ser Leu Gly



	90	95	100	
tat cag ctg ccc att ttg tca gcg ctc ggc acg gat cct acc gcc tgt				451
Tyr Gln Leu Pro Ile Leu Ser Ala Leu Gly Thr Asp Pro Thr Ala Cys				
	105	110	115	
gcg ttg tat cta act ccc acc aag gct ttg gga tct gat cag cta acc				499
Ala Leu Tyr Leu Thr Pro Thr Lys Ala Leu Gly Ser Asp Gln Leu Thr				
	120	125	130	
tcc acg tcc acg ttg ctg cgc gac att ccg gat ttc cac ccg att aat				547
Ser Thr Ser Thr Leu Leu Arg Asp Ile Pro Asp Phe His Pro Ile Asn				
	135	140	145	
ccg gcg ccc tac gat ggc gat acc ccc tcc gag gcg cgg tcc gcc atc				595
Pro Ala Pro Tyr Asp Gly Asp Thr Pro Ser Glu Ala Arg Ser Gly Ile				
	150	155	160	
cgc gat ttg agt cgt ttt gtg ttc acc aat ccg gat atg gtg cat gcg				643
Arg Asp Leu Ser Arg Phe Val Phe Thr Asn Pro Asp Met Val His Ala				
	170	175	180	
tcg atg ctg gcg aat cat ccc cgc tgg gcc agg ttg ttg cgc cat ttg				691
Ser Met Leu Ala Asn His Pro Arg Trp Ala Arg Leu Leu Arg His Leu				
	185	190	195	
aag ttc atc gtg att gat gaa tgc cat gcc tac cgt ggt gtg ttt ggc				739
Lys Phe Ile Val Ile Asp Glu Cys His Ala Tyr Arg Gly Val Phe Gly				
	200	205	210	
gcg aac gtg tcg atg gtg ctt cgt cgt cta ctg cgc atc gcc gcg ttt				787
Ala Asn Val Ser Met Val Leu Arg Arg Leu Leu Arg Ile Ala Ala Phe				
	215	220	225	
tat gga tcc cac ccg acg gtc att ttg gcg tcc gcg acc agc tcc gat				835
Tyr Gly Ser His Pro Thr Val Ile Leu Ala Ser Ala Thr Ser Ser Asp				
	230	235	240	
ccg gaa att cat gct tcc aga ttg ttg ggc gcg ccg gtt aaa gca gtg				883
Pro Glu Ile His Ala Ser Arg Leu Leu Gly Ala Pro Val Lys Ala Val				
	250	255	260	
acg gaa gat ggc gcc ccg acg ggt gaa cgc acc gtt ttg ctg tgg gag				931
Thr Glu Asp Gly Ala Pro Thr Gly Glu Arg Thr Val Leu Leu Trp Glu				
	265	270	275	
ccc ggt ttc atc gaa ggc gcc gag ggc gag aac ggc gcg ccg gtg cgt				979
Pro Gly Phe Ile Glu Gly Ala Glu Gly Glu Asn Gly Ala Pro Val Arg				
	280	285	290	
cgc gca gcc agc acc gaa gca gca aac att atg gcc acg ctc att tcc				1027
Arg Ala Ala Ser Thr Glu Ala Ala Asn Ile Met Ala Thr Leu Ile Ser				
	295	300	305	
gag ggt gca cgc acg ttg acg ttc gtc cgt tca cgt cga caa gca gaa				1075
Glu Gly Ala Arg Thr Leu Thr Phe Val Arg Ser Arg Arg Gln Ala Glu				
	310	315	320	
atc gtt gcc ctg cgc gcg cag gaa gag ctc agc acg ctg ggc cgc ccc				1123
Ile Val Ala Leu Arg Ala Gln Glu Glu Leu Ser Thr Leu Gly Arg Pro				
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 Asp Phe Ala Arg Arg Val Ala Ser Tyr Arg Ala Gly Tyr Leu Ala Glu  
 345 350 355

gac cgc cgt agg ttg gag aga ttg ctt gac gac ggc acc ctc ctc ggt 1219  
 Asp Arg Arg Arg Leu Glu Arg Leu Leu Asp Asp Gly Thr Leu Leu Gly  
 360 365 370

gtt gct tcc acc aat gcg ctt gaa ctg ggc att gat gtc ggt gga ctg 1267  
 Val Ala Ser Thr Asn Ala Leu Glu Leu Gly Ile Asp Val Gly Gly Leu  
 375 380 385

gat gct gtg gtc acg gct ggt ttt cca gga act gtg gcg tcg ttt tgg 1315  
 Asp Ala Val Val Thr Ala Gly Phe Pro Gly Thr Val Ala Ser Phe Trp  
 390 395 400 405

cag cag gcg ggg cga gct ggt cgg cgt ggg cag ggt tcg ttg gtg gtg 1363  
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 410 415 420

ctt gtt gct cgt gat gag ccg atg gat acg tat ttg gtg cat cat ccg 1411  
 Leu Val Ala Arg Asp Glu Pro Met Asp Thr Tyr Leu Val His His Pro  
 425 430 435

gca gcc ctg ttg gag aag ccg gtt gag gct gcg gtg ttt gat ccg acg 1459  
 Ala Ala Leu Leu Glu Lys Pro Val Glu Ala Ala Val Phe Asp Pro Thr  
 440 445 450

aat ccg cat gtt att ccg ggt cat gtt tat tgc gct gcg gtg gaa aag 1507  
 Asn Pro His Val Ile Arg Gly His Val Tyr Cys Ala Ala Val Glu Lys  
 455 460 465

cct ctg aca gag gcg gag gtc gcg gcg ttt ggt gcc caa aag gtg gtg 1555  
 Pro Leu Thr Glu Ala Glu Val Ala Ala Phe Gly Ala Gln Lys Val Val  
 470 475 480 485

gag aag ctc gag att gaa ggg ctg ttg gcg aag cgt ccg cgt ggc tgg 1603  
 Glu Lys Leu Glu Ile Glu Gly Leu Leu Arg Lys Arg Pro Arg Gly Trp  
 490 495 500

ttt gcg gtg gaa aag ccc atg tca gag gat ccg gat gag ctg agt cct 1651  
 Phe Ala Val Glu Lys Pro Met Ser Glu Asp Pro Asp Glu Leu Ser Pro  
 505 510 515

gat tcg gca cac cag cag gtg agt ttg cgt ggt ggg tct ggt tcg gag 1699  
 Asp Ser Ala His Gln Gln Val Ser Leu Arg Gly Gly Ser Gly Ser Glu  
 520 525 530

ttc atg att gtt gat atc act gac ggc cgg ttg tta ggc acc atc gat 1747  
 Phe Met Ile Val Asp Ile Thr Asp Gly Arg Leu Leu Gly Thr Ile Asp  
 535 540 545

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 550 555 560 565

cag ggt gaa tcc ttt gtc att gat gag ttg gat ttg gag gag aat ctg 1843  
 Gln Gly Glu Ser Phe Val Ile Asp Glu Leu Asp Leu Glu Glu Asn Leu  
 570 575 580

gca ctg gcc agg cct gag ctg cct gat tac acc acc tat gcc aga agt 1891  
 Ala Leu Ala Arg Pro Glu Leu Pro Asp Tyr Thr Thr Tyr Ala Arg Ser  
 585 590 595

gac acg gac atc agg att acc tct gcc ccg ttg gag gac gag gtt ttt 1939  
 Asp Thr Asp Ile Arg Ile Thr Ser Ala Pro Leu Glu Asp Glu Val Phe  
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 615 620 625

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 630 635 640 645

gat gcg act ccg ttg tat ctt cct cct caa att ctt cag act cgt gcg 2083  
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gtg gcg tac acg att gat ccg ttg gcg ttg gaa gcg atg ggc att ccc 2131  
 Val Ala Tyr Thr Ile Asp Pro Leu Ala Leu Glu Ala Met Gly Ile Pro  
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gcc gct gat att ccc ggt gct ctt cac gca gcg gag cat gcg gcg att 2179  
 Ala Ala Asp Ile Pro Gly Ala Leu His Ala Ala Glu His Ala Ala Ile  
 680 685 690

ggt atg ttg ccg ctg ctt gcg acg tgt gat cgt tgg gat atc ggc ggc 2227  
 Gly Met Leu Pro Leu Leu Ala Thr Cys Asp Arg Trp Asp Ile Gly Gly  
 695 700 705

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 Val Ser Thr Ala Leu His Ala Asp Thr Gly Tyr Pro Thr Val Phe Val  
 710 715 720 725

tat gac ggt atg gac ggc gga gct ggt ttt gcg gat act ggt ttt cga 2323  
 Tyr Asp Gly Met Asp Gly Gly Ala Gly Phe Ala Asp Thr Gly Phe Arg  
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&lt;400&gt; 88

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 Gly Lys Ser Leu Gly Tyr Gln Leu Pro Ile Leu Ser Ala Leu Gly Thr  
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 Asp Met Val His Ala Ser Met Leu Ala Asn His Pro Arg Trp Ala Arg  
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 Ala Thr Ser Ser Asp Pro Glu Ile His Ala Ser Arg Leu Leu Gly Ala  
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 Pro Val Lys Ala Val Thr Glu Asp Gly Ala Pro Thr Gly Glu Arg Thr  
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 Val Phe Asp Pro Thr Asn Pro His Val Ile Arg Gly His Val Tyr Cys  
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 Gly Ser Gly Ser Glu Phe Met Ile Val Asp Ile Thr Asp Gly Arg Leu  
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 580 585 590  
 Thr Tyr Ala Arg Ser Asp Thr Asp Ile Arg Ile Thr Ser Ala Pro Leu  
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<223> FRXA00809
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atg gtg acg ttg ccc gca tgc aaa gct aaa tac gtc gat tgg ccg agt 259  
Met Val Thr Leu Pro Ala Ser Lys Ala Lys Tyr Val Asp Trp Pro Ser  
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tgg gta cct gct agc ctg cgc gat gcg ttg gtg aat cgt ggt atc aat 307  
 Trp Val Pro Ala Ser Leu Arg Asp Ala Leu Val Asn Arg Gly Ile Asn  
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aag ctc ttt tcc cac cag gag cag acc gca cat ctg gcg tgg aat ggc 355  
 Lys Leu Phe Ser His Gln Glu Thr Ala His Leu Ala Trp Asn Gly  
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cag cat gtg gtg gtt gcc acc ggt aca tct tcg gga aaa tct ttg ggt 403  
 Gln His Val Val Val Ala Thr Gly Thr Ser Ser Gly Lys Ser Leu Gly  
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gcg ttg tat cta act ccc acc aag gct ttg gga tct gat cag cta acc 499  
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Val Asp Trp Pro Ser Trp Val Pro Ala Ser Leu Arg Asp Ala Leu Val  
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Asn Arg Gly Ile Asn Lys Leu Phe Ser His Gln Glu Thr Ala His  
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Leu Ala Trp Asn Gly Gln His Val Val Val Ala Thr Gly Thr Ser Ser  
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Gly Lys Ser Leu Gly Tyr Gln Leu Pro Ile Leu Ser Ala Leu Gly Thr  
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Asp Pro Thr Ala Cys Ala Leu Tyr Leu Thr Pro Thr Lys Ala Leu Gly  
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Ser Asp Gln Leu Thr Ser Thr Ser Thr Leu Leu Arg Asp Ile Pro Asp  
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 Asp Pro Glu Ile His Ala Ser Arg Leu Leu Gly Ala Pro Val Lys Ala  
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Leu Asp Ala Val Val Thr Ala Gly Phe Pro Gly Thr Val Ala Ser Phe	
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Trp Gln Gln Ala Gly Arg Ala Gly Arg Gly Gln Gly Ser Leu Val	
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Val Leu Val Ala Arg Asp Glu Pro Met Asp Thr Tyr Leu Val His His	
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Pro Ala Ala Leu Leu Glu Lys Pro Val Glu Ala Val Phe Asp Pro	
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Thr Asn Pro His Val Ile Arg Gly His Val Tyr Cys Ala Ala Val Glu	
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Lys Pro Leu Thr Glu Ala Glu Val Ala Ala Phe Gly Ala Gln Lys Val	
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Val Glu Lys Leu Glu Ile Glu Gly Leu Leu Arg Lys Arg Pro Arg Gly	
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Trp Phe Ala Val Glu Lys Pro Met Ser Glu Asp Pro Asp Glu Leu Ser	
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Pro Asp Ser Ala His Gln Gln Val Ser Leu Arg Gly Gly Ser Gly Ser	
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His Gln Gly Glu Ser Phe Val Ile Asp Glu Leu Asp Leu Glu Glu Asn	
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Phe Asp Ala Gly Gly Gly Leu Trp Val Ala Asn Val Glu Val Gln Val	

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Thr Asp Arg Val Thr Gly Tyr Val Thr Arg Leu Ser Asp Gly Thr Thr	405	410	415	
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Leu Asp Ala Thr Pro Leu Tyr Leu Pro Pro Gln Ile Leu Gln Thr Arg	420	425	430	
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Ala Val Ala Tyr Thr Ile Asp Pro Leu Ala Leu Glu Ala Met Gly Ile	435	440	445	
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Pro Ala Ala Asp Ile Pro Gly Ala Leu His Ala Ala Glu His Ala Ala	450	455	460	
att ggt atg ttg cgc ctg ctt gcg acg tgt gat cgt tgg gat atc ggc				1440
Ile Gly Met Leu Pro Leu Leu Ala Thr Cys Asp Arg Trp Asp Ile Gly	465	470	475	480
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Gly Val Ser Thr Ala Leu His Ala Asp Thr Gly Tyr Pro Thr Val Phe	485	490	495	
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Val Tyr Asp Gly Met Asp Gly Gly Ala Gly Phe Ala Asp Thr Gly Phe	500	505	510	
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Arg Arg Phe Ala Gln Trp Ile Glu Ala Thr Phe Glu Val Val Arg Ser	515	520	525	
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Cys Ser Cys Glu Ser Gly Cys Pro Ser Cys Val Gln Ser Pro Lys Cys	530	535	540	
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Gly Asn Gly Asn Asn Pro Leu Asp Lys Ala Gly Ala Ile Lys Leu Leu	545	550	555	560
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Met Ala Lys Ser Ile  
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Ala Ser Pro Thr Pro Val Gln Glu Gly Thr Trp Glu Ala Val Ser Lys				
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Gly Lys Asn Ala Leu Val Val Ala Pro Thr Gly Ser Gly Lys Thr Leu				
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gct gcg ttt ttg tgg gcg tta gat tcc ctc act gaa caa aca ggt caa				307
Ala Ala Phe Leu Trp Ala Leu Asp Ser Leu Thr Glu Gln Thr Gly Gln				
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cag gtt tta gac acg gga aca ccg gtg cct gtt cgt ggt ggg aaa gtg				355
Gln Val Leu Asp Thr Gly Thr Pro Val Pro Val Arg Gly Gly Lys Val				
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Lys Val Leu Tyr Ile Ser Pro Leu Lys Ala Leu Gly Val Asp Val Glu				
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Asn Asn Leu Arg Ala Pro Leu Thr Gly Ile Ala Arg Thr Ala Ser Arg				
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atg ggt ttg gat gtg ccc aat atc act gtg gcg gtt cgt tcg ggt gat				499
Met Gly Leu Asp Val Pro Asn Ile Thr Val Ala Val Arg Ser Gly Asp				
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Thr Pro Ser Ala Glu Arg Ala Arg Gln Val Arg Lys Pro Pro Asp Ile				
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Gly Ala Thr Leu Ser Asp Val Asp Val Val Ile Ile Asp Glu Ile His				
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gcc atg gcc gga acc aaa ccg gga gtg cat ctg gcg ttg acg ctg gag				691
Ala Met Ala Gly Thr Lys Arg Gly Val His Leu Ala Leu Thr Leu Glu				
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Arg Leu Glu Lys Leu Val Gly Arg Pro Val Gln Arg Val Gly Leu Ser				
	200	205	210	
gca acg gtg cgt cct ttg gaa acg gtg gcg ggt ttc ttg gcc ggt gcc				787
Ala Thr Val Arg Pro Leu Glu Thr Val Ala Gly Phe Leu Gly Gly Gly				
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Arg Pro Val Glu Ile Val Ala Pro Pro Ala Glu Lys Lys Trp Asp Leu				
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act gtc act gtg ccg gtg gaa gac atg tcg gat ttg ccg gtt cag gag				883
Thr Val Thr Val Pro Val Glu Asp Met Ser Asp Leu Pro Val Gln Glu				
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 Asn Ala Leu Asp Val Leu Ala Gln Gln Thr Val Ala Ala Val Ser Ile  
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 Lys Asp Val Gln Val Asp Glu Trp Tyr Glu Thr Ile Arg Lys Ala Tyr  
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ccg tac cgg gat ttg gcg cgc gaa gtc ttc gat tcc gtc atc gac ctg 1651  
 Pro Tyr Arg Asp Leu Ala Arg Glu Val Phe Asp Ser Val Ile Asp Leu  
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gtc agc ggt gtg tat ccc tcc aca gat ttt gcc gag ctg aag cca cgt 1699  
 Val Ser Gly Val Tyr Pro Ser Thr Asp Phe Ala Glu Leu Lys Pro Arg  
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gtg gtg tac gac cgg gtt tca gcc gtg ctg gag gcc cgg cca gga tcc 1747  
 Val Val Tyr Asp Arg Val Ser Gly Val Leu Glu Gly Arg Pro Gly Ser  
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caa cgc gta gca gtg acc agt gcc gga aca att ccc gat cga gga atg 1795  
 Gln Arg Val Ala Val Thr Ser Gly Gly Thr Ile Pro Asp Arg Gly Met  
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ttc gga gtc ttc ctc gtc gcc gat ggt ccc cgg cgc gtc gcc gag ctc 1843  
 Phe Gly Val Phe Leu Val Gly Asp Gly Pro Arg Arg Val Gly Glu Leu  
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gat gag gaa atg gtc tac gaa tcc cgc gtg gcc gat gtg ttt acg ctc 1891  
 Asp Glu Glu Met Val Tyr Glu Ser Arg Val Gly Asp Val Phe Thr Leu  
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ggg cgc tcg agt tgg cgg att gaa gag atc acc cgc gac cag gta ctg 1939  
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gtc act ccc cgc ccg ggt cac acg ggt cgg ctg cct ttt tgg acg gcc 1987  
 Val Thr Pro Ala Pro Gly His Thr Gly Arg Leu Pro Phe Trp Thr Gly  
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gat gcc gca gcc cgg ccc gct gag ctg ggt aaa gct tta gcc gct ttt 2035  
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cga cgc tcg acc ctc acc gat cca tcc agc tcc gcc ttg gaa gcc tgg 2083  
 Arg Arg Ser Thr Leu Thr Asp Pro Ser Ser Ser Gly Leu Glu Gly Trp  
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gcg cac gac aac ctg atc gcc ttt tta cag gag cag gaa gaa tcc acc 2131  
 Ala His Asp Asn Leu Ile Ala Phe Leu Gln Glu Gln Glu Glu Ser Thr  
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 Glu Leu Gly Asp Trp Arg Ile Val Leu His Thr Pro Tyr Gly Arg Gly  
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 710 715 720 725

acc gcc atg gat gcg caa gcc gtg gca ggt gat gat gcc att gtg ctt 2323  
 Thr Gly Met Asp Ala Gln Ala Val Ala Gly Asp Asp Gly Ile Val Leu  
 730 735 740

cgg ttg ccg gaa ggg gat gaa gat ccc agc gca cgc ttg ttt atg ttt 2371

Arg Leu Pro Glu Gly Asp Glu Asp Pro Ser Ala Ala Leu Phe Met Phe	
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Glu Ala Glu Glu Ile Glu Thr Leu Val Thr Glu Gln Val Gly Asn Ser	
760 765 770	
gcg ctg ttt gcc agc agg ttc cgt gaa tgc gcc gcg agg gcc cta ttg	2467
Ala Leu Phe Ala Ser Arg Phe Arg Glu Cys Ala Ala Arg Ala Leu Leu	
775 780 785	
ctg ccg aga cga aac ccc gcc aag cgc gca ccg ctg tgg cag caa cga	2515
Leu Pro Arg Arg Asn Pro Gly Lys Arg Ala Pro Leu Trp Gln Gln Arg	
790 795 800 805	
caa cga gca gca cag ctt ctt gat gtg gcc aga aag tac ccg agt ttc	2563
Gln Arg Ala Ala Gln Leu Leu Asp Val Ala Arg Lys Tyr Pro Ser Phe	
810 815 820	
ccg atc att ttg gaa aca gtg cgc gaa tgt ctt caa gat gtt tac gat	2611
Pro Ile Ile Leu Glu Thr Val Arg Glu Cys Leu Gln Asp Val Tyr Asp	
825 830 835	
ctg ccc gct ctg aag aat ctc att gag gat cta cag ctg cgg aag gta	2659
Leu Pro Ala Leu Lys Asn Leu Ile Glu Asp Leu Gln Leu Arg Lys Val	
840 845 850	
aga atc gcg gaa gtc acc acc cag cag ccc agt cct ttt gcc tcc gca	2707
Arg Ile Ala Glu Val Thr Thr Gln Gln Pro Ser Pro Phe Ala Ser Ala	
855 860 865	
ttg ctg ttc aat tac acc ggt gca ttc atg tac gaa ggc gac agc ccg	2755
Leu Leu Phe Asn Tyr Thr Gly Ala Phe Met Tyr Glu Gly Asp Ser Pro	
870 875 880 885	
ctc gca gag aaa cgt gcc gca gcg ttg gcc ctg gat ccg gca ctg ttg	2803
Leu Ala Glu Lys Arg Ala Ala Leu Ala Leu Asp Pro Ala Leu Leu	
890 895 900	
gcg aaa ttg ctg ggt gag gtg gag ctt cga caa tta ctg gat ccc gac	2851
Ala Lys Leu Leu Gly Glu Val Glu Leu Arg Gln Leu Leu Asp Pro Asp	
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Ile Ile Ala Glu Val His Gln Gln Leu Arg Arg Gln Gly Asp Arg Ala	
920 925 930	
gcg aga aac aat gaa gaa ctc gca gat tct ttg agg att tta gga ccg	2947
Ala Arg Asn Asn Glu Glu Leu Ala Asp Ser Leu Arg Ile Leu Gly Pro	
935 940 945	
att cct ttg gat gaa ttg gcc gaa cac atc acc ttt gaa aac cca gac	2995
Ile Pro Leu Asp Glu Leu Gly Glu His Ile Thr Phe Glu Asn Pro Asp	
950 955 960 965	
ctg gag gat cga gca atg act gtt cgg atc aac ggt cgg gaa cat tta	3043
Leu Glu Asp Arg Ala Met Thr Val Arg Ile Asn Gly Arg Glu His Leu	
970 975 980	
gcg cag gtc ttg gat gca cct ttg ctt cga gat gcc tta ggt gtt ccc	3091
Ala Gln Val Leu Asp Ala Pro Leu Leu Arg Asp Ala Leu Gly Val Pro	



985	990	995	
gta ccg cct ggt gtg cct gcg cag gta gaa acc att acg gat gcg ttg			3139
Val Pro Pro Gly Val Pro Ala Gln Val Glu Thr Ile Thr Asp Ala Leu			
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gaa cag tta gtc aac agg tgg gtt cgt acc aga ggg cca ttt act gcg			3187
Glu Gln Leu Val Asn Arg Trp Val Arg Thr Arg Gly Pro Phe Thr Ala			
1015	1020	1025	
aat gat ttg gca gaa gcc ttt gga ctg ggc atc gcc acg gcg atc acc			3235
Asn Asp Leu Ala Glu Ala Phe Gly Leu Gly Ile Ala Thr Ala Ile Thr			
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gcc ctt caa agc gca cct gtg att gaa ggc cgc tac cga caa ggc gtg			3283
Ala Leu Gln Ser Ala Pro Val Ile Glu Gly Arg Tyr Arg Gln Gly Val			
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gac gtg cag gaa tac tgt gcg aca gaa gtg ttg tgc atc ata agg cga			3331
Asp Val Gln Glu Tyr Cys Ala Thr Glu Val Leu Ser Ile Ile Arg Arg			
1065	1070	1075	
cgc agc ctc gca gca gcg agg aaa caa acc agg ccg gta tgc caa tca			3379
Arg Ser Leu Ala Ala Ala Arg Lys Gln Thr Arg Pro Val Ser Gln Ser			
1080	1085	1090	
gcc ttt gcg cga ttc ctg ctt gat tgg caa cag atc gca ccg gtg ggc			3427
Ala Phe Ala Arg Phe Leu Leu Asp Trp Gln Gln Ile Ala Pro Val Gly			
1095	1100	1105	
gcc aca cct gaa ctt cga ggc gtt gat ggc acc tac aca gtc att gaa			3475
Ala Thr Pro Glu Leu Arg Gly Val Asp Gly Tyr Thr Val Ile Glu			
1110	1115	1120	1125
caa ctc gcc ggt gta cgt ctt ccc gcc agt gcg tgg gaa gat ctc gtg			3523
Gln Leu Ala Gly Val Arg Leu Pro Ala Ser Ala Trp Glu Asp Leu Val			
1130	1135	1140	
ttg ccg cgc cgg gtt gcc gac tat tca ccg atc cat ctc gat gag ctg			3571
Leu Pro Arg Arg Val Ala Asp Tyr Ser Pro Ile His Leu Asp Glu Leu			
1145	1150	1155	
acc tcc aat ggg gaa gtc ctc atc gtg gga gcg ggc caa gcc gga agc			3619
Thr Ser Asn Gly Glu Val Leu Ile Val Gly Ala Gly Gln Ala Gly Ser			
1160	1165	1170	
cgc gat ccg tgg att agc ttg ctg ccc gcg gat tat gcg gcg cag ttg			3667
Arg Asp Pro Trp Ile Ser Leu Leu Pro Val Asp Tyr Ala Ala Gln Leu			
1175	1180	1185	
gtg ggg gag gcg tgc aca agc atg agc cca ttg cag gac gcc gtg ctt			3715
Val Gly Glu Ala Ser Thr Ser Met Ser Pro Leu Gln Asp Ala Val Leu			
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gac cag ctg cgt gcg gga ggc gcc ttc ctg ttt tct gac att ctc gaa			3763
Asp Gln Leu Arg Ala Gly Gly Ala Phe Leu Phe Ser Asp Ile Leu Glu			
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gag aat ttc ggc tac acc aca gcc cag ctg caa gaa gcg atg tgg ggg			3811
Glu Asn Phe Gly Tyr Thr Thr Ala Gln Leu Gln Glu Ala Met Trp Gly			
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gcg cgc cta gcg tgg gga acc acg gcg cat cgg gcg aaa cgt cga cca 3907  
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gcg aga tcc cgg ctg cgc acc cgc acc agc ttc gcg agc gac gtg ccc 3955  
 Ala Arg Ser Arg Leu Arg Thr Arg Thr Ser Phe Ala Ser Asp Val Pro  
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cca gac atg cgc gga cga tgg acg ctg tcc gtg caa ccc gcc gac gcc 4003  
 Pro Asp Met Arg Gly Arg Trp Thr Leu Ser Val Gln Pro Ala Asp Ala  
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acc agc cgc tcc gtc gca cac ggc gaa ggc tgg ctc gac cgc tac gcc 4051  
 Thr Ser Arg Ser Val Ala His Gly Glu Gly Trp Leu Asp Arg Tyr Gly  
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gtg ctc acc cgc ggg agc gtc gtc gcc gaa gac atc gtc gga gcc ttc 4099  
 Val Leu Thr Arg Gly Ser Val Val Ala Glu Asp Ile Val Gly Gly Phe  
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gcc ctg gcc tac aaa gtg ctc tcc ggc ttc gaa gaa agc gcc aaa gcg 4147  
 Ala Leu Ala Tyr Lys Val Leu Ser Gly Phe Glu Glu Ser Gly Lys Ala  
 1335 1340 1345

atg cgc ggc tac ttc atc gaa ggg ctc ggc gcc gcg caa ttc tcc acg 4195  
 Met Arg Gly Tyr Phe Ile Glu Gly Leu Gly Ala Ala Gln Phe Ser Thr  
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ccc gcc atc atc gac cgc ctc cgc ggc cac gac gat tcc ccc gac gtc 4243  
 Pro Ala Ile Ile Asp Arg Leu Arg Gly His Asp Asp Ser Pro Asp Val  
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gaa ggc tgg ccc tcc ggc gcc acc gac cca gac gtc tac ctc ata gcc 4291  
 Glu Gly Trp Pro Ser Gly Ala Thr Asp Pro Asp Val Tyr Leu Ile Ala  
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gcc gcc gac ccc gca aac ccc tac ggc gcc gca ctt ccc tgg cct gag 4339  
 Ala Ala Asp Pro Ala Asn Pro Tyr Gly Ala Ala Leu Pro Trp Pro Glu  
 1400 1405 1410

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 Gln Gly Pro Ser Arg Ala Ala Gly Ala Met Val Val Leu Cys Asp Gly  
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ctc ctc ctc gcc cac ctc acc cgc ggc ggg cgc acc ctc acc gtg ttc 4435  
 Leu Leu Leu Ala His Leu Thr Arg Gly Gly Arg Thr Leu Thr Val Phe  
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tcc gac aat atc ccc aaa atc gcg aca gcc cta atc aca tac gaa agg 4483  
 Ser Asp Asn Ile Pro Lys Ile Ala Thr Ala Leu Ile Thr Tyr Glu Arg  
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ctc acg gta gaa aaa atc aac ggc gac aac gtc ttc gac tcc cca ctc 4531  
 Leu Thr Val Glu Lys Ile Asn Gly Asp Asn Val Phe Asp Ser Pro Leu  
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 Arg Phe Arg Pro Pro Val Ala Arg Glu Thr Pro Ser Asp Thr Leu Pro  
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agg 4683

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Glu Ala Val Ser Lys Gly Lys Asn Ala Leu Val Val Ala Pro Thr Gly  
 35 40 45

Ser Gly Lys Thr Leu Ala Ala Phe Leu Trp Ala Leu Asp Ser Leu Thr  
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Glu Gln Thr Gly Gln Gln Val Leu Asp Thr Gly Thr Pro Val Pro Val  
 65 70 75 80

Arg Gly Gly Lys Val Lys Val Leu Tyr Ile Ser Pro Leu Lys Ala Leu  
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Gly Val Asp Val Glu Asn Asn Leu Arg Ala Pro Leu Thr Gly Ile Ala  
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Arg Thr Ala Ser Arg Met Gly Leu Asp Val Pro Asn Ile Thr Val Ala  
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Val Arg Ser Gly Asp Thr Pro Ser Ala Glu Arg Ala Arg Gln Val Arg  
 130 135 140

Lys Pro Pro Asp Ile Leu Ile Thr Thr Pro Glu Ser Ala Tyr Leu Met  
 145 150 155 160

Leu Thr Ser Lys Ala Gly Ala Thr Leu Ser Asp Val Asp Val Val Ile  
 165 170 175

Ile Asp Glu Ile His Ala Met Ala Gly Thr Lys Arg Gly Val His Leu  
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Ala Leu Thr Leu Glu Arg Leu Glu Lys Leu Val Gly Arg Pro Val Gln  
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Arg Val Gly Leu Ser Ala Thr Val Arg Pro Leu Glu Thr Val Ala Gly

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Lys Lys Trp Asp Leu Thr Val Thr Val	Pro Val Glu Asp Met Ser Asp	
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Asp Pro Leu Gly Ile Thr Gly Glu Ser Ala Leu Pro Thr Gln Gly Ser		
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Ile Trp Pro His Ile Glu Gln Gln Val Tyr Asn Gln Val Met Ser Ala		
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Lys Ser Thr Ile Val Phe Val Asn Ser Arg Arg Ser Ala Glu Arg Leu		
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Thr Ser Arg Leu Asn Glu Ile Trp Ala Met Glu His Asp Pro Glu Ser		
325	330	335
Leu Ser Pro Gln Leu Arg Arg Asp Pro Ala Gln Ile Met Ser Ser Ala		
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Asp Val Ala Gly Lys Ala Pro Gln Val Ile Ala Arg Ala His His Gly		
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Ser Val Ser Lys Asp Glu Arg Ala Thr Thr Glu Thr Met Leu Lys Glu		
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Gly Arg Leu Arg Ala Val Ile Ser Thr Ser Ser Leu Glu Leu Gly Ile		
385	390	395 400
Asp Met Gly Ala Val Asp Leu Val Ile Gln Val Glu Ser Pro Pro Ser		
405	410	415
Val Ala Ser Gly Leu Gln Arg Val Gly Arg Ala Gly His Thr Val Gly		
420	425	430
Ala Thr Ser Ile Gly Ser Phe Tyr Pro Lys His Arg Ser Asp Leu Val		
435	440	445
Gln Thr Ala Val Thr Val Gln Arg Met Lys Glu Gly Leu Ile Glu Glu		
450	455	460
Ile His Val Pro Lys Asn Ala Leu Asp Val Leu Ala Gln Gln Thr Val		
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Ala Ala Val Ser Ile Lys Asp Val Gln Val Asp Glu Trp Tyr Glu Thr		
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Ile Arg Lys Ala Tyr Pro Tyr Arg Asp Leu Ala Arg Glu Val Phe Asp		
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Ser Val Ile Asp Leu Val Ser Gly Val Tyr Pro Ser Thr Asp Phe Ala		
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Glu Leu Lys Pro Arg Val Val Tyr Asp Arg Val Ser Gly Val Leu Glu		
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Gly Arg Pro Gly Ser Gln Arg Val Ala Val Thr Ser Gly Gly Thr Ile  
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 Pro Asp Arg Gly Met Phe Gly Val Phe Leu Val Gly Asp Gly Pro Arg  
 565 570 575  
 Arg Val Gly Glu Leu Asp Glu Glu Met Val Tyr Glu Ser Arg Val Gly  
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 595 600 605  
 Arg Asp Gln Val Leu Val Thr Pro Ala Pro Gly His Thr Gly Arg Leu  
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 Pro Phe Trp Thr Gly Asp Ala Ala Gly Arg Pro Ala Glu Leu Gly Lys  
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 Ala Leu Gly Ala Phe Arg Arg Ser Thr Leu Thr Asp Pro Ser Ser Ser  
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 Gly Leu Glu Gly Trp Ala His Asp Asn Leu Ile Ala Phe Leu Gln Glu  
 660 665 670  
 Gln Glu Glu Ser Thr Gly Val Leu Pro Asp Glu Lys Thr Leu Val Leu  
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 690 695 700  
 Pro Tyr Gly Arg Gly Val Asn Ala Ala Trp Ala Leu Ala Val Gly Ala  
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 725 730 735  
 Asp Gly Ile Val Leu Arg Leu Pro Glu Gly Asp Glu Asp Pro Ser Ala  
 740 745 750  
 Ala Leu Phe Met Phe Glu Ala Glu Glu Ile Glu Thr Leu Val Thr Glu  
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 Gln Val Gly Asn Ser Ala Leu Phe Ala Ser Arg Phe Arg Glu Cys Ala  
 770 775 780  
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 785 790 795 800  
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 805 810 815  
 Lys Tyr Pro Ser Phe Pro Ile Ile Leu Glu Thr Val Arg Glu Cys Leu  
 820 825 830  
 Gln Asp Val Tyr Asp Leu Pro Ala Leu Lys Asn Leu Ile Glu Asp Leu  
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 Gln Leu Arg Lys Val Arg Ile Ala Glu Val Thr Thr Gln Gln Pro Ser  
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Pro Phe Ala Ser Ala Leu Leu Phe Asn Tyr Thr Gly Ala Phe Met Tyr  
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 Glu Gly Asp Ser Pro Leu Ala Glu Lys Arg Ala Ala Ala Leu Ala Leu  
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 Leu Leu Asp Pro Asp Ile Ile Ala Glu Val His Gln Gln Leu Arg Arg  
 915 920 925  
 Gln Gly Asp Arg Ala Ala Arg Asn Asn Glu Glu Leu Ala Asp Ser Leu  
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 Arg Ile Leu Gly Pro Ile Pro Leu Asp Glu Leu Gly Glu His Ile Thr  
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 Phe Glu Asn Pro Asp Leu Glu Asp Arg Ala Met Thr Val Arg Ile Asn  
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 Gly Arg Glu His Leu Ala Gln Val Leu Asp Ala Pro Leu Leu Arg Asp  
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 Ala Leu Gly Val Pro Val Pro Gly Val Pro Ala Gln Val Glu Thr  
 995 1000 1005  
 Ile Thr Asp Ala Leu Glu Gln Leu Val Asn Arg Trp Val Arg Thr Arg  
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 Pro Val Ser Gln Ser Ala Phe Ala Arg Phe Leu Leu Asp Trp Gln Gln  
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 Tyr Thr Val Ile Glu Gln Leu Ala Gly Val Arg Leu Pro Ala Ser Ala  
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 Trp Glu Asp Leu Val Leu Pro Arg Arg Val Ala Asp Tyr Ser Pro Ile  
 1140 1145 1150  
 His Leu Asp Glu Leu Thr Ser Asn Gly Glu Val Leu Ile Val Gly Ala  
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 Gly Gln Ala Gly Ser Arg Asp Pro Trp Ile Ser Leu Leu Pro Val Asp  
 1170 1175 1180  
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1185	1190	1195	1200
Gln Asp Ala Val Leu Asp Gln Leu Arg Ala Gly Gly Ala Phe Leu Phe	1205	1210	1215
Ser Asp Ile Leu Glu Glu Asn Phe Gly Tyr Thr Thr Ala Gln Leu Gln	1220	1225	1230
Glu Ala Met Trp Gly Leu Val Glu Ala Gly Leu Val Ser Pro Asp Ser	1235	1240	1245
Phe Ala Pro Ile Arg Ala Arg Leu Ala Ser Gly Thr Thr Ala His Arg	1250	1255	1260
Ala Lys Arg Arg Pro Ala Arg Ser Arg Leu Arg Thr Arg Thr Ser Phe	1265	1270	1275
Ala Ser Asp Val Pro Pro Asp Met Arg Gly Arg Trp Thr Leu Ser Val	1285	1290	1295
Gln Pro Ala Asp Ala Thr Ser Arg Ser Val Ala His Gly Glu Gly Trp	1300	1305	1310
Leu Asp Arg Tyr Gly Val Leu Thr Arg Gly Ser Val Val Ala Glu Asp	1315	1320	1325
Ile Val Gly Gly Phe Ala Leu Ala Tyr Lys Val Leu Ser Gly Phe Glu	1330	1335	1340
Glu Ser Gly Lys Ala Met Arg Gly Tyr Phe Ile Glu Gly Leu Gly Ala	1345	1350	1355
Ala Gln Phe Ser Thr Pro Ala Ile Ile Asp Arg Leu Arg Gly His Asp	1365	1370	1375
Asp Ser Pro Asp Val Glu Gly Trp Pro Ser Gly Ala Thr Asp Pro Asp	1380	1385	1390
Val Tyr Leu Ile Ala Ala Ala Asp Pro Ala Asn Pro Tyr Gly Ala Ala	1395	1400	1405
Leu Pro Trp Pro Glu Gln Gly Pro Ser Arg Ala Ala Gly Ala Met Val	1410	1415	1420
Val Leu Cys Asp Gly Leu Leu Leu Ala His Leu Thr Arg Gly Gly Arg	1425	1430	1435
Thr Leu Thr Val Phe Ser Asp Asn Ile Pro Lys Ile Ala Thr Ala Leu	1445	1450	1455
Ile Thr Tyr Glu Arg Leu Thr Val Glu Lys Ile Asn Gly Asp Asn Val	1460	1465	1470
Phe Asp Ser Pro Leu Leu Glu Gln Phe Arg Lys His Gly Ala Thr Ile	1475	1480	1485
Thr Pro Lys Gly Met Arg Phe Arg Pro Pro Val Ala Arg Glu Thr Pro	1490	1495	1500
Ser Asp Thr Leu Pro Thr Arg Thr Phe Arg Gly Phe Gly Arg Arg	1505	1510	1515
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 Leu Ser Arg Phe Arg Pro Gln Val Ala Glu Trp Phe Arg Asp Val Phe  
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 Ala Ser Pro Thr Pro Val Gln Glu Gly Thr Trp Glu Ala Val Ser Lys  
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 Gly Lys Asn Ala Leu Val Val Ala Pro Thr Gly Ser Gly Lys Thr Leu  
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 gct gcg ttt ttg tgg gcg tta gat tcc ctc act gaa caa aca ggt caa 307  
 Ala Ala Phe Leu Trp Ala Leu Asp Ser Leu Thr Glu Gln Thr Gly Gln  
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 Gln Val Leu Asp Thr Gly Thr Pro Val Pro Val Arg Gly Gly Lys Val  
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 Lys Val Leu Tyr Ile Ser Pro Leu Lys Ala Leu Gly Val Asp Val Glu  
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 Asn Asn Leu Arg Ala Pro Leu Thr Gly Ile Ala Arg Thr Ala Ser Arg  
 105 110 115  
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 Met Gly Leu Asp Val Pro Asn Ile Thr Val Ala Val Arg Ser Gly Asp  
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 Thr Pro Ser Ala Glu Arg Ala Arg Gln Val Arg Lys Pro Ala His Ile  
 135 140 145  
 ttg atc acc act ccg gag tcg gcg tat ttg atg ttg acc tca aaa gcg 595  
 Leu Ile Thr Thr Pro Glu Ser Ala Tyr Leu Met Leu Thr Ser Lys Ala  
 150 155 160 165



ggg gcg acc ctt tcg gat gtt gat gtg gtg atc atc gat gaa atc cac 643  
 Gly Ala Thr Leu Ser Asp Val Asp Val Val Ile Ile Asp Glu Ile His  
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gcc atg gcc gga acc aaa cgg gga gtg cac ctg gcg ttg act ctg gag 691  
 Ala Met Ala Gly Thr Lys Arg Gly Val His Leu Ala Leu Thr Leu Glu  
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cgt ttg gaa aag ctc gtg ggg cgg cct gtg cag cga gtt ggt ttg tct 739  
 Arg Leu Glu Lys Leu Val Gly Arg Pro Val Gln Arg Val Gly Leu Ser  
 200 205 210

gca acg gtg cgt cct ttg gaa acg gtg gcg gga ttc ttg ggc ggt ggc 787  
 Ala Thr Val Arg Pro Leu Glu Thr Val Ala Gly Phe Leu Gly Gly Gly  
 215 220 225

aga ccc gtt gag att gtg gct cca cct gcg gag aaa aag tgg gat ctc 835  
 Arg Pro Val Glu Ile Val Ala Pro Pro Ala Glu Lys Lys Trp Asp Leu  
 230 235 240 245

act gtc act gtg ccg gtg gaa gac atg tcg gat ttg ccg gtt cag gag 883  
 Thr Val Thr Val Pro Val Glu Asp Met Ser Asp Leu Pro Val Gln Glu  
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ccg gga tca act att ggt gaa cta gtc atg gat gat ccg ttg ggg att 931  
 Pro Gly Ser Thr Ile Gly Glu Leu Val Met Asp Asp Pro Leu Gly Ile  
 265 270 275

act ggc gaa tca gcg ctg cct act caa ggc tcg att tgg cca cac att 979  
 Thr Gly Glu Ser Ala Leu Pro Thr Gln Gly Ser Ile Trp Pro His Ile  
 280 285 290

gag cag cag gtg tac aac cag gtg atg tcg gcg aaa tcg acc atc gtg 1027  
 Glu Gln Gln Val Tyr Asn Gln Val Met Ser Ala Lys Ser Thr Ile Val  
 295 300 305

ttt gta aat tcc agg cgt tcc gcg gag cgt tta acc agt cgg ttg aat 1075  
 Phe Val Asn Ser Arg Arg Ser Ala Glu Arg Leu Thr Ser Arg Leu Asn  
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gaa atc tgg gcg atg gaa cac gat ccg gaa tcg ctg tcg ccg cag ctg 1123  
 Glu Ile Trp Ala Met Glu His Asp Pro Glu Ser Leu Ser Pro Gln Leu  
 330 335 340

cga aga gat ccg gcg cag att atg tcg tca gcg gat gtg gca gga aaa 1171  
 Arg Arg Asp Pro Ala Gln Ile Met Ser Ser Ala Asp Val Ala Gly Lys  
 345 350 355

gca cca cag gtg atc gca cgt gcg cac cac gga tcc gta tcc aaa gat 1219  
 Ala Pro Gln Val Ile Ala Arg Ala His His Gly Ser Val Ser Lys Asp  
 360 365 370

gaa cgt gcc acc acc gaa acc atg ctg aag gaa ggt cgg ttg gcg gca 1267  
 Glu Arg Ala Thr Thr Glu Thr Met Leu Lys Glu Gly Arg Leu Arg Ala  
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gtt att tcc acc tcc tcg ctg gag ttg ggc att gat atg ggt gcc gtg 1315  
 Val Ile Ser Thr Ser Ser Leu Glu Leu Gly Ile Asp Met Gly Ala Val  
 390 395 400 405

gac ctg gtg att cag gtg gaa tgc cca ccg tcc gtg gca agt ggc ctg 1363  
 Asp Leu Val Ile Gln Val Glu Ser Pro Ser Val Ala Ser Gly Leu  
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cag cgc gtg ggg cgt gcg ggg cac acg gtg ggg gcg acg tgc ata ggc 1411  
 Gln Arg Val Gly Arg Ala Gly His Thr Val Gly Ala Thr Ser Ile Gly  
 425 430 435

tcc ttt tat ccc aag cac cgc tcc gac ttg gtg caa acc gcg gtg acc 1459  
 Ser Phe Tyr Pro Lys His Arg Ser Asp Leu Val Gln Thr Ala Val Thr  
 440 445 450

gtg cag cgg atg aag gaa ggg ctg atc gaa gag atc cac gtg ccc aaa 1507  
 Val Gln Arg Met Lys Glu Gly Leu Ile Glu Glu Ile His Val Pro Lys  
 455 460 465

aac cgc ctt gat gta ctg gca cag cag acg gtg gcg gct gtc tgc att 1555  
 Asn Ala Leu Asp Val Leu Ala Gln Gln Thr Val Ala Ala Val Ser Ile  
 470 475 480 485

aaa gat gtg cag gtc gat gag tgg tac gag act att cgc aag gcg tat 1603  
 Lys Asp Val Gln Val Asp Glu Trp Tyr Glu Thr Ile Arg Lys Ala Tyr  
 490 495 500

ccg tac cgg gat ttg gcg cgc gaa gtc ttc gat tcc gtc atc gac ctg 1651  
 Pro Tyr Arg Asp Leu Ala Arg Glu Val Phe Asp Ser Val Ile Asp Leu  
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gtc agc ggt gtg tat ccc tcc aca gat ttt gcc gag ctg aag cca cgt 1699  
 Val Ser Gly Val Tyr Pro Ser Thr Asp Phe Ala Glu Leu Lys Pro Arg  
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gtg gtg tac gac cgg gtt tca ggc gtg ctg gag ggc cgg cca gga tcc 1747  
 Val Val Tyr Asp Arg Val Ser Gly Val Leu Glu Gly Arg Pro Gly Ser  
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caa cgc gta gca gtg acc agt ggc gga aca att ccc gat cga gga atg 1795  
 Gln Arg Val Ala Val Thr Ser Gly Gly Thr Ile Pro Asp Arg Gly Met  
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 Phe Gly Val Phe Leu Val Gly Asp Gly Pro Arg Arg Val Gly Glu Leu  
 570 575 580

gat gag gaa atg gtc tac gaa tcc cgc gtg ggc gat gtg ttt acg ctc 1891  
 Asp Glu Glu Met Val Tyr Glu Ser Arg Val Gly Asp Val Phe Thr Leu  
 585 590 595

ggg gcg tgc agt tgg cgg att gaa gag atc acc cgc gac cag gta ctg 1939  
 Gly Ala Ser Ser Trp Arg Ile Glu Glu Ile Thr Arg Asp Gln Val Leu  
 600 605 610

gtc act ccc gcg cgg ggt cac acg ggt cgg ctg cct ttt tgg acg ggc 1987  
 Val Thr Pro Ala Pro Gly His Thr Gly Arg Leu Pro Phe Trp Thr Gly  
 615 620 625

gat gcc gca ggc cgg ccc gct gag ctg ggt aaa gct tta ggc gct ttt 2035  
 Asp Ala Ala Gly Arg Pro Ala Glu Leu Gly Lys Ala Leu Gly Ala Phe  
 630 635 640 645

cga cgc tgc acc ctc acc gat cca tcc agc tcc ggc ttg gaa ggc tgg 2083

Arg	Arg	Ser	Thr	Leu	Thr	Asp	Pro	Ser	Ser	Ser	Gly	Leu	Glu	Gly	Trp		
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gcg	cac	gac	aac	ctg	atc	gcc	ttt	tta	cag	gag	cag	gaa	gaa	tcc	acc	2131	
Ala	His	Asp	Asn	Leu	Ile	Ala	Phe	Leu	Gln	Glu	Gln	Glu	Glu	Ser	Thr		
			665				670						675				
ggt	gtg	ttg	ccg	gat	gag	aag	acg	ttg	gtg	ttg	gag	cgt	ttc	aaa	gat	2179	
Gly	Val	Leu	Pro	Asp	Glu	Lys	Thr	Leu	Val	Leu	Glu	Arg	Phe	Lys	Asp		
		680				685						690					
gaa	cta	ggc	gac	tgg	cgc	att	gtc	ctg	cac	act	cct	tat	gga	cga	gga	2227	
Glu	Leu	Gly	Asp	Trp	Arg	Ile	Val	Leu	His	Thr	Pro	Tyr	Gly	Arg	Gly		
	695				700						705						
gta	aac	gca	gca	tgg	gct	ttg	gcc	gtc	ggg	gcg	aaa	atc	gct	gaa	gag	2275	
Val	Asn	Ala	Ala	Trp	Ala	Leu	Ala	Val	Gly	Ala	Lys	Ile	Ala	Glu	Glu		
	710				715				720					725			
acc	ggc	atg	gat	gcg	caa	gcc	gtg	gca	ggt	gat	gat	ggc	att	gtg	ctt	2323	
Thr	Gly	Met	Asp	Ala	Gln	Ala	Val	Ala	Gly	Asp	Asp	Gly	Ile	Val	Leu		
			730						735					740			
cgg	ttg	ccg	gaa	ggg	gat	gaa	gat	ccc	agc	gca	gcg	ttg	ttt	atg	ttt	2371	
Arg	Leu	Pro	Glu	Gly	Asp	Glu	Asp	Pro	Ser	Ala	Ala	Leu	Phe	Met	Phe		
		745					750						755				
gag	gcg	gaa	gag	atc	gaa	acg	cta	gtg	aca	gag	cag	gtg	ggt	aac	tct	2419	
Glu	Ala	Glu	Glu	Ile	Glu	Thr	Leu	Val	Thr	Glu	Gln	Val	Gly	Asn	Ser		
		760				765						770					
gcg	ctg	ttt	gcc	agc	agg	ttc	cgt	gaa	tgc	gcc	gcg	agg	gcc	cta	ttg	2467	
Ala	Leu	Phe	Ala	Ser	Arg	Phe	Arg	Glu	Cys	Ala	Ala	Arg	Ala	Leu	Leu		
	775				780					785							
ctg	ccg	aga	cga	aac	ccc	ggc	aag	cgc	gca	ccg	ctg	tgg	cag	caa	cga	2515	
Leu	Pro	Arg	Arg	Asn	Pro	Gly	Lys	Arg	Ala	Pro	Leu	Trp	Gln	Gln	Arg		
	790			795					800						805		
caa	cga	gca	gca	cag	ctt	ctt	gat	gtg	gcc	aga	aag	tac	ccg	agt	ttc	2563	
Gln	Arg	Ala	Ala	Gln	Leu	Leu	Asp	Val	Ala	Arg	Lys	Tyr	Pro	Ser	Phe		
			810					815					820				
ccg	atc	att	ttg	gaa	aca	gtg	cgc	gaa	tgt	ctt	caa	gat	ggt	tac	gat	2611	
Pro	Ile	Ile	Leu	Glu	Thr	Val	Arg	Glu	Cys	Leu	Gln	Asp	Val	Tyr	Asp		
		825				830							835				
ctg	ccc	gct	ctg	aag	aat	ctc	att	gag	gat	cta	cag	ctg	cgg	aag	gta	2659	
Leu	Pro	Ala	Leu	Lys	Asn	Leu	Ile	Glu	Asp	Leu	Gln	Leu	Arg	Lys	Val		
		840				845						850					
aga	atc	gcg	gaa	gtc	acc	acc	cag	cag	ccc	agt	cct	ttt	gcc	tcc	gca	2707	
Arg	Ile	Ala	Glu	Val	Thr	Thr	Gln	Gln	Pro	Ser	Pro	Phe	Ala	Ser	Ala		
	855				860						865						
ttg	ctg	ttc	aat	tac	acc	ggt	gca	ttc	atg	tac	gaa	ggc	gac	agc	ccg	2755	
Leu	Leu	Phe	Asn	Tyr	Thr	Gly	Ala	Phe	Met	Tyr	Glu	Gly	Asp	Ser	Pro		
	870				875				880						885		
ctc	gca	gag	aaa	cgt	gcc	gca	gcg	ttg	gcc	ctg	gat	ccg	gca	ctg	ttg	2803	
Leu	Ala	Glu	Lys	Arg	Ala	Ala	Ala	Leu	Ala	Leu	Asp	Pro	Ala	Leu	Leu		

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atc atc gca gaa gtg cac caa caa ttg cgc agg caa ggc gat cgt gcg Ile Ile Ala Glu Val His Gln Gln Leu Arg Arg Gln Gly Asp Arg Ala 920 925 930			2899
gcg aga aac aat gaa gaa ctc gca gat tct ttg agg att tta gga cgg Ala Arg Asn Asn Glu Glu Leu Ala Asp Ser Leu Arg Ile Leu Gly Pro 935 940 945			2947
att cct ttg gat gaa ttg ggc gaa cac atc acc ttt gaa aac cca gac Ile Pro Leu Asp Glu Leu Gly Glu His Ile Thr Phe Glu Asn Pro Asp 950 955 960 965			2995
ctg gag gat cga gca atg act gtt cgg atc aac ggt cgg gaa cat tta Leu Glu Asp Arg Ala Met Thr Val Arg Ile Asn Gly Arg Glu His Leu 970 975 980			3043
gcg cag gtc ttg gat gca cct ttg ctt cga gat gcc tta ggt gtt ccc Ala Gln Val Leu Asp Ala Pro Leu Leu Arg Asp Ala Leu Gly Val Pro 985 990 995			3091
gta ccg cct ggt gtg cct gcg cag gta gaa acc att acg gat gcg ttg Val Pro Pro Gly Val Pro Ala Gln Val Glu Thr Ile Thr Asp Ala Leu 1000 1005 1010			3139
gaa cag tta gtc aac agg tgg gtt cgt acc aga ggg cca ttt act gcg Glu Gln Leu Val Asn Arg Trp Val Arg Thr Arg Gly Pro Phe Thr Ala 1015 1020 1025			3187
aat gat ttg gca gaa gcc ttt gga ctg ggc atc gcc acg gcg atc acc Asn Asp Leu Ala Glu Ala Phe Gly Leu Gly Ile Ala Thr Ala Ile Thr 1030 1035 1040 1045			3235
gcc ctt caa agc gca cct gtg att gaa ggc cgc tac cga caa ggc gtg Ala Leu Gln Ser Ala Pro Val Ile Glu Gly Arg Tyr Arg Gln Gly Val 1050 1055 1060			3283
gac gtg cag gaa tac tgt gcg aca gaa gtg ttg tgc atc ata agg cga Asp Val Gln Glu Tyr Cys Ala Thr Glu Val Leu Ser Ile Ile Arg Arg 1065 1070 1075			3331
gcg agc ctc gca gca gcg agg aaa caa acc agg ccg gta tgc caa tca Arg Ser Leu Ala Ala Ala Arg Lys Gln Thr Arg Pro Val Ser Gln Ser 1080 1085 1090			3379
gcc ttt gcg cga ttc ctg ctt gat tgg caa cag atc gca cgg gtg ggc Ala Phe Ala Arg Phe Leu Leu Asp Trp Gln Gln Ile Ala Pro Val Gly 1095 1100 1105			3427
gcc aca cct gaa ctt cga ggc gtt gat ggc acc tac aca gtc att gaa Ala Thr Pro Glu Leu Arg Gly Val Asp Gly Thr Tyr Thr Val Ile Glu 1110 1115 1120 1125			3475
caa ctc gcc ggt gta cgt ctt ccc gcc agt gcg tgg gaa gat ctc gtg Gln Leu Ala Gly Val Arg Leu Pro Ala Ser Ala Trp Glu Asp Leu Val 1130 1135 1140			3523

ttg ccg cgc cgg gtt gcc gac tat tca ccg atc cat ctc gat gag ctg 3571  
 Leu Pro Arg Arg Val Ala Asp Tyr Ser Pro Ile His Leu Asp Glu Leu  
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acc tcc aat ggg gaa gtc ctc atc gtg gga cgc ggc caa gcc gga agc 3619  
 Thr Ser Asn Gly Glu Val Leu Ile Val Gly Ala Gly Gln Ala Gly Ser  
 1160 1165 1170

cgc gat ccg tgg att agc ttg ctg ccc gtg gat tat gcg gcg cag ttg 3667  
 Arg Asp Pro Trp Ile Ser Leu Leu Pro Val Asp Tyr Ala Ala Gln Leu  
 1175 1180 1185

gtg ggg gag cgc tgc aca agc atg agc cca ttg cag gac gcc gtg ctt 3715  
 Val Gly Glu Ala Ser Thr Ser Met Ser Pro Leu Gln Asp Ala Val Leu  
 1190 1195 1200 1205

gac cag ctg cgt gcg gga ggc gcc ttc ctg ttt tct gac att ctc gaa 3763  
 Asp Gln Leu Arg Ala Gly Gly Ala Phe Leu Phe Ser Asp Ile Leu Glu  
 1210 1215 1220

gag aat ttc ggc tac acc aca gcc cag ctg caa gaa gcg atg tgg ggg 3811  
 Glu Asn Phe Gly Tyr Thr Thr Ala Gln Leu Gln Glu Ala Met Trp Gly  
 1225 1230 1235

ctg gtg gaa gca ggc ctg gtc agc cct gat agc ttc gcg ccg atc cgc 3859  
 Leu Val Glu Ala Gly Leu Val Ser Pro Asp Ser Phe Ala Pro Ile Arg  
 1240 1245 1250

gcg cgc cta gcg tgc gga acc acg gcg cat cgg gcg aaa cgt cga cca 3907  
 Ala Arg Leu Ala Ser Gly Thr Thr Ala His Arg Ala Lys Arg Arg Pro  
 1255 1260 1265

gcg aga tcc ccg ctg cgc acc cgc acc agc ttc gcg agc gac gtg ccc 3955  
 Ala Arg Ser Arg Leu Arg Thr Arg Thr Ser Phe Ala Ser Asp Val Pro  
 1270 1275 1280 1285

cca gac atg cgc gga cga tgg acg ctg tcc gtg caa ccc gcc gac gcc 4003  
 Pro Asp Met Arg Gly Arg Trp Thr Leu Ser Val Gln Pro Ala Asp Ala  
 1290 1295 1300

acc agc cgc tcc gtc gca cac ggc gaa ggc tgg ctc gac cgc tac ggc 4051  
 Thr Ser Arg Ser Val Ala His Gly Glu Gly Trp Leu Asp Arg Tyr Gly  
 1305 1310 1315

gtg ctc acc cgc ggg agc gtc gtc gcc gaa gac atc gtc gga ggc ttc 4099  
 Val Leu Thr Arg Gly Ser Val Val Ala Glu Asp Ile Val Gly Gly Phe  
 1320 1325 1330

gcc ctg gcc tac aaa gtg ctc tcc ggc ttc gaa gaa agc ggc aaa gcg 4147  
 Ala Leu Ala Tyr Lys Val Leu Ser Gly Phe Glu Glu Ser Gly Lys Ala  
 1335 1340 1345

atg cgc ggc tac ttc atc gaa ggg ctc ggc gcc gcg caa ttc tcc acg 4195  
 Met Arg Gly Tyr Phe Ile Glu Gly Leu Gly Ala Ala Gln Phe Ser Thr  
 1350 1355 1360 1365

ccc gcc atc atc gac cgc ctc cgc ggc cac gac gat tcc ccc gac gtc 4243  
 Pro Ala Ile Ile Asp Arg Leu Arg Gly His Asp Asp Ser Pro Asp Val  
 1370 1375 1380

gaa ggc tgg ccc tcc ggc gcc acc gac cca gac gtc tac ctc ata gcc 4291  
 Glu Gly Trp Pro Ser Gly Ala Thr Asp Pro Asp Val Tyr Leu Ile Ala  
 1385 1390 1395

gcc gcc gac ccc gca aac ccc tac ggc gcc gca ctt ccc tgg cct gag 4339  
 Ala Ala Asp Pro Ala Asn Pro Tyr Gly Ala Ala Leu Pro Trp Pro Glu  
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cag ggg ccc agc cgc gcc gcc gga gct atg gtc gtg ctt tgc gac gga 4387  
 Gln Gly Pro Ser Arg Ala Ala Gly Ala Met Val Val Leu Cys Asp Gly  
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 Leu Leu Leu Ala His Leu Thr Arg Gly Gly Arg Thr Leu Thr Val Phe  
 1430 1435 1440 1445

tcc gac aat atc ccc aaa atc gcg aca gcc cta atc aca tac gaa agg 4483  
 Ser Asp Asn Ile Pro Lys Ile Ala Thr Ala Leu Ile Thr Tyr Glu Arg  
 1450 1455 1460

ctc acg gta gaa aaa atc aac ggc gac aac gtc ttc gac tcc cca ctc 4531  
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 1465 1470 1475

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acc agg act ttt cgt gga ggc ttc gga cgg cgc taacctgatg acatgccaga 4680  
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agg 4683

&lt;210&gt; 96

&lt;211&gt; 1520

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 96

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Phe Arg Asp Val Phe Ala Ser Pro Thr Pro Val Gln Glu Gly Thr Trp  
 20 25 30

Glu Ala Val Ser Lys Gly Lys Asn Ala Leu Val Val Ala Pro Thr Gly  
 35 40 45

Ser Gly Lys Thr Leu Ala Ala Phe Leu Trp Ala Leu Asp Ser Leu Thr  
 50 55 60

Glu Gln Thr Gly Gln Gln Val Leu Asp Thr Gly Thr Pro Val Pro Val  
 65 70 75 80

Arg Gly Gly Lys Val Lys Val Leu Tyr Ile Ser Pro Leu Lys Ala Leu

85										90										95																			
Gly Val Asp Val Glu Asn Asn Leu Arg Ala Pro Leu Thr Gly Ile Ala																																							
100										105										110																			
Arg Thr Ala Ser Arg Met Gly Leu Asp Val Pro Asn Ile Thr Val Ala																																							
115										120										125																			
Val Arg Ser Gly Asp Thr Pro Ser Ala Glu Arg Ala Arg Gln Val Arg																																							
130										135										140																			
Lys Pro Ala His Ile Leu Ile Thr Thr Pro Glu Ser Ala Tyr Leu Met																																							
145										150										155										160									
Leu Thr Ser Lys Ala Gly Ala Thr Leu Ser Asp Val Asp Val Val Ile																																							
165										170										175																			
Ile Asp Glu Ile His Ala Met Ala Gly Thr Lys Arg Gly Val His Leu																																							
180										185										190																			
Ala Leu Thr Leu Glu Arg Leu Glu Lys Leu Val Gly Arg Pro Val Gln																																							
195										200										205																			
Arg Val Gly Leu Ser Ala Thr Val Arg Pro Leu Glu Thr Val Ala Gly																																							
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Phe Leu Gly Gly Gly Arg Pro Val Glu Ile Val Ala Pro Pro Ala Glu																																							
225										230										235										240									
Lys Lys Trp Asp Leu Thr Val Thr Val Pro Val Glu Asp Met Ser Asp																																							
245										250										255																			
Leu Pro Val Gln Glu Pro Gly Ser Thr Ile Gly Glu Leu Val Met Asp																																							
260										265										270																			
Asp Pro Leu Gly Ile Thr Gly Glu Ser Ala Leu Pro Thr Gln Gly Ser																																							
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Ile Trp Pro His Ile Glu Gln Gln Val Tyr Asn Gln Val Met Ser Ala																																							
290										295										300																			
Lys Ser Thr Ile Val Phe Val Asn Ser Arg Arg Ser Ala Glu Arg Leu																																							
305										310										315										320									
Thr Ser Arg Leu Asn Glu Ile Trp Ala Met Glu His Asp Pro Glu Ser																																							
325										330										335																			
Leu Ser Pro Gln Leu Arg Arg Asp Pro Ala Gln Ile Met Ser Ser Ala																																							
340										345										350																			
Asp Val Ala Gly Lys Ala Pro Gln Val Ile Ala Arg Ala His His Gly																																							
355										360										365																			
Ser Val Ser Lys Asp Glu Arg Ala Thr Thr Glu Thr Met Leu Lys Glu																																							
370										375										380																			
Gly Arg Leu Arg Ala Val Ile Ser Thr Ser Ser Leu Glu Leu Gly Ile																																							
385										390										395										400									
Asp Met Gly Ala Val Asp Leu Val Ile Gln Val Glu Ser Pro Pro Ser																																							
405										410										415																			

Val Ala Ser Gly Leu Gln Arg Val Gly Arg Ala Gly His Thr Val Gly  
420 425 430

Ala Thr Ser Ile Gly Ser Phe Tyr Pro Lys His Arg Ser Asp Leu Val  
435 440 445

Gln Thr Ala Val Thr Val Gln Arg Met Lys Glu Gly Leu Ile Glu Glu  
450 455 460

Ile His Val Pro Lys Asn Ala Leu Asp Val Leu Ala Gln Gln Thr Val  
465 470 475 480

Ala Ala Val Ser Ile Lys Asp Val Gln Val Asp Glu Trp Tyr Glu Thr  
485 490 495

Ile Arg Lys Ala Tyr Pro Tyr Arg Asp Leu Ala Arg Glu Val Phe Asp  
500 505 510

Ser Val Ile Asp Leu Val Ser Gly Val Tyr Pro Ser Thr Asp Phe Ala  
515 520 525

Glu Leu Lys Pro Arg Val Val Tyr Asp Arg Val Ser Gly Val Leu Glu  
530 535 540

Gly Arg Pro Gly Ser Gln Arg Val Ala Val Thr Ser Gly Gly Thr Ile  
545 550 555 560

Pro Asp Arg Gly Met Phe Gly Val Phe Leu Val Gly Asp Gly Pro Arg  
565 570 575

Arg Val Gly Glu Leu Asp Glu Glu Met Val Tyr Glu Ser Arg Val Gly  
580 585 590

Asp Val Phe Thr Leu Gly Ala Ser Ser Trp Arg Ile Glu Glu Ile Thr  
595 600 605

Arg Asp Gln Val Leu Val Thr Pro Ala Pro Gly His Thr Gly Arg Leu  
610 615 620

Pro Phe Trp Thr Gly Asp Ala Ala Gly Arg Pro Ala Glu Leu Gly Lys  
625 630 635 640

Ala Leu Gly Ala Phe Arg Arg Ser Thr Leu Thr Asp Pro Ser Ser Ser  
645 650 655

Gly Leu Glu Gly Trp Ala His Asp Asn Leu Ile Ala Phe Leu Gln Glu  
660 665 670

Gln Glu Glu Ser Thr Gly Val Leu Pro Asp Glu Lys Thr Leu Val Leu  
675 680 685

Glu Arg Phe Lys Asp Glu Leu Gly Asp Trp Arg Ile Val Leu His Thr  
690 695 700

Pro Tyr Gly Arg Gly Val Asn Ala Ala Trp Ala Leu Ala Val Gly Ala  
705 710 715 720

Lys Ile Ala Glu Glu Thr Gly Met Asp Ala Gln Ala Val Ala Gly Asp  
725 730 735



Asp Gly Ile Val Leu Arg Leu Pro Glu Gly Asp Glu Asp Pro Ser Ala  
 740 745 750  
 Ala Leu Phe Met Phe Glu Ala Glu Glu Ile Glu Thr Leu Val Thr Glu  
 755 760 765  
 Gln Val Gly Asn Ser Ala Leu Phe Ala Ser Arg Phe Arg Glu Cys Ala  
 770 775 780  
 Ala Arg Ala Leu Leu Leu Pro Arg Arg Asn Pro Gly Lys Arg Ala Pro  
 785 790 795 800  
 Leu Trp Gln Gln Arg Gln Arg Ala Ala Gln Leu Leu Asp Val Ala Arg  
 805 810 815  
 Lys Tyr Pro Ser Phe Pro Ile Ile Leu Glu Thr Val Arg Glu Cys Leu  
 820 825 830  
 Gln Asp Val Tyr Asp Leu Pro Ala Leu Lys Asn Leu Ile Glu Asp Leu  
 835 840 845  
 Gln Leu Arg Lys Val Arg Ile Ala Glu Val Thr Thr Gln Gln Pro Ser  
 850 855 860  
 Pro Phe Ala Ser Ala Leu Leu Phe Asn Tyr Thr Gly Ala Phe Met Tyr  
 865 870 875 880  
 Glu Gly Asp Ser Pro Leu Ala Glu Lys Arg Ala Ala Ala Leu Ala Leu  
 885 890 895  
 Asp Pro Ala Leu Leu Ala Lys Leu Leu Gly Glu Val Glu Leu Arg Gln  
 900 905 910  
 Leu Leu Asp Pro Asp Ile Ile Ala Glu Val His Gln Gln Leu Arg Arg  
 915 920 925  
 Gln Gly Asp Arg Ala Ala Arg Asn Asn Glu Glu Leu Ala Asp Ser Leu  
 930 935 940  
 Arg Ile Leu Gly Pro Ile Pro Leu Asp Glu Leu Gly Glu His Ile Thr  
 945 950 955 960  
 Phe Glu Asn Pro Asp Leu Glu Asp Arg Ala Met Thr Val Arg Ile Asn  
 965 970 975  
 Gly Arg Glu His Leu Ala Gln Val Leu Asp Ala Pro Leu Leu Arg Asp  
 980 985 990  
 Ala Leu Gly Val Pro Val Pro Pro Gly Val Pro Ala Gln Val Glu Thr  
 995 1000 1005  
 Ile Thr Asp Ala Leu Glu Gln Leu Val Asn Arg Trp Val Arg Thr Arg  
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 Gly Pro Phe Thr Ala Asn Asp Leu Ala Glu Ala Phe Gly Leu Gly Ile  
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 Tyr Arg Gln Gly Val Asp Val Gln Glu Tyr Cys Ala Thr Glu Val Leu

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     1365                      1370                      1375  
 Asp Ser Pro Asp Val Glu Gly Trp Pro Ser Gly Ala Thr Asp Pro Asp  
     1380                      1385                      1390

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 Met Ser Ser Leu Ile  
 1 5

cct gtc cat gcg gct ggc agc att caa gaa ggc atc acc gaa tat ttg 163  
 Pro Val His Ala Ala Gly Ser Ile Gln Glu Gly Ile Thr Glu Tyr Leu  
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 Thr Thr Ser Phe Ser Leu Ala Asp Lys Gln Val Ala Thr Glu Leu Lys  
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 Arg Phe Leu Gly His Gly Asp Ser Gly Met Phe His Gly Pro Tyr Val  
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 Ser Trp Leu Pro Glu Asn Phe Val Pro Tyr His His Gln Lys Ala Ala  
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 Phe Gln Arg Leu Ser Ser Leu Asp Asn Arg Gly Lys Asp Arg Arg Pro  
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 Arg Val Ser Pro Pro Asp Ile Leu Leu Thr Asn Tyr Lys Met Leu Asp  
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 Arg Pro Leu Gly Ile Ile Thr Pro Val Ala Thr Ser Ala Thr Leu Gly  
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 Lys Arg Leu Pro Gly Val Glu Thr His Leu Trp Val Arg Glu Val Ser  
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 Arg Ile Asp Arg Ala Leu Gly Val Gly Asp Glu Gln Ser Met Phe Arg  
 490 495 500

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 Trp Ser Asp Asp Gly Pro Ala Glu Asp Ala Asn Thr Gln Gln Trp Leu  
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ccg cgc tgt tat tgc cgc agt tgt ggc cgt tcc ggc tgg atg gtc agc 1699  
 Pro Ala Cys Tyr Cys Arg Ser Cys Gly Arg Ser Gly Trp Met Val Ser  
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acc tct gag cag cgc gca gcc att gag cag ggg cgc agc gtt gct ggg	1843
Thr Ser Glu Gln Arg Ala Ala Ile Glu Gln Gly Arg Ser Val Ala Gly	
570 575 580	
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Pro Arg Gly Val Asp Gly Thr Ser Ala Val Leu Trp Phe His Ser Ala	
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Ser Asn Glu Leu Ser Thr Arg Gln Pro Ser Pro Glu Glu Glu Gln Ser	
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Gly Ser Ser Ile Ala Val Leu Thr His Phe Gly Pro Glu Ala Asp Asp	
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Arg Tyr Ile Gly Ser Gly Ile Ser Thr Leu Leu Ser Val Ser Leu Ser	
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Asn Leu Phe Gly Met Ala Asp Leu Asp Ser Ala Glu Lys Lys Thr Leu	
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Val Phe Ala Asp Ser Val Gln Asp Ala Ala His Arg Ala Gly Tyr Val	
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Gln Ala Arg Ser Arg Ala Phe Ala Leu Arg Thr Tyr Thr Arg Arg Ala	
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Val Gly Asp Asn Glu Val Thr Leu Pro Ser Ile Ser Arg Ala Leu Met	
710 715 720 725	
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Asp Asn Ala Thr Ser Gly Arg Thr Arg Tyr Glu Leu Leu Pro Pro Asp	
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Leu Thr Asp Leu Asp Ile Tyr Lys Pro Tyr Trp His Pro Ala Ser	
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Lys Ala Glu Arg Arg Glu Ala Ser Arg Asn Val His Lys Arg Leu Ser	
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Phe Asp Leu Ala Leu Glu Phe Gly Gln Arg Ala Asp Leu Pro Arg Ser	
775 780 785	
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Val Ala Leu Ser	Ala Ala Ala Glu Ala Leu	Tyr Ala Ile Glu	Val Pro	
	810	815	820	
acc tta gat att gag gat gag aac ctg cga ctg cgc tgg gtg caa ggt				2611
Thr Leu Asp	Ile Glu Asp Glu Asn Leu Arg Leu Arg Trp	Val Gln Gly		
	825	830	835	
gcc ctg gaa ctt ttg cgc gcc cgc ggg ggc atc aac cat gag tgg ttt				2659
Ala Leu Glu Leu Leu Arg Ala Arg Gly Gly Ile Asn His Glu Trp Phe				
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ggc gcc tac ctg cgc acc gat ggc aac ccc tat atg ctt aac cgc cgc				2707
Gly Ala Tyr Leu Arg Thr Asp Gly Asn Pro Tyr Met Leu Asn Arg Arg				
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Gln Ala Arg Ala Glu Gly Ile Pro Gly Phe Val Arg Gly Gly Ala Pro				
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Glu Phe Pro Arg Val Gly Ser Ala Leu Ser Gly Ser Leu Arg Ser Ser				
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Thr Gly Thr Thr Pro Leu Gly Ser Pro Arg Gly Arg Tyr Ala Ser Trp				
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acc tgc cag gtg ctt ggc atc agc acc cac gat gcc gcc acc gcc atc				2899
Thr Ser Gln Val Leu Gly Ile Ser Thr His Asp Ala Ala Thr Ala Ile				
	920	925	930	
aca aag ctt ttc gac gct tta agc aac cgc agc att ctc tcc tca ata				2947
Thr Lys Leu Phe Asp Ala Leu Ser Asn Arg Ser Ile Leu Ser Ser Ile				
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tct acc gac agc ggc gga aaa atc tac tgc ctc gag gcc gaa cgc atc				2995
Ser Thr Asp Ser Gly Gly Lys Ile Tyr Cys Leu Glu Ala Glu Arg Ile				
	950	955	960	965
cgt att ttt agc gaa gac cat ccc gaa gtt ctg gaa tgc agc gtg tgc				3043
Arg Ile Phe Ser Glu Asp His Pro Glu Val Leu Glu Cys Ser Val Cys				
	970	975	980	
cat gcc caa act ggt gta act gat cat gtg cgt gac ttc ctt gat ggc				3091
His Ala Gln Thr Gly Val Thr Asp His Val Arg Asp Phe Leu Asp Gly				
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gct ccg tgt ttt agc cct agt tgt ggg ggc gtt ctc cat atc gag gaa				3139
Ala Pro Cys Phe Ser Pro Ser Cys Gly Gly Val Leu His Ile Glu Glu				
	1000	1005	1010	
gta gaa gac aac tac tac cgc agg ctt tat tcc gca att gaa ccg cgc				3187
Val Glu Asp Asn Tyr Tyr Arg Arg Leu Tyr Ser Ala Ile Glu Pro Arg				
	1015	1020	1025	
act gtc att gcc cgc gag cac acc agc atg ctc aag aaa aaa gac cgc				3235
Thr Val Ile Ala Arg Glu His Thr Ser Met Leu Lys Lys Lys Asp Arg				
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 1270 1275 1280 1285



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Phe Arg Ala Thr Ala Glu Lys Ser Leu Arg Ala Ile Leu Leu Asn Ser	
1690 1695 1700	
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Ser Arg Pro Glu Glu Ile Thr Asp Leu Ser Ala Val Pro Asp Trp Thr	
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Phe Leu Glu Lys Arg Pro Glu Asn Thr Leu Gly Ser Gln Leu Glu Leu	
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cgt ttc cgc gtg atg ctg cga cgc gcc tta aaa aat cgc cat gcc aaa	5347
Arg Phe Arg Val Met Leu Arg Arg Ala Leu Lys Asn Arg His Ala Lys	
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Leu Val Asp Arg Val Asn Gly Ser Asn Ser Tyr Val Asp Ile Glu Met	
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Ser Ser Gly Val Arg Trp Arg Met Ser Glu Gln Val Asp Arg Gly Tyr	

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Thr Arg Pro Asp Phe Trp Phe Glu Pro Leu Asn Gly Asn Tyr Pro Thr			
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Val Ala Val Phe Thr Asp Gly Ala Ala Phe His Ile Ser Ser Ala Asn			
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Tyr Arg Leu Asp Gly Asp Ile Gln Lys Arg Met Lys Leu Ala Leu Asp			
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Pro Asp Asn Ile Leu Pro Trp Asn Ile Thr Ser Leu Asp Leu Asp Arg			
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Phe Ser Asn Pro Ala Ala Gln Gly Glu Glu Pro Ala Trp Phe Ser Pro			
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Ile Gly Arg Gln Leu Ser Lys Ala Asn Leu Ile Leu Asp Pro Gln Ser			
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Thr Ala Leu Leu Ala Ala Thr Pro Met Asp Gln Leu Leu Ala Phe Leu			
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Asp Asn Pro Ala Ala Ser Ser Trp Lys Glu Phe Ala His Ile Ala Ala			
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Leu Glu Val Asp Thr Trp Thr Ala Phe Leu Asn Leu Ala Asn Leu Met			
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Trp Leu Ala Pro Glu Ser Val Tyr Val Ser Thr Asn Gly Ser Pro His			
1975	1980	1985	
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Lys Ile Asp Ile Val Pro Ala Pro Ala Ala Pro Leu Val Val Glu Val			
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Pro Glu Leu Trp Ala Pro Ile Leu Asp Gly Phe Thr Ala Asp Glu Asp			
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 Val Pro Glu Thr Thr Gly Asp Glu Leu Ser Ser Ile Pro Thr Ile Ala  
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 Thr Trp Pro Ser Val Lys Ile Ala Leu Leu Tyr Gly Ser Asp Pro Asp  
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 Trp Glu Asn Val Leu Ser Trp Leu Pro Glu Asn Phe Val Pro Tyr His  
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 His Asn Asn Pro Ala Leu Lys Gly Val Thr Ala Gly Ile Tyr Thr Gly

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Asn His Glu Trp Phe Gly Ala Tyr Leu Arg Thr Asp Gly Asn Pro Tyr  
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Gly Leu Asp Pro Leu Leu Glu Glu Phe Val Arg Thr Leu Asn Met Gln 1205	1210	1215
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Arg Phe Asn Gln His Val Ser Phe Val Val Pro Pro Asp Gly His Gly 1460	1465	1470



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Glu Leu Arg Phe Arg Val Met Leu Arg Arg Ala Leu Lys Asn Arg His  
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Ala Lys Leu Val Asp Arg Val Asn Gly Ser Asn Ser Tyr Val Asp Ile  
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Glu Met Ser Ser Gly Val Arg Trp Arg Met Ser Glu Gln Val Asp Arg  
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Gly Tyr Thr Arg Pro Asp Phe Trp Phe Glu Pro Leu Asn Gly Asn Tyr  
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ccc acc gtg gct gtt ttt acc gat ggc gct gcg ttc cat atc tct tca 336  
Pro Thr Val Ala Val Phe Thr Asp Gly Ala Ala Phe His Ile Ser Ser  
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gct aac tac cgt ctt gat ggc gat att cag aaa cgg atg aaa cta gcg 384  
Ala Asn Tyr Arg Leu Asp Gly Asp Ile Gln Lys Arg Met Lys Leu Ala  
115 120 125

ctc gat cca gac aat att ttg ccg tgg aat atc act agc tta gac ctc 432  
Leu Asp Pro Asp Asn Ile Leu Pro Trp Asn Ile Thr Ser Leu Asp Leu  
130 135 140

gac cgc ttt agt aat ccc gct gca caa ggt gag gaa cca gca tgg ttt 480  
Asp Arg Phe Ser Asn Pro Ala Ala Gln Gly Glu Glu Pro Ala Trp Phe  
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agc ccc atc ggc agg cag etc agc aaa gca aat ttg att ctt gat cca 528  
Ser Pro Ile Gly Arg Gln Leu Ser Lys Ala Asn Leu Ile Leu Asp Pro

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Phe	Leu	Asp	Asn	Pro	Ala	Ala	Ser	Ser	Trp	Lys	Glu	Phe	Ala	His	Ile					
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Ala	Ala	Ala	His	Met	Leu	Gly	His	Asn	Pro	Gln	Lys	Asn	Gly	Asp	Gly					
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Pro	His	Lys	Ile	Asp	Ile	Val	Pro	Ala	Pro	Ala	Ala	Pro	Leu	Val	Val					
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Glu	Val	Pro	Glu	Leu	Trp	Ala	Pro	Ile	Leu	Asp	Gly	Phe	Thr	Ala	Asp					
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Glu	Asp	Glu	Glu	Ala	Glu	Gly	Ala	Leu	Gln	Ile	Leu	Ala	Lys	Glu	His					
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Ala	Leu	Val	Pro	Glu	Thr	Thr	Gly	Asp	Glu	Leu	Ser	Ser	Ile	Pro	Thr					
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Leu	Phe	Ala	Asn	Asp	Leu	Glu	Thr	Ser	Asp	Ile	Pro	Ala	Ala	Leu	Arg					
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Pro																				

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                   20                  25                  30  
 Glu Leu Arg Phe Arg Val Met Leu Arg Arg Ala Leu Lys Asn Arg His  
           35                  40                  45  
 Ala Lys Leu Val Asp Arg Val Asn Gly Ser Asn Ser Tyr Val Asp Ile  
           50                  55                  60  
 Glu Met Ser Ser Gly Val Arg Trp Arg Met Ser Glu Gln Val Asp Arg  
           65                  70                  75                  80  
 Gly Tyr Thr Arg Pro Asp Phe Trp Phe Glu Pro Leu Asn Gly Asn Tyr  
                   85                  90                  95  
 Pro Thr Val Ala Val Phe Thr Asp Gly Ala Ala Phe His Ile Ser Ser  
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 Ala Asn Tyr Arg Leu Asp Gly Asp Ile Gln Lys Arg Met Lys Leu Ala  
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 Leu Asp Pro Asp Asn Ile Leu Pro Trp Asn Ile Thr Ser Leu Asp Leu  
           130                  135                  140  
 Asp Arg Phe Ser Asn Pro Ala Ala Gln Gly Glu Glu Pro Ala Trp Phe  
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 Ser Pro Ile Gly Arg Gln Leu Ser Lys Ala Asn Leu Ile Leu Asp Pro  
           165                  170                  175  
 Gln Ser Thr Ala Leu Leu Ala Ala Thr Pro Met Asp Gln Leu Leu Ala  
           180                  185                  190  
 Phe Leu Asp Asn Pro Ala Ala Ser Ser Trp Lys Glu Phe Ala His Ile  
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 Ala Ala Ala His Met Leu Gly His Asn Pro Gln Lys Asn Gly Asp Gly  
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 Ile Val Gly Thr Phe Arg Asn Lys Ile Ser Leu Arg Ala Thr Met Val  
           225                  230                  235                  240  
 Asn Arg Glu Leu Arg Ala Arg Gln Leu Trp Leu Ala Pro Thr Thr Pro  
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 Glu Glu Leu Glu Val Asp Thr Trp Thr Ala Phe Leu Asn Leu Ala Asn  
           260                  265                  270  
 Leu Met Trp Leu Ala Pro Glu Ser Val Tyr Val Ser Thr Asn Gly Ser  
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Pro His Lys Ile Asp Ile Val Pro Ala Pro Ala Ala Pro Leu Val Val  
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Glu Val Pro Glu Leu Trp Ala Pro Ile Leu Asp Gly Phe Thr Ala Asp  
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Glu Asp Glu Glu Ala Glu Gly Ala Leu Gln Ile Leu Ala Lys Glu His  
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Ala Leu Val Pro Glu Thr Thr Gly Asp Glu Leu Ser Ser Ile Pro Thr  
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Ile Ala Thr Trp Pro Ser Val Lys Ile Ala Leu Leu Tyr Glu Ser Asp  
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Pro

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Ile Ala Thr Ala Gln His Glu Asp Asp Tyr Ala Gln Leu Cys Phe Arg  
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gtt ttt tgt gag aaa gtg tgg ctg tgt gag gct gat ctg cac gca gcg 144  
Val Phe Cys Glu Lys Val Trp Leu Cys Glu Ala Asp Leu His Ala Ala  
35 40 45

atc agt gct tat gcg gct cat gat tta act gct gcg att ttg cag cat 192  
Ile Ser Ala Tyr Ala Ala His Asp Leu Thr Ala Ala Ile Leu Gln His  
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gct gct gat tcc acc ccg ctt agc agg cgt gat caa gat gag gtc act 240  
Ala Ala Asp Ser Thr Pro Leu Ser Arg Arg Asp Gln Asp Glu Val Thr  
65 70 75 80

gcc ctt ccg gag ctg gta ttg ggg gct acc gcc cgc atc tta ggt gag 288  
Ala Leu Pro Glu Leu Val Leu Gly Ala Thr Ala Arg Ile Leu Gly Glu  
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cag cgc gca gcc att gag cag ggg cgc agc gtt gct ggg ccg cga gga Gln Arg Ala Ala Ile Glu Gln Gly Arg Ser Val Ala Gly Pro Arg Gly 225 230 235 240	720
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aat	gaa	gtc	acc	ttg	cca	tca	atc	tcc	cgg	cgc	ctg	atg	gat	aac	gcc	1152
Asn	Glu	Val	Thr	Leu	Pro	Ser	Ile	Ser	Arg	Ala	Leu	Met	Asp	Asn	Ala	
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Thr	Ser	Gly	Arg	Thr	Arg	Tyr	Glu	Leu	Leu	Pro	Pro	Asp	Leu	Thr	Asp	
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Leu	Asp	Ile	Tyr	Lys	Pro	Tyr	Trp	His	Pro	Asp	Ala	Ser	Lys	Ala	Glu	
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Arg	Arg	Glu	Ala	Ser	Arg	Asn	Val	His	Lys	Arg	Leu	Ser	Phe	Asp	Leu	
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Ala	Leu	Glu	Phe	Gly	Gln	Arg	Ala	Asp	Leu	Pro	Arg	Ser	Leu	Ala	Leu	
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acc	ggc	gct	ttg	agt	gct	ttt	gtg	gat	ttg	ccc	aaa	ggt	ggt	gca	ttg	1392
Thr	Gly	Ala	Leu	Ser	Ala	Phe	Val	Asp	Leu	Pro	Lys	Gly	Val	Ala	Leu	
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Ser	Ala	Ala	Ala	Glu	Ala	Leu	Tyr	Ala	Ile	Glu	Val	Pro	Thr	Leu	Asp	
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Ile	Glu	Asp	Glu	Asn	Leu	Arg	Leu	Arg	Trp	Val	Gln	Gly	Ala	Leu	Glu	
			485							490			495			
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Leu	Leu	Arg	Ala	Arg	Gly	Gly	Ile	Asn	His	Glu	Trp	Phe	Gly	Ala	Tyr	
			500							505			510			
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Leu	Arg	Thr	Asp	Gly	Asn	Pro	Tyr	Met	Leu	Asn	Arg	Arg	Gln	Ala	Arg	
			515							520			525			
gct	gag	ggc	att	ccc	ggt	ttt	gtc	cgc	ggt	ggt	gca	cct	gaa	ttc	cca	1632
Ala	Glu	Gly	Ile	Pro	Gly	Phe	Val	Arg	Gly	Gly	Ala	Pro	Glu	Phe	Pro	
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Arg	Val	Gly	Ser	Ala	Leu	Ser	Gly	Ser	Leu	Arg	Ser	Ser	Thr	Gly	Thr	
			545							555			560			
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Thr	Pro	Leu	Gly	Ser	Pro	Arg	Gly	Arg	Tyr	Ala	Ser	Trp	Thr	Ser	Gln	
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 915 920 925

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 980 985 990

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 Ala Gly Ala Asn Ser Arg Trp Asp His Arg Pro Trp Cys Pro His Arg  
 1185 1190 1195 1200

tat gag caa aaa gaa gat acc gta tct ttc gct ttg ggt cgt act ctt 3648  
 Tyr Glu Gln Lys Glu Asp Thr Val Ser Phe Ala Leu Gly Arg Thr Leu  
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aaa acc caa ggc gtg ctc atg ctg ctg ccc gaa tat ttt ggc agt gaa 3696  
 Lys Thr Gln Gly Val Leu Met Leu Leu Pro Glu Tyr Phe Gly Ser Glu  
 1220 1225 1230

gcc gat tct atg gtg gta acc agc ctc att gct gct atc aaa tta gga 3744  
 Ala Asp Ser Met Val Val Thr Ser Leu Ile Ala Ala Ile Lys Leu Gly  
 1235 1240 1245

ttt cgt gag gtg ttg ggt ggc gat cct gac cac ctg gat gtc acc agt 3792  
 Phe Arg Glu Val Leu Gly Gly Asp Pro Asp His Leu Asp Val Thr Ser  
 1250 1255 1260

gtg cag gtc ccc cgt act tct ggc gat ggt gca ctt gat gcc ctt ttg 3840  
 Val Gln Val Pro Arg Thr Ser Gly Asp Gly Ala Leu Asp Ala Leu Leu  
 1265 1270 1275 1280

ctg cac gat cag gtt 3855  
 Leu His Asp Gln Val  
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&lt;210&gt; 104

&lt;211&gt; 1285

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

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 Val Phe Cys Glu Lys Val Trp Leu Cys Glu Ala Asp Leu His Ala Ala  
 35 40 45  
 Ile Ser Ala Tyr Ala Ala His Asp Leu Thr Ala Ala Ile Leu Gln His  
 50 55 60  
 Ala Ala Asp Ser Thr Pro Leu Ser Arg Arg Asp Gln Asp Glu Val Thr  
 65 70 75 80  
 Ala Leu Pro Glu Leu Val Leu Gly Ala Thr Ala Arg Ile Leu Gly Glu  
 85 90 95  
 Val Lys Ala Ala Glu Phe Ile Ser His Ala Leu Ala Ala Met Ala Phe  
 100 105 110  
 Val Arg Ala Glu Tyr Gly Lys Val Ala Ala Trp Gly Ala Lys Arg Leu  
 115 120 125  
 Pro Gly Val Glu Thr His Leu Trp Val Arg Glu Val Ser Arg Ile Asp  
 130 135 140  
 Arg Ala Leu Gly Val Gly Asp Glu Gln Ser Met Phe Arg Trp Ser Asp  
 145 150 155 160  
 Asp Gly Pro Ala Glu Asp Ala Asn Thr Gln Gln Trp Leu Pro Ala Cys  
 165 170 175  
 Tyr Cys Arg Ser Cys Gly Arg Ser Gly Trp Met Val Ser Leu Glu Gln  
 180 185 190  
 Gly Thr Asn Ile Pro Val Leu Glu Glu Gln Lys Ile Arg Leu Asn Ser  
 195 200 205  
 Phe Glu Gln Pro His Lys Gln Arg Ala Leu Leu Asp Ala Thr Ser Glu  
 210 215 220  
 Gln Arg Ala Ala Ile Glu Gln Gly Arg Ser Val Ala Gly Pro Arg Gly  
 225 230 235 240  
 Val Asp Gly Thr Ser Ala Val Leu Trp Phe His Ser Ala Ser Asn Glu  
 245 250 255  
 Leu Ser Thr Arg Gln Pro Ser Pro Glu Glu Glu Gln Ser Gly Ser Ser  
 260 265 270  
 Ile Ala Val Leu Thr His Phe Gly Pro Glu Ala Asp Asp Leu Ser Ala  
 275 280 285  
 Lys Gln Thr Cys Pro Ser Cys Gly Asp Val Asp Ser Ile Arg Tyr Ile  
 290 295 300  
 Gly Ser Gly Ile Ser Thr Leu Leu Ser Val Ser Leu Ser Asn Leu Phe  
 305 310 315 320

Gly Met Ala Asp Leu Asp Ser Ala Glu Lys Lys Thr Leu Val Phe Ala  
 325 330 335  
 Asp Ser Val Gln Asp Ala Ala His Arg Ala Gly Tyr Val Gln Ala Arg  
 340 345 350  
 Ser Arg Ala Phe Ala Leu Arg Thr Tyr Thr Arg Arg Ala Val Gly Asp  
 355 360 365  
 Asn Glu Val Thr Leu Pro Ser Ile Ser Arg Ala Leu Met Asp Asn Ala  
 370 375 380  
 Thr Ser Gly Arg Thr Arg Tyr Glu Leu Leu Pro Pro Asp Leu Thr Asp  
 385 390 395 400  
 Leu Asp Ile Tyr Lys Pro Tyr Trp His Pro Asp Ala Ser Lys Ala Glu  
 405 410 415  
 Arg Arg Glu Ala Ser Arg Asn Val His Lys Arg Leu Ser Phe Asp Leu  
 420 425 430  
 Ala Leu Glu Phe Gly Gln Arg Ala Asp Leu Pro Arg Ser Leu Ala Leu  
 435 440 445  
 Thr Gly Ala Leu Ser Ala Phe Val Asp Leu Pro Lys Gly Val Ala Leu  
 450 455 460  
 Ser Ala Ala Ala Glu Ala Leu Tyr Ala Ile Glu Val Pro Thr Leu Asp  
 465 470 475 480  
 Ile Glu Asp Glu Asn Leu Arg Leu Arg Trp Val Gln Gly Ala Leu Glu  
 485 490 495  
 Leu Leu Arg Ala Arg Gly Gly Ile Asn His Glu Trp Phe Gly Ala Tyr  
 500 505 510  
 Leu Arg Thr Asp Gly Asn Pro Tyr Met Leu Asn Arg Arg Gln Ala Arg  
 515 520 525  
 Ala Glu Gly Ile Pro Gly Phe Val Arg Gly Gly Ala Pro Glu Phe Pro  
 530 535 540  
 Arg Val Gly Ser Ala Leu Ser Gly Ser Leu Arg Ser Ser Thr Gly Thr  
 545 550 555 560  
 Thr Pro Leu Gly Ser Pro Arg Gly Arg Tyr Ala Ser Trp Thr Ser Gln  
 565 570 575  
 Val Leu Gly Ile Ser Thr His Asp Ala Ala Thr Ala Ile Thr Lys Leu  
 580 585 590  
 Phe Asp Ala Leu Ser Asn Arg Ser Ile Leu Ser Ser Ile Ser Thr Asp  
 595 600 605  
 Ser Gly Gly Lys Ile Tyr Cys Leu Glu Ala Glu Arg Ile Arg Ile Phe  
 610 615 620  
 Ser Glu Asp His Pro Glu Val Leu Glu Cys Ser Val Cys His Ala Gln  
 625 630 635 640

Thr Gly Val Thr Asp His Val Arg Asp Phe Leu Asp Gly Ala Pro Cys  
 645 650 655  
 Phe Ser Pro Ser Cys Gly Gly Val Leu His Ile Glu Glu Val Glu Asp  
 660 665 670  
 Asn Tyr Tyr Arg Arg Leu Tyr Ser Ala Ile Glu Pro Arg Thr Val Ile  
 675 680 685  
 Ala Arg Glu His Thr Ser Met Leu Lys Lys Lys Asp Arg Leu Ala Leu  
 690 695 700  
 Glu Gln Ser Phe Arg Gly Gly Glu Gly Ser Ala Lys Gln Ser Pro Asp  
 705 710 715 720  
 Ala Pro Asn Val Leu Val Ala Thr Pro Thr Leu Glu Met Gly Ile Asp  
 725 730 735  
 Ile Gly Asp Leu Ser Thr Val Met Leu Ala Ser Leu Pro Thr Ser Val  
 740 745 750  
 Ala Ser Tyr Val Gln Arg Val Gly Arg Ala Gly Arg Leu Ser Gly Asn  
 755 760 765  
 Ser Leu Val Leu Ala Val Val Arg Gly Arg Gly Val Thr Leu Pro Arg  
 770 775 780  
 Leu Asn Gln Pro Leu Ser Met Ile Lys Gly Ala Ile Thr Pro Pro Val  
 785 790 795 800  
 Ala Tyr Leu Ser Ala Ser Glu Ile Leu His Arg Gln Phe Leu Ala Tyr  
 805 810 815  
 Val Ile Asp Cys Leu Asp Thr Arg Ala Glu Leu Pro Lys Leu Glu Thr  
 820 825 830  
 Ala Ile Asp Val Phe Asp Asn Ala Ala Gly Lys Thr Pro Leu Val Ala  
 835 840 845  
 Leu Leu Lys Ala Gln Ile His Ala Gly Leu Asp Pro Leu Leu Glu Glu  
 850 855 860  
 Phe Val Arg Thr Leu Asn Met Gln Ile Ser Ile Asp Asn Ile Phe Glu  
 865 870 875 880  
 Leu Arg Thr Trp Ala Ser Gly Asn Ser Thr Asp Ser Leu Leu Ala Leu  
 885 890 895  
 Leu Glu Thr Ser Gln Lys Glu Trp Met Glu Glu Arg Arg Ser Leu Thr  
 900 905 910  
 Ala Arg Arg Gly Glu Leu Glu Lys Ile Phe Asp Lys Leu Asp Ala Arg  
 915 920 925  
 Asn Asp Ala His Asp Glu Glu Leu Lys Glu Glu Lys Arg Lys Thr Ala  
 930 935 940  
 Ala Ser Leu Lys Ala Val Lys Leu Gln Ile Arg Asp Leu Leu Gly Glu  
 945 950 955 960  
 Phe Trp Ile Ala Ala Leu Glu Arg Tyr Gly Leu Leu Pro Asn Phe Thr



965                      970                      975

Leu Val Asp Asp Ser Val Glu Leu Asn Val Ala Val Thr Ser Phe Asn  
                  980                      985                      990

Pro Gln Glu Val Glu Phe Asp Thr Lys Asn His Ala Tyr Ser Arg Gly  
                  995                      1000                      1005

Ile Ser Ala Ala Leu Phe Glu Leu Ala Pro Gly Ala Thr Phe Tyr Ala  
                  1010                      1015                      1020

Gln Gly Ile Ala Ala Lys Val Asp Ser Ile Glu Ile Gly Glu His Gly  
1025                      1030                      1035                      1040

Ser Ala Ile Glu Gln Trp Arg Leu Cys Pro Val Cys Ser His Ser Glu  
                  1045                      1050                      1055

Ile Leu Gln Pro Gly Val Ser Thr Pro Gly Ser Cys Pro Thr Cys Gly  
                  1060                      1065                      1070

Ser Pro Ala Phe Ala Asp Lys Gly Gln Ile Leu Glu Val Val Gln Met  
                  1075                      1080                      1085

Arg Lys Val Ser Ser Ala Val Glu Lys Thr Arg Ala Ala Ile Ser Asp  
                  1090                      1095                      1100

Asp Arg Glu Asp Arg Phe Ser Thr Arg Phe Asn Gln His Val Ser Phe  
1105                      1110                      1115                      1120

Val Val Pro Pro Asp Gly His Gly Lys Ser Trp Tyr Leu Asn Asp Gly  
                  1125                      1130                      1135

Phe Gly Ile Glu His Leu Pro Lys Val Glu Leu Arg Trp Leu Asn Leu  
                  1140                      1145                      1150

Gly Ile Gly Asn Gly Gln Lys Arg Arg Leu Gly Gly Phe Glu Val Thr  
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Ser Pro Leu Phe Asn Val Cys Arg His Cys Gly His Leu Asp Ser Glu  
                  1170                      1175                      1180

Ala Gly Ala Asn Ser Arg Trp Asp His Arg Pro Trp Cys Pro His Arg  
1185                      1190                      1195                      1200

Tyr Glu Gln Lys Glu Asp Thr Val Ser Phe Ala Leu Gly Arg Thr Leu  
                  1205                      1210                      1215

Lys Thr Gln Gly Val Leu Met Leu Leu Pro Glu Tyr Phe Gly Ser Glu  
                  1220                      1225                      1230

Ala Asp Ser Met Val Val Thr Ser Leu Ile Ala Ala Ile Lys Leu Gly  
                  1235                      1240                      1245

Phe Arg Glu Val Leu Gly Gly Asp Pro Asp His Leu Asp Val Thr Ser  
                  1250                      1255                      1260

Val Gln Val Pro Arg Thr Ser Gly Asp Gly Ala Leu Asp Ala Leu Leu  
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Leu His Asp Gln Val  
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 <223> RXA01740

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 Val Ala Glu Glu Phe  
 1 5  
 cgc cag cag tat cgc agc ttt gtg gtc gat gag tat cag gat gtg acg 163  
 Arg Gln Gln Tyr Arg Ser Phe Val Val Asp Glu Tyr Gln Asp Val Thr  
 10 15 20  
 cct ctg cag cag cgg gtg ctc gat gcg tgg ctc ggc gat cgc gat gac 211  
 Pro Leu Gln Gln Arg Val Leu Asp Ala Trp Leu Gly Asp Arg Asp Asp  
 25 30 35  
 ctg acg gtt gtc ggc gat gct aac cag aca att tat tgc ttc acg ggg 259  
 Leu Thr Val Val Gly Asp Ala Asn Gln Thr Ile Tyr Ser Phe Thr Gly  
 40 45 50  
 gca aca cct gaa ttt ttg ctt aat ttc tgc agg aaa tat ccg gag gca 307  
 Ala Thr Pro Glu Phe Leu Leu Asn Phe Ser Arg Lys Tyr Pro Glu Ala  
 55 60 65  
 acc gtc gtc aag ctg cag cgc gac tac cgc tca acg ccg cag gtc acc 355  
 Thr Val Val Lys Leu Gln Arg Asp Tyr Arg Ser Thr Pro Gln Val Thr  
 70 75 80 85  
 gcg ctg gcc aat acc gtc atc ggc cag gcg cgg ggg cgc gtt gct ggc 403  
 Ala Leu Ala Asn Thr Val Ile Gly Gln Ala Arg Gly Arg Val Ala Gly  
 90 95 100  
 acg cgc ctg gag ctt cag gga atg cgg atc gcc ggg ccg gag ccc gaa 451  
 Thr Arg Leu Glu Leu Gln Gly Met Arg Ile Ala Gly Pro Glu Pro Glu  
 105 110 115  
 ttt tgc gct ttc gac gac gaa ccc acc gaa gcc cgc gaa gtt gcg ggc 499  
 Phe Ser Ala Phe Asp Asp Glu Pro Thr Glu Ala Arg Glu Val Ala Gly  
 120 125 130  
 cgc att ttg acg ctg ctt aaa aac ggc gtt cag gcc tca gaa atc gcc 547  
 Arg Ile Leu Thr Leu Leu Lys Asn Gly Val Gln Ala Ser Glu Ile Ala  
 135 140 145  
 gtt ttg tac cgc atc aac gcg cag tgc gcg gtt ttc gag caa gcg ctt 595  
 Val Leu Tyr Arg Ile Asn Ala Gln Ser Ala Val Phe Glu Gln Ala Leu  
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 gcc gac gcc ggc atc gta tat cag gtg cgc ggc gcc gaa gcc ttt ttc 643  
 Ala Asp Ala Gly Ile Val Thr Gln Val Arg Gly Glu Gly Phe Phe

170	175	180	
acc cgc cca gaa att cgc caa gcc ctg agt caa ctg atc cgc act tcc Thr Arg Pro Glu Ile Arg Gln Ala Leu Ser Gln Leu Ile Arg Thr Ser 185 190 195			691
caa cgc gac gtc gat gaa agc gat ctg gtg cgt ctg acg caa cgc aca Gln Arg Asp Val Asp Glu Ser Asp Leu Val Arg Leu Thr Gln Arg Thr 200 205 210			739
ctc gtg cca ctt ggg ttg agt tgc gaa gag ccc agc ggt gcc caa gag Leu Val Pro Leu Gly Leu Ser Ser Glu Glu Pro Ser Gly Ala Gln Glu 215 220 225			787
cgg gaa cgc tgg caa tgc ctc aac gct tta gtc gat ctg gtg aaa gac Arg Glu Arg Trp Gln Ser Leu Asn Ala Leu Val Asp Leu Val Lys Asp 230 235 240 245			835
ctt gtt aaa gcc aca cca gat ttg gat ctc aca ggc ttg ctg ctg aaa Leu Val Lys Ala Thr Pro Asp Leu Asp Leu Thr Gly Leu Arg Leu Lys 250 255 260			883
ctt cgg gaa cgc caa gag gcg aag cat ccg ccg acc gtc gaa ggt gtc Leu Arg Glu Arg Gln Glu Ala Lys His Pro Pro Thr Val Glu Gly Val 265 270 275			931
acc ttg gca tgc cta cac gcg gcg aaa ggc ctc gaa tgg gat gcg gtg Thr Leu Ala Ser Leu His Ala Ala Lys Gly Leu Glu Trp Asp Ala Val 280 285 290			979
ttt ctt gtc gga ctt gtc gat tcc acg tta ccg atc agc cac gcc att Phe Leu Val Gly Leu Val Asp Ser Thr Leu Pro Ile Ser His Ala Ile 295 300 305			1027
aaa tct ggc gat gaa gca atc gaa gag gaa cgt cgc ctg ttc tat gtc Lys Ser Gly Asp Glu Ala Ile Glu Glu Glu Arg Leu Phe Tyr Val 310 315 320 325			1075
ggt gtg acc cgt gcc cgc gaa cac ctc cac tgc agt tgg gca ctc gcg Gly Val Thr Arg Ala Arg Glu His Leu His Cys Ser Trp Ala Leu Ala 330 335 340			1123
agg caa gaa ggc gga cgg aaa tgc aga aag cgg agt cga ttc ctc gat Arg Gln Glu Gly Gly Arg Lys Ser Arg Lys Arg Ser Arg Phe Leu Asp 345 350 355			1171
ggc ata gtc gtg gag atg gcc tcc gaa tgc ggc aca cct cgc agc aat Gly Ile Val Val Glu Met Ala Ser Glu Ser Gly Thr Pro Arg Ser Asn 360 365 370			1219
cgt ccg aaa aac tgc cga gtg tgc gga tgc gtt ctt tca agc cct gcc Arg Pro Lys Asn Cys Arg Val Cys Gly Ser Val Leu Ser Ser Pro Ala 375 380 385			1267
gaa aaa gct gtc ggt cgg tgt gcg agt tgc ccg atc caa gcg gat gaa Glu Lys Ala Val Gly Arg Cys Ala Ser Cys Pro Ile Gln Ala Asp Glu 390 395 400 405			1315
cga gtc ttc gaa cag ctg cga acg tgg cgc aat gac acc cgc aag cgc Arg Val Phe Glu Gln Leu Arg Thr Trp Arg Asn Asp Thr Ala Lys Arg 410 415 420			1363

Leu Ile Arg Thr Ser Gln Arg Asp Val Asp Glu Ser Asp Leu Val Arg

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210				215				220							
Ser	Gly	Ala	Gln	Glu	Arg	Glu	Arg	Trp	Gln	Ser	Leu	Asn	Ala	Leu	Val
225				230				235				240			
Asp	Leu	Val	Lys	Asp	Leu	Val	Lys	Ala	Thr	Pro	Asp	Leu	Asp	Leu	Thr
				245				250				255			
Gly	Leu	Leu	Leu	Lys	Leu	Arg	Glu	Arg	Gln	Glu	Ala	Lys	His	Pro	Pro
				260				265				270			
Thr	Val	Glu	Gly	Val	Thr	Leu	Ala	Ser	Leu	His	Ala	Ala	Lys	Gly	Leu
				275				280				285			
Glu	Trp	Asp	Ala	Val	Phe	Leu	Val	Gly	Leu	Val	Asp	Ser	Thr	Leu	Pro
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Ile	Ser	His	Ala	Ile	Lys	Ser	Gly	Asp	Glu	Ala	Ile	Glu	Glu	Glu	Arg
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Arg	Leu	Phe	Tyr	Val	Gly	Val	Thr	Arg	Ala	Arg	Glu	His	Leu	His	Cys
				320				325				330			
Ser	Trp	Ala	Leu	Ala	Arg	Gln	Glu	Gly	Gly	Arg	Lys	Ser	Arg	Lys	Arg
				335				340				345			
Ser	Arg	Phe	Leu	Asp	Gly	Ile	Val	Val	Glu	Met	Ala	Ser	Glu	Ser	Gly
				350				355				360			
Thr	Pro	Arg	Ser	Asn	Arg	Pro	Lys	Asn	Cys	Arg	Val	Cys	Gly	Ser	Val
				365				370				375			
Leu	Ser	Ser	Pro	Ala	Glu	Lys	Ala	Val	Gly	Arg	Cys	Ala	Ser	Cys	Pro
				380				385				390			
Ile	Gln	Ala	Asp	Glu	Arg	Val	Phe	Glu	Gln	Leu	Arg	Thr	Trp	Arg	Asn
				400				405				410			
Asp	Thr	Ala	Lys	Arg	Glu	Asn	Lys	Ala	Ala	Tyr	Met	Val	Phe	Ser	Asn
				415				420				425			
Ala	Thr	Leu	Met	Ala	Ile	Ala	Glu	Met	Asn	Pro	Thr	Asn	Glu	Asn	Glu
				430				435				440			
Leu	Leu	Ser	Val	Pro	Gly	Val	Gly	Pro	Met	Lys	Ile	Glu	Asn	Tyr	Gly
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Asp	Asp	Val	Leu	Ala	Ile	Leu	Gly	Ala	Leu						
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&lt;223&gt; RXN01683

&lt;400&gt; 107

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 Val Ser Asp Asp Asn  
 1 5

acc gga caa ttt gac cgc gtt aat ccc att gat atc aat gag gaa atg 163  
 Thr Gly Gln Phe Asp Arg Val Asn Pro Ile Asp Ile Asn Glu Met  
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cag tcg agc tac atc gac tac cgc atg tca gtc atc gtc gga cgt gcc 211  
 Gln Ser Ser Tyr Ile Asp Tyr Ala Met Ser Val Ile Val Gly Arg Ala  
 25 30 35

ctc cca gag gtg cga gac ggc ctg aag cca gtc cac cgc cgc gtc ttg 259  
 Leu Pro Glu Val Arg Asp Gly Leu Lys Pro Val His Arg Arg Val Leu  
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tac cgc atg ttc gac aac ggc tac cgc ccc gac cgc agc tac gtg aag 307  
 Tyr Ala Met Phe Asp Asn Gly Tyr Arg Pro Asp Arg Ser Tyr Val Lys  
 55 60 65

tct gca aaa cca gtg gca gac acc atg ggt aac ttc cac cca cac ggc 355  
 Ser Ala Lys Pro Val Ala Asp Thr Met Gly Asn Phe His Pro His Gly  
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gac acc gca att tat gac acg ttg gtg cgc atg gct cag cca tgg tcc 403  
 Asp Thr Ala Ile Tyr Asp Thr Leu Val Arg Met Ala Gln Pro Trp Ser  
 90 95 100

atg cga tac ccg ctg gta gac ggc cag ggt aac ttc ggt tcc cgc ggc 451  
 Met Arg Tyr Pro Leu Val Asp Gly Gln Gly Asn Phe Gly Ser Arg Gly  
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aac gac ggc cct gca gca atg cgt tac acc gag tgc cgc atg acc cca 499  
 Asn Asp Gly Pro Ala Ala Met Arg Tyr Thr Glu Cys Arg Met Thr Pro  
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ctg gcc atg gag atg gtg cgc gac atc cgc gaa aac acc gtc aac ttc 547  
 Leu Ala Met Glu Met Val Arg Asp Ile Arg Glu Asn Thr Val Asn Phe  
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tca cca aac tac gac ggt aaa acc ctc gaa cca gac gtt ttg cca tcg 595  
 Ser Pro Asn Tyr Asp Gly Lys Thr Leu Glu Pro Asp Val Leu Pro Ser  
 150 155 160 165

cgc gtt cca aac ttg ttg atg aac ggt tcg ggc ggc att cgc gtc ggc 643  
 Arg Val Pro Asn Leu Leu Met Asn Gly Ser Gly Gly Ile Ala Val Gly  
 170 175 180

atg gcc acc aac atc cca ccg cac aac ctc aac gag ctt gcc gac gcc 691  
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 185 190 195

atc ttc tgg ctc ctg gaa aac cca gac gcc gaa gaa tcc gaa gct ctc 739  
 Ile Phe Trp Leu Leu Glu Asn Pro Asp Ala Glu Glu Ser Glu Ala Leu  
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gaa gcc tgc atg aag ttt gtg aag ggc cca gac ttc cca acc gct ggc 787  
 Glu Ala Cys Met Lys Phe Val Lys Gly Pro Asp Phe Pro Thr Ala Gly  
 215 220 225

ctc atc atc ggt gac aag ggc atc cac gat gcc tac acc acc ggc cgc 835  
 Leu Ile Ile Gly Asp Lys Gly Ile His Asp Ala Tyr Thr Thr Gly Arg  
 230 235 240 245

ggc tcc atc cgc atg cgc ggt gtc acc tcc atc gag gag gaa ggc aac 883  
 Gly Ser Ile Arg Met Arg Gly Val Thr Ser Ile Glu Glu Glu Gly Asn  
 250 255 260

cgc acc gtc atc gtt atc acc gag ctg cca tac cag gtc aac ccg gat 931  
 Arg Thr Val Ile Val Ile Thr Glu Leu Pro Tyr Gln Val Asn Pro Asp  
 265 270 275

aac ctg atc tct aat atc cgc gag cag gtc cgc gac ggc aag ctc gtg 979  
 Asn Leu Ile Ser Asn Ile Ala Glu Gln Val Arg Asp Gly Lys Leu Val  
 280 285 290

ggc atc tcc aag att gaa gat gaa tcc tcc gac cgc gtc ggc atg cgc 1027  
 Gly Ile Ser Lys Ile Glu Asp Glu Ser Ser Asp Arg Val Gly Met Arg  
 295 300 305

att gtg gtc acc ctc aag cgc gac gca gtt gcc cgc gtg gtg ctg aac 1075  
 Ile Val Val Thr Leu Lys Arg Asp Ala Val Ala Arg Val Val Leu Asn  
 310 315 320 325

aac ctg ttc aag cac tcc cag ctg caa gcc aac ttt ggt cgc aac atg 1123  
 Asn Leu Phe Lys His Ser Gln Leu Gln Ala Asn Phe Gly Ala Asn Met  
 330 335 340

ctc tcc atc gtc gat ggc gtg cca cgc acc ctt cgc ctg gac cag atg 1171  
 Leu Ser Ile Val Asp Gly Val Pro Arg Thr Leu Arg Leu Asp Gln Met  
 345 350 355

ctg cgc tac tac gtg gca cac cag atc gaa gtc atc gtg cgc cgc acc 1219  
 Leu Arg Tyr Tyr Val Ala His Gln Ile Glu Val Ile Val Arg Arg Thr  
 360 365 370

caa tac cgc ctc gac aag gct gaa gag cgc gcc cac ctc ctc cgc ggc 1267  
 Gln Tyr Arg Leu Asp Lys Ala Glu Glu Arg Ala His Leu Leu Arg Gly  
 375 380 385

ctg gtc aag gcc ctg gac atg ctg gac gag gtc atc cgc ctc atc cgc 1315  
 Leu Val Lys Ala Leu Asp Met Leu Asp Glu Val Ile Ala Leu Ile Arg  
 390 395 400 405

cgc agc cca acc cca gat gaa gcc cgc acc ggc ctc atg tgc ctt ctc 1363  
 Arg Ser Pro Thr Pro Asp Glu Ala Arg Thr Gly Leu Met Ser Leu Leu  
 410 415 420

gac gtc gac gag cgc cag gct gac gca att ctg gca atg cag ctg cgt 1411  
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 425 430 435

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 Arg Leu Ala Ala Leu Glu Arg Gln Lys Ile Ile Asp Glu Leu Ala Glu  
 440 445 450

atc gag ctg gaa atc gct gac ctg aag gcc atc ctg gca agc cca gaa 1507  
 Ile Glu Leu Glu Ile Ala Asp Leu Lys Ala Ile Leu Ala Ser Pro Glu  
 455 460 465

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 470 475 480 485

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tct gaa gaa gac ctc att gcg cgt gaa aac gtt gtc atc acc att acc 1651  
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 505 510 515

tcc acc ggt tac gca aag cgc acc aag gtc gat gcc tac aag tcg caa 1699  
 Ser Thr Gly Tyr Ala Lys Arg Thr Lys Val Asp Ala Tyr Lys Ser Gln  
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aag cgt ggc ggc aag ggt gtt cgt ggc gca gag ctc aag caa gat gac 1747  
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 535 540 545

att gtt cgt cac ttc ttc gtc agc tcc acc cac gac tgg att ttg ttc 1795  
 Ile Val Arg His Phe Phe Val Ser Ser Thr His Asp Trp Ile Leu Phe  
 550 555 560 565

ttc acc aac tac ggt cgc gtg tac cgc ctc aag gca ttc gaa ctt cca 1843  
 Phe Thr Asn Tyr Gly Arg Val Tyr Arg Leu Lys Ala Phe Glu Leu Pro  
 570 575 580

gag gca tcc cgc acc gca cgt gga cag cac gtg gcc aac ctt ctg gaa 1891  
 Glu Ala Ser Arg Thr Ala Arg Gly Gln His Val Ala Asn Leu Leu Glu  
 585 590 595

ttc caa cct ggt gag caa atc gcc cag gtc atc cag ttg gaa agc tac 1939  
 Phe Gln Pro Gly Glu Gln Ile Ala Gln Val Ile Gln Leu Glu Ser Tyr  
 600 605 610

aac gac ttc cca tac ctg gtg ctc gca acc gca cac ggt cgc gtg aag 1987  
 Asn Asp Phe Pro Tyr Leu Val Leu Ala Thr Ala His Gly Arg Val Lys  
 615 620 625

aag tcc cgc ctg ctc gac tac gaa tca gca cgt tcc ggt ggc ctc atc 2035  
 Lys Ser Arg Leu Leu Asp Tyr Glu Ser Ala Arg Ser Gly Gly Leu Ile  
 630 635 640 645

gcc atc aac ctg aac gag gac gat cgc ctc atc ggc gcc gca ctt tgc 2083  
 Ala Ile Asn Leu Asn Glu Asp Asp Arg Leu Ile Gly Ala Ala Leu Cys  
 650 655 660

ggt gaa gaa gac gat ctg ctg ctg gtc tct gaa ttc gga cag tcc atc 2131  
 Gly Glu Glu Asp Asp Leu Leu Leu Val Ser Glu Phe Gly Gln Ser Ile  
 665 670 675

cgc ttc acc gcc gac gat gag cag ctc cgc ccc atg ggc cgc gcc acc 2179  
 Arg Phe Thr Ala Asp Asp Glu Gln Leu Arg Pro Met Gly Arg Ala Thr  
 680 685 690

gcc ggt gtc aag ggc atg cgc ttc cgc gac aac gac caa ctg ctg tcc 2227



Ala Gly Val Lys Gly Met Arg Phe Arg Asp Asn Asp Gln Leu Leu Ser  
695 700 705

atg tcc gtg gtc cgc gac ggc gaa ttc ctc gtt gcc acc tcc ggc 2275  
Met Ser Val Val Arg Asp Gly Glu Phe Leu Leu Val Ala Thr Ser Gly  
710 715 720 725

ggc tac ggc aag cgc acc cca ctt gag gat tac tcc acc cag ggc cgt 2323  
Gly Tyr Gly Lys Arg Thr Pro Leu Glu Asp Tyr Ser Thr Gln Gly Arg  
730 735 740

ggc ggc ctc ggc gtg gtg acc ttc aag tac acc cag aag cgc ggt cgc 2371  
Gly Gly Leu Gly Val Val Thr Phe Lys Tyr Thr Pro Lys Arg Gly Arg  
745 750 755

ctc gtc agc gcc atc gca gtt gag gaa gat gac gag atc ttc gcc atc 2419  
Leu Val Ser Ala Ile Ala Val Glu Glu Asp Asp Glu Ile Phe Ala Ile  
760 765 770

acc tcc gcc ggc ggc gtt gtt cgc acc gaa gtc aag cag atc cga cca 2467  
Thr Ser Ala Gly Gly Val Val Arg Thr Glu Val Lys Gln Ile Arg Pro  
775 780 785

tcc tcc cgt gca aca atg ggt gtt cga ctg gtc aac ttg gaa gaa ggt 2515  
Ser Ser Arg Ala Thr Met Gly Val Arg Leu Val Asn Leu Glu Glu Gly  
790 795 800 805

gta gaa ctg ctt gcc atc gac aag aac gtc gaa gac cag ggc gaa gca 2563  
Val Glu Leu Leu Ala Ile Asp Lys Asn Val Glu Asp Gln Gly Glu Ala  
810 815 820

tcc gca gaa gca gta gca aag ggt gca gtc gaa gga cca gca tcc aag 2611  
Ser Ala Glu Ala Val Ala Lys Gly Ala Val Glu Gly Pro Ala Ser Lys  
825 830 835

act gct gcc gaa gaa acc gac tcc gtt gac aac gga tcc gac gaa aac 2659  
Thr Ala Ala Glu Glu Thr Asp Ser Val Asp Asn Gly Ser Asp Glu Asn  
840 845 850

ggc gag gaa taatttatgg catcccgaga agt 2691  
Gly Glu Glu  
855

<210> 108

<211> 856

<212> PRT

<213> Corynebacterium glutamicum

<400> 108

Val Ser Asp Asp Asn Thr Gly Gln Phe Asp Arg Val Asn Pro Ile Asp  
1 5 10 15

Ile Asn Glu Glu Met Gln Ser Ser Tyr Ile Asp Tyr Ala Met Ser Val  
20 25 30

Ile Val Gly Arg Ala Leu Pro Glu Val Arg Asp Gly Leu Lys Pro Val  
35 40 45

His Arg Arg Val Leu Tyr Ala Met Phe Asp Asn Gly Tyr Arg Pro Asp  
50 55 60

Arg Ser Tyr Val Lys Ser Ala Lys Pro Val Ala Asp Thr Met Gly Asn  
 65 70 75 80  
 Phe His Pro His Gly Asp Thr Ala Ile Tyr Asp Thr Leu Val Arg Met  
 85 90 95  
 Ala Gln Pro Trp Ser Met Arg Tyr Pro Leu Val Asp Gly Gln Gly Asn  
 100 105 110  
 Phe Gly Ser Arg Gly Asn Asp Gly Pro Ala Ala Met Arg Tyr Thr Glu  
 115 120 125  
 Cys Arg Met Thr Pro Leu Ala Met Glu Met Val Arg Asp Ile Arg Glu  
 130 135 140  
 Asn Thr Val Asn Phe Ser Pro Asn Tyr Asp Gly Lys Thr Leu Glu Pro  
 145 150 155 160  
 Asp Val Leu Pro Ser Arg Val Pro Asn Leu Leu Met Asn Gly Ser Gly  
 165 170 175  
 Gly Ile Ala Val Gly Met Ala Thr Asn Ile Pro Pro His Asn Leu Asn  
 180 185 190  
 Glu Leu Ala Asp Ala Ile Phe Trp Leu Leu Glu Asn Pro Asp Ala Glu  
 195 200 205  
 Glu Ser Glu Ala Leu Glu Ala Cys Met Lys Phe Val Lys Gly Pro Asp  
 210 215 220  
 Phe Pro Thr Ala Gly Leu Ile Ile Gly Asp Lys Gly Ile His Asp Ala  
 225 230 235 240  
 Tyr Thr Thr Gly Arg Gly Ser Ile Arg Met Arg Gly Val Thr Ser Ile  
 245 250 255  
 Glu Glu Glu Gly Asn Arg Thr Val Ile Val Ile Thr Glu Leu Pro Tyr  
 260 265 270  
 Gln Val Asn Pro Asp Asn Leu Ile Ser Asn Ile Ala Glu Gln Val Arg  
 275 280 285  
 Asp Gly Lys Leu Val Gly Ile Ser Lys Ile Glu Asp Glu Ser Ser Asp  
 290 295 300  
 Arg Val Gly Met Arg Ile Val Val Thr Leu Lys Arg Asp Ala Val Ala  
 305 310 315 320  
 Arg Val Val Leu Asn Asn Leu Phe Lys His Ser Gln Leu Gln Ala Asn  
 325 330 335  
 Phe Gly Ala Asn Met Leu Ser Ile Val Asp Gly Val Pro Arg Thr Leu  
 340 345 350  
 Arg Leu Asp Gln Met Leu Arg Tyr Tyr Val Ala His Gln Ile Glu Val  
 355 360 365  
 Ile Val Arg Arg Thr Gln Tyr Arg Leu Asp Lys Ala Glu Glu Arg Ala  
 370 375 380

His Leu Leu Arg Gly Leu Val Lys Ala Leu Asp Met Leu Asp Glu Val  
 385 390 395 400  
 Ile Ala Leu Ile Arg Arg Ser Pro Thr Pro Asp Glu Ala Arg Thr Gly  
 405 410 415  
 Leu Met Ser Leu Leu Asp Val Asp Glu Ala Gln Ala Asp Ala Ile Leu  
 420 425 430  
 Ala Met Gln Leu Arg Arg Leu Ala Ala Leu Glu Arg Gln Lys Ile Ile  
 435 440 445  
 Asp Glu Leu Ala Glu Ile Glu Leu Glu Ile Ala Asp Leu Lys Ala Ile  
 450 455 460  
 Leu Ala Ser Pro Glu Arg Gln Arg Thr Ile Val Arg Asp Glu Leu Thr  
 465 470 475 480  
 Glu Ile Val Glu Lys Tyr Gly Asp Glu Arg Arg Ser Gln Ile Ile Ala  
 485 490 495  
 Ala Thr Gly Asp Val Ser Glu Glu Asp Leu Ile Ala Arg Glu Asn Val  
 500 505 510  
 Val Ile Thr Ile Thr Ser Thr Gly Tyr Ala Lys Arg Thr Lys Val Asp  
 515 520 525  
 Ala Tyr Lys Ser Gln Lys Arg Gly Gly Lys Gly Val Arg Gly Ala Glu  
 530 535 540  
 Leu Lys Gln Asp Asp Ile Val Arg His Phe Phe Val Ser Ser Thr His  
 545 550 555 560  
 Asp Trp Ile Leu Phe Phe Thr Asn Tyr Gly Arg Val Tyr Arg Leu Lys  
 565 570 575  
 Ala Phe Glu Leu Pro Glu Ala Ser Arg Thr Ala Arg Gly Gln His Val  
 580 585 590  
 Ala Asn Leu Leu Glu Phe Gln Pro Gly Glu Gln Ile Ala Gln Val Ile  
 595 600 605  
 Gln Leu Glu Ser Tyr Asn Asp Phe Pro Tyr Leu Val Leu Ala Thr Ala  
 610 615 620  
 His Gly Arg Val Lys Lys Ser Arg Leu Leu Asp Tyr Glu Ser Ala Arg  
 625 630 635 640  
 Ser Gly Gly Leu Ile Ala Ile Asn Leu Asn Glu Asp Asp Arg Leu Ile  
 645 650 655  
 Gly Ala Ala Leu Cys Gly Glu Glu Asp Asp Leu Leu Leu Val Ser Glu  
 660 665 670  
 Phe Gly Gln Ser Ile Arg Phe Thr Ala Asp Asp Glu Gln Leu Arg Pro  
 675 680 685  
 Met Gly Arg Ala Thr Ala Gly Val Lys Gly Met Arg Phe Arg Asp Asn  
 690 695 700  
 Asp Gln Leu Leu Ser Met Ser Val Val Arg Asp Gly Glu Phe Leu Leu

705                      710                      715                      720

Val Ala Thr Ser Gly Gly Tyr Gly Lys Arg Thr Pro Leu Glu Asp Tyr  
725                      730                      735

Ser Thr Gln Gly Arg Gly Gly Leu Gly Val Val Thr Phe Lys Tyr Thr  
740                      745                      750

Pro Lys Arg Gly Arg Leu Val Ser Ala Ile Ala Val Glu Asp Asp  
755                      760                      765

Glu Ile Phe Ala Ile Thr Ser Ala Gly Gly Val Val Arg Thr Glu Val  
770                      775                      780

Lys Gln Ile Arg Pro Ser Ser Arg Ala Thr Met Gly Val Arg Leu Val  
785                      790                      795                      800

Asn Leu Glu Glu Gly Val Glu Leu Leu Ala Ile Asp Lys Asn Val Glu  
805                      810                      815

Asp Gln Gly Glu Ala Ser Ala Glu Ala Val Ala Lys Gly Ala Val Glu  
820                      825                      830

Gly Pro Ala Ser Lys Thr Ala Ala Glu Glu Thr Asp Ser Val Asp Asn  
835                      840                      845

Gly Ser Asp Glu Asn Gly Glu Glu  
850                      855

<210> 109  
<211> 257  
<212> DNA  
<213> Corynebacterium glutamicum

<220>  
<221> CDS  
<222> (1)..(234)  
<223> FRXA01682

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Arg Thr Lys Val Asp Ala Tyr Lys Ser Gln Lys Arg Gly Gly Lys Gly  
1                      5                      10                      15

ggt tgt ggc gca gag ctc aag caa gat gac att gtt cgt cac ttc ttc 96  
Val Cys Gly Ala Glu Leu Lys Gln Asp Asp Ile Val Arg His Phe Phe  
20                      25                      30

gtc agc tcc acc cac gac tgg att ttg ttt ctt cac caa cta cgg tcg 144  
Val Ser Ser Thr His Asp Trp Ile Leu Phe Leu His Gln Leu Arg Ser  
35                      40                      45

cgt gta ccg cct caa ggc att cga act tcc aga ggc atc ccg cac cgc 192  
Arg Val Pro Pro Gln Gly Ile Arg Thr Ser Arg Gly Ile Pro His Arg  
50                      55                      60

acg tgg aca gca cgt ggc caa cct tct gga att cca acc tgg 234  
Thr Trp Thr Ala Arg Gly Gln Pro Ser Gly Ile Pro Thr Trp  
65                      70                      75

tgagcaaatc gccaggtca tcc

257

&lt;210&gt; 110

&lt;211&gt; 78

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 110

Arg Thr Lys Val Asp Ala Tyr Lys Ser Gln Lys Arg Gly Gly Lys Gly  
 1 5 10 15

Val Cys Gly Ala Glu Leu Lys Gln Asp Asp Ile Val Arg His Phe Phe  
 20 25 30

Val Ser Ser Thr His Asp Trp Ile Leu Phe Leu His Gln Leu Arg Ser  
 35 40 45

Arg Val Pro Pro Gln Gly Ile Arg Thr Ser Arg Gly Ile Pro His Arg  
 50 55 60

Thr Trp Thr Ala Arg Gly Gln Pro Ser Gly Ile Pro Thr Trp  
 65 70 75

&lt;210&gt; 111

&lt;211&gt; 850

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(850)

&lt;223&gt; FRXA01683

&lt;400&gt; 111

gggtgtttgtg ggcagagct caagcaagat gacattgttc gtcacttctt cgtagctcc 60

accacagact ggattttgtt tcttcaccaa ctacgggtcgc gtg tac cgc ctc aag 115  
 Val Tyr Arg Leu Lys  
 1 5

gca ttc gaa ctt cca gag gca tcc cgc acc gca cgt gga cag cac gtg 163  
 Ala Phe Glu Leu Pro Glu Ala Ser Arg Thr Ala Arg Gly Gln His Val  
 10 15 20

gcc aac ctt ctg gaa ttc caa cct ggt gag caa atc gcc cag gtc atc 211  
 Ala Asn Leu Leu Glu Phe Gln Pro Gly Glu Gln Ile Ala Gln Val Ile  
 25 30 35

cag ttg gaa agc tac aac gac ttc cca tac ctg gtg ctc gca acc gca 259  
 Gln Leu Glu Ser Tyr Asn Asp Phe Pro Tyr Leu Val Leu Ala Thr Ala  
 40 45 50

cac ggt cgc gtg aag aag tcc cgc ctg ctc gac tac gaa tca gca cgt 307  
 His Gly Arg Val Lys Lys Ser Arg Leu Leu Asp Tyr Glu Ser Ala Arg  
 55 60 65

tcc ggt ggc ctc atc gcc atc aac ctg aac gag gac gat cgc ctc atc 355  
 Ser Gly Gly Leu Ile Ala Ile Asn Leu Asn Glu Asp Asp Arg Leu Ile  
 70 75 80 85

ggc gcc gca ctt tgc ggt gaa gaa gac gat ctg ctg ctg gtc tct gaa 403  
 Gly Ala Ala Leu Cys Gly Glu Glu Asp Asp Leu Leu Leu Val Ser Glu  
 90 95 100  
 ttc gga cag tcc atc cgc ttc acc gcc gac gat gag cag etc cgc ccc 451  
 Phe Gly Gln Ser Ile Arg Phe Thr Ala Asp Asp Glu Gln Leu Arg Pro  
 105 110 115  
 atg ggc cgc gcc acc gcc ggt gtc aag ggc atg cgc ttc cgc gac aac 499  
 Met Gly Arg Ala Thr Ala Gly Val Lys Gly Met Arg Phe Arg Asp Asn  
 120 125 130  
 gac caa ctg ctg tcc atg tcc gtg gtc cgc gac ggc gaa ttc etc etc 547  
 Asp Gln Leu Leu Ser Met Ser Val Val Arg Asp Gly Glu Phe Leu Leu  
 135 140 145  
 gtt gcc acc tcc ggc ggc tac ggc aag cgc acc cca ctt gag gat tac 595  
 Val Ala Thr Ser Gly Gly Tyr Gly Lys Arg Thr Pro Leu Glu Asp Tyr  
 150 155 160 165  
 tcc acc cag ggc cgt ggt ggc etc ggc gtg gtg acc ttc aag tac acc 643  
 Ser Thr Gln Gly Arg Gly Gly Leu Gly Val Val Thr Phe Lys Tyr Thr  
 170 175 180  
 ccg aag cgc ggt cgc etc gtc agc gcc atc gca gtt gag gaa gat gac 691  
 Pro Lys Arg Gly Arg Leu Val Ser Ala Ile Ala Val Glu Glu Asp Asp  
 185 190 195  
 gag atc ttc gcc atc acc tcc gcc ggc ggc gtt gtt cgc acc gaa gtc 739  
 Glu Ile Phe Ala Ile Thr Ser Ala Gly Gly Val Val Arg Thr Glu Val  
 200 205 210  
 aag cag atc cga cca tcc tcc cgt gca aca atg ggt gtt cga ctg gtc 787  
 Lys Gln Ile Arg Pro Ser Ser Arg Ala Thr Met Gly Val Arg Leu Val  
 215 220 225  
 aac ttg gaa gaa ggt gta gaa ctg ctt gcc atc gac aag aac gtc gaa 835  
 Asn Leu Glu Glu Gly Val Glu Leu Leu Ala Ile Asp Lys Asn Val Glu  
 230 235 240 245  
 gac cag ggc gaa gca 850  
 Asp Gln Gly Glu Ala  
 250

&lt;210&gt; 112

&lt;211&gt; 250

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 112

Val Tyr Arg Leu Lys Ala Phe Glu Leu Pro Glu Ala Ser Arg Thr Ala  
 1 5 10 15

Arg Gly Gln His Val Ala Asn Leu Leu Glu Phe Gln Pro Gly Glu Gln  
 20 25 30

Ile Ala Gln Val Ile Gln Leu Glu Ser Tyr Asn Asp Phe Pro Tyr Leu  
 35 40 45

Val Leu Ala Thr Ala His Gly Arg Val Lys Lys Ser Arg Leu Leu Asp  
50 55 60

Tyr Glu Ser Ala Arg Ser Gly Gly Leu Ile Ala Ile Asn Leu Asn Glu  
65 70 75 80

Asp Asp Arg Leu Ile Gly Ala Ala Leu Cys Gly Glu Glu Asp Asp Leu  
85 90 95

Leu Leu Val Ser Glu Phe Gly Gln Ser Ile Arg Phe Thr Ala Asp Asp  
100 105 110

Glu Gln Leu Arg Pro Met Gly Arg Ala Thr Ala Gly Val Lys Gly Met  
115 120 125

Arg Phe Arg Asp Asn Asp Gln Leu Leu Ser Met Ser Val Val Arg Asp  
130 135 140

Gly Glu Phe Leu Leu Val Ala Thr Ser Gly Gly Tyr Gly Lys Arg Thr  
145 150 155 160

Pro Leu Glu Asp Tyr Ser Thr Gln Gly Arg Gly Gly Leu Gly Val Val  
165 170 175

Thr Phe Lys Tyr Thr Pro Lys Arg Gly Arg Leu Val Ser Ala Ile Ala  
180 185 190

Val Glu Glu Asp Asp Glu Ile Phe Ala Ile Thr Ser Ala Gly Gly Val  
195 200 205

Val Arg Thr Glu Val Lys Gln Ile Arg Pro Ser Ser Arg Ala Thr Met  
210 215 220

Gly Val Arg Leu Val Asn Leu Glu Glu Gly Val Glu Leu Leu Ala Ile  
225 230 235 240

Asp Lys Asn Val Glu Asp Gln Gly Glu Ala  
245 250

<210> 113

<211> 873

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(873)

<223> FRXA01684

<400> 113

ggc gac acc gca att tat gac acg ttg gtg cgc atg gct cag cca tgg 48  
Gly Asp Thr Ala Ile Tyr Asp Thr Leu Val Arg Met Ala Gln Pro Trp  
1 5 10 15

tcc atg cga tac ccg ctg gta gac ggc cag ggt aac ttc ggt tcc cgc 96  
Ser Met Arg Tyr Pro Leu Val Asp Gly Gln Gly Asn Phe Gly Ser Arg  
20 25 30

ggc aac gac ggc cct gca gca atg cgt tac acc gag tgc cgc atg acc 144  
Gly Asn Asp Gly Pro Ala Ala Met Arg Tyr Thr Glu Cys Arg Met Thr

35	40	45	
cca ctg gcc atg gag atg gtg cgc gac atc cgc gaa aac acc gtc aac Pro Leu Ala Met Glu Met Val Arg Asp Ile Arg Glu Asn Thr Val Asn 50 55 60			192
ttc tca cca aac tac gac ggt aaa acc ctc gaa cca gac gtt ttg cca Phe Ser Pro Asn Tyr Asp Gly Lys Thr Leu Glu Pro Asp Val Leu Pro 65 70 75 80			240
tcg cgc gtt cca aac ttg ttg atg aac ggt tcg ggc ggc att gcg gtc Ser Arg Val Pro Asn Leu Leu Met Asn Gly Ser Gly Gly Ile Ala Val 85 90 95			288
ggc atg gcc acc aac atc cca ccg cac aac ctc aac gag ctt gcc gac Gly Met Ala Thr Asn Ile Pro Pro His Asn Leu Asn Glu Leu Ala Asp 100 105 110			336
gcc atc ttc tgg ctc ctg gaa aac cca gac gcc gaa gaa tcc gaa gct Ala Ile Phe Trp Leu Leu Glu Asn Pro Asp Ala Glu Glu Ser Glu Ala 115 120 125			384
ctc gaa gcc tgc atg aag ttt gtg aag ggc cca gac ttc cca acc gct Leu Glu Ala Cys Met Lys Phe Val Lys Gly Pro Asp Phe Pro Thr Ala 130 135 140			432
ggc ctc atc atc ggt gac aag ggc atc cac gat gcc tac acc acc ggc Gly Leu Ile Ile Gly Asp Lys Gly Ile His Asp Ala Tyr Thr Thr Gly 145 150 155 160			480
cgc ggc tcc atc cgc atg cgc ggt gtc acc tcc atc gag gag gaa ggc Arg Gly Ser Ile Arg Met Arg Gly Val Thr Ser Ile Glu Glu Glu Gly 165 170 175			528
aac cgc acc gtc atc gtt atc acc gag ctg cca tac cag gtc aac cgc Asn Arg Thr Val Ile Val Ile Thr Glu Leu Pro Tyr Gln Val Asn Pro 180 185 190			576
gat aac ctg atc tct aat atc gcg gag cag gtg cgc gac ggc aag ctc Asp Asn Leu Ile Ser Asn Ile Ala Glu Gln Val Arg Asp Gly Lys Leu 195 200 205			624
gtg ggc atc tcc aag att gaa gat gaa tcc tcc gac cgc gtc ggc atg Val Gly Ile Ser Lys Ile Glu Asp Glu Ser Ser Asp Arg Val Gly Met 210 215 220			672
cgc att gtg gtc acc ctc aag cgc gac gca gtt gcc cgc gtg gtg ctg Arg Ile Val Val Thr Leu Lys Arg Asp Ala Val Ala Arg Val Val Leu 225 230 235 240			720
aac aac ctg ttc aag cac tcc cag ctg caa gcc aac ttt ggt gcg aac Asn Asn Leu Phe Lys His Ser Gln Leu Leu Ala Asn Phe Gly Ala Asn 245 250 255			768
atg ctc tcc atc gtc gat ggc gtg cca cgc acc ctt cgc ctg gac cag Met Leu Ser Ile Val Asp Gly Val Pro Arg Thr Leu Arg Leu Asp Gln 260 265 270			816
atg ctg cgc tac tac gtg gca cac cag atc gaa gtc atc gtg cgc cgc Met Leu Arg Tyr Tyr Val Ala His Gln Ile Glu Val Ile Val Arg Arg 275 280 285			864



acc caa tac  
Thr Gln Tyr  
290

<210> 114  
<211> 291  
<212> PRT  
<213> *Corynebacterium glutamicum*

<400> 114  
Gly Asp Thr Ala Ile Tyr Asp Thr Leu Val Arg Met Ala Gln Pro Trp  
1 5 10 15  
Ser Met Arg Tyr Pro Leu Val Asp Gly Gln Gly Asn Phe Gly Ser Arg  
20 25 30  
Gly Asn Asp Gly Pro Ala Ala Met Arg Tyr Thr Glu Cys Arg Met Thr  
35 40 45  
Pro Leu Ala Met Glu Met Val Arg Asp Ile Arg Glu Asn Thr Val Asn  
50 55 60  
Phe Ser Pro Asn Tyr Asp Gly Lys Thr Leu Glu Pro Asp Val Leu Pro  
65 70 75 80  
Ser Arg Val Pro Asn Leu Leu Met Asn Gly Ser Gly Gly Ile Ala Val  
85 90 95  
Gly Met Ala Thr Asn Ile Pro Pro His Asn Leu Asn Glu Leu Ala Asp  
100 105 110  
Ala Ile Phe Trp Leu Leu Glu Asn Pro Asp Ala Glu Glu Ser Glu Ala  
115 120 125  
Leu Glu Ala Cys Met Lys Phe Val Lys Gly Pro Asp Phe Pro Thr Ala  
130 135 140  
Gly Leu Ile Ile Gly Asp Lys Gly Ile His Asp Ala Tyr Thr Thr Gly  
145 150 155 160  
Arg Gly Ser Ile Arg Met Arg Gly Val Thr Ser Ile Glu Glu Glu Gly  
165 170 175  
Asn Arg Thr Val Ile Val Ile Thr Glu Leu Pro Tyr Gln Val Asn Pro  
180 185 190  
Asp Asn Leu Ile Ser Asn Ile Ala Glu Gln Val Arg Asp Gly Lys Leu  
195 200 205  
Val Gly Ile Ser Lys Ile Glu Asp Glu Ser Ser Asp Arg Val Gly Met  
210 215 220  
Arg Ile Val Val Thr Leu Lys Arg Asp Ala Val Ala Arg Val Val Leu  
225 230 235 240  
Asn Asn Leu Phe Lys His Ser Gln Leu Gln Ala Asn Phe Gly Ala Asn  
245 250 255  
Met Leu Ser Ile Val Asp Gly Val Pro Arg Thr Leu Arg Leu Asp Gln

260 265 270

Met Leu Arg Tyr Tyr Val Ala His Gln Ile Glu Val Ile Val Arg Arg  
 275 280 285

Thr Gln Tyr  
 290

<210> 115  
 <211> 953  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (1)..(930)  
 <223> RXN01688

<400> 115  
 cag ttc gaa ggc cag acc aaa acc aag ctg ggc aac acg gag atc aaa 48  
 Gln Phe Glu Gly Gln Thr Lys Thr Lys Leu Gly Asn Thr Glu Ile Lys  
 1 5 10 15

tcc ttc gtg cag cgc atg gcc aac gag cac atc ggc cac tgg ttg gaa 96  
 Ser Phe Val Gln Arg Met Ala Asn Glu His Ile Gly His Trp Leu Glu  
 20 25 30

gca aac cct gct gaa gcc aag gtc atc atc aac aag gct gtc ggt tcc 144  
 Ala Asn Pro Ala Glu Ala Lys Val Ile Ile Asn Lys Ala Val Gly Ser  
 35 40 45

gcg cag gca cgc ctt gct gct cga aaa gcc cgt gac ctg gtc cga cgg 192  
 Ala Gln Ala Arg Leu Ala Ala Arg Lys Ala Arg Asp Leu Val Arg Arg  
 50 55 60

aag tca gca acc gat ctg ggt gga ctg ccc ggt aag ctt gcc gac tgc 240  
 Lys Ser Ala Thr Asp Leu Gly Gly Leu Pro Gly Lys Leu Ala Asp Cys  
 65 70 75 80

cgt tcc aag gat cca gaa aag tcc gaa ctt tac atc gtg gag ggc gac 288  
 Arg Ser Lys Asp Pro Glu Lys Ser Glu Leu Tyr Ile Val Glu Gly Asp  
 85 90 95

tcc gca ggt ggt tct gcg aag tcc ggc cgt gac tcc atg ttc cag gca 336  
 Ser Ala Gly Gly Ser Ala Lys Ser Gly Arg Asp Ser Met Phe Gln Ala  
 100 105 110

atc ctt cca ctg cga ggc aag atc ctc aac gtg gaa aag gcc cgc cta 384  
 Ile Leu Pro Leu Arg Gly Lys Ile Leu Asn Val Glu Lys Ala Arg Leu  
 115 120 125

gac aag gtt ctg aag aac gcc gaa gtc caa gcg atc atc acc gca ctg 432  
 Asp Lys Val Leu Lys Asn Ala Glu Val Gln Ala Ile Ile Thr Ala Leu  
 130 135 140

ggt acc ggc atc cac gac gag ttc gac atc aac aag ctg cgc tac cac 480  
 Gly Thr Gly Ile His Asp Glu Phe Asp Ile Asn Lys Leu Arg Tyr His  
 145 150 155 160

aag atc gtg ctg atg gcc gac gcc gat gtt gac ggc cag cac atc gca 528

Lys Ile Val Leu Met Ala Asp Ala Asp Val Asp Gly Gln His Ile Ala  
 165 170 175  
 acg ctg ctg ctc acc ctg ctt ttc cgc ttc atg cca gac ctc gtc gcc 576  
 Thr Leu Leu Leu Thr Leu Leu Phe Arg Phe Met Pro Asp Leu Val Ala  
 180 185 190  
 gaa ggc cac gtc tac ttg gca cag cca cct ttg tac aaa ctg aag tgg 624  
 Glu Gly His Val Tyr Leu Ala Gln Pro Pro Leu Tyr Lys Leu Lys Trp  
 195 200 205  
 cag cgc gga gag cca gga ttc gca tac tcc gat gag gag cgc gat gag 672  
 Gln Arg Gly Glu Pro Gly Phe Ala Tyr Ser Asp Glu Glu Arg Asp Glu  
 210 215 220  
 cag ctc aac gaa ggc ctt gcc gct gga cgc aag atc aac aag gac gac 720  
 Gln Leu Asn Glu Gly Leu Ala Ala Gly Arg Lys Ile Asn Lys Asp Asp  
 225 230 235 240  
 ggc atc cag cgc tac aag ggt ctc ggc gag atg aac gcc agc gag ctg 768  
 Gly Ile Gln Arg Thr Lys Gly Leu Gly Glu Met Asn Ala Ser Glu Leu  
 245 250 255  
 tgg gaa acc acc atg gac cca act gtt cgt att ctg cgc cgc gtg gac 816  
 Trp Glu Thr Thr Met Asp Pro Thr Val Arg Ile Leu Arg Arg Val Asp  
 260 265 270  
 atc acc gat gct cag cgt gct gat gaa ctg ttc tcc atc ttg atg ggt 864  
 Ile Thr Asp Ala Gln Arg Ala Asp Glu Leu Phe Ser Ile Leu Met Gly  
 275 280 285  
 gac gac gtt gtg gct cgc cgc agc ttc atc acc cga aat gcc aag gat 912  
 Asp Asp Val Val Val Ala Arg Arg Ser Phe Ile Thr Arg Asn Ala Lys Asp  
 290 295 300  
 gtt cgt ttc ctc gat atc taaagcgcct tacttaaccc gcc 953  
 Val Arg Phe Leu Asp Ile  
 305 310

&lt;210&gt; 116

&lt;211&gt; 310

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 116

Gln Phe Glu Gly Gln Thr Lys Thr Lys Leu Gly Asn Thr Glu Ile Lys  
 1 5 10 15

Ser Phe Val Gln Arg Met Ala Asn Glu His Ile Gly His Trp Leu Glu  
 20 25 30

Ala Asn Pro Ala Glu Ala Lys Val Ile Ile Asn Lys Ala Val Gly Ser  
 35 40 45

Ala Gln Ala Arg Leu Ala Ala Arg Lys Ala Arg Asp Leu Val Arg Arg  
 50 55 60

Lys Ser Ala Thr Asp Leu Gly Gly Leu Pro Gly Lys Leu Ala Asp Cys  
 65 70 75 80

Arg Ser Lys Asp Pro Glu Lys Ser Glu Leu Tyr Ile Val Glu Gly Asp  
                   85                                  90                  95  
 Ser Ala Gly Gly Ser Ala Lys Ser Gly Arg Asp Ser Met Phe Gln Ala  
                   100                                  105                  110  
 Ile Leu Pro Leu Arg Gly Lys Ile Leu Asn Val Glu Lys Ala Arg Leu  
                   115                                  120                  125  
 Asp Lys Val Leu Lys Asn Ala Glu Val Gln Ala Ile Ile Thr Ala Leu  
                   130                                  135                  140  
 Gly Thr Gly Ile His Asp Glu Phe Asp Ile Asn Lys Leu Arg Tyr His  
                   145                                  150                  155                  160  
 Lys Ile Val Leu Met Ala Asp Ala Asp Val Asp Gly Gln His Ile Ala  
                   165                                  170                  175  
 Thr Leu Leu Leu Thr Leu Leu Phe Arg Phe Met Pro Asp Leu Val Ala  
                   180                                  185                  190  
 Glu Gly His Val Tyr Leu Ala Gln Pro Pro Leu Tyr Lys Leu Lys Trp  
                   195                                  200                  205  
 Gln Arg Gly Glu Pro Gly Phe Ala Tyr Ser Asp Glu Glu Arg Asp Glu  
                   210                                  215                  220  
 Gln Leu Asn Glu Gly Leu Ala Ala Gly Arg Lys Ile Asn Lys Asp Asp  
                   225                                  230                  235                  240  
 Gly Ile Gln Arg Tyr Lys Gly Leu Gly Glu Met Asn Ala Ser Glu Leu  
                   245                                  250                  255  
 Trp Glu Thr Thr Met Asp Pro Thr Val Arg Ile Leu Arg Arg Val Asp  
                   260                                  265                  270  
 Ile Thr Asp Ala Gln Arg Ala Asp Glu Leu Phe Ser Ile Leu Met Gly  
                   275                                  280                  285  
 Asp Asp Val Val Ala Arg Arg Ser Phe Ile Thr Arg Asn Ala Lys Asp  
                   290                                  295                  300  
 Val Arg Phe Leu Asp Ile  
                   305                  310

&lt;210&gt; 117

&lt;211&gt; 564

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(564)

&lt;223&gt; FRXA01688

&lt;400&gt; 117

cag ttc gaa ggc cag acc aaa acc aag ctg ggc aac acg gag atc aaa 48  
 Gln Phe Glu Gly Gln Thr Lys Thr Lys Leu Gly Asn Thr Glu Ile Lys  
           1                  5                  10                  15

tcc ttc gtg cag cgc atg gcc aac gag cac atc ggc cac tgg ttg gaa 96  
 Ser Phe Val Gln Arg Met Ala Asn Glu His Ile Gly His Trp Leu Glu  
 20 25 30  
 gca aac cct gct gaa gcc aag gtc atc atc aac aag gct gtc ggt tcc 144  
 Ala Asn Pro Ala Glu Ala Lys Val Ile Ile Asn Lys Ala Val Gly Ser  
 35 40 45  
 gcg cag gca cgc ctt gct gct cga aaa gcc cgt gac ctg gtc cga cgg 192  
 Ala Gln Ala Arg Leu Ala Ala Arg Lys Ala Arg Asp Leu Val Arg Arg  
 50 55 60  
 aag tca gca acc gat ctg ggt gga ctg ccc ggt aag ctt gcc gac tgc 240  
 Lys Ser Ala Thr Asp Leu Gly Gly Leu Pro Gly Lys Leu Ala Asp Cys  
 65 70 75 80  
 cgt tcc aag gat cca gaa aag tcc gaa ctt tac atc gtg gag ggc gac 288  
 Arg Ser Lys Asp Pro Glu Lys Ser Glu Leu Tyr Ile Val Glu Gly Asp  
 85 90 95  
 tcc gca ggt ggt tct gcg aag tcc ggc cgt gac tcc atg ttc cag gca 336  
 Ser Ala Gly Gly Ser Ala Lys Ser Gly Arg Asp Ser Met Phe Gln Ala  
 100 105 110  
 atc ctt cca ctg cga gcc aag atc ctc aac gtg gaa aag gcc cgc cta 384  
 Ile Leu Pro Leu Arg Gly Lys Ile Leu Asn Val Glu Lys Ala Arg Leu  
 115 120 125  
 gac aag gtt ctg aag aac gcc gaa gtc caa gcg atc atc acc gca ctg 432  
 Asp Lys Val Leu Lys Asn Ala Glu Val Gln Ala Ile Ile Thr Ala Leu  
 130 135 140  
 ggt acc ggc atc cac gac gag ttc gac atc aac aag ctg cgc tac cac 480  
 Gly Thr Gly Ile His Asp Glu Phe Asp Ile Asn Lys Leu Arg Tyr His  
 145 150 155 160  
 aag atc gtg ctg atg gcc gac gcc gat gtt gac ggc cag cac atc gca 528  
 Lys Ile Val Leu Met Ala Asp Ala Asp Val Asp Gly Gln His Ile Ala  
 165 170 175  
 acg ctg ctg ctc acc ctg ctt ttc cgc ttc atg cca 564  
 Thr Leu Leu Leu Thr Leu Leu Phe Arg Phe Met Pro  
 180 185

&lt;210&gt; 118

&lt;211&gt; 188

&lt;212&gt; FRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 118

Gln Phe Glu Gly Gln Thr Lys Thr Lys Leu Gly Asn Thr Glu Ile Lys  
 1 5 10 15

Ser Phe Val Gln Arg Met Ala Asn Glu His Ile Gly His Trp Leu Glu  
 20 25 30

Ala Asn Pro Ala Glu Ala Lys Val Ile Ile Asn Lys Ala Val Gly Ser  
 35 40 45

Ala Gln Ala Arg Leu Ala Ala Arg Lys Ala Arg Asp Leu Val Arg Arg

50 55 60

Lys Ser Ala Thr Asp Leu Gly Gly Leu Pro Gly Lys Leu Ala Asp Cys  
65 70 75 80

Arg Ser Lys Asp Pro Glu Lys Ser Glu Leu Tyr Ile Val Glu Gly Asp  
85 90 95

Ser Ala Gly Gly Ser Ala Lys Ser Gly Arg Asp Ser Met Phe Gln Ala  
100 105 110

Ile Leu Pro Leu Arg Gly Lys Ile Leu Asn Val Glu Lys Ala Arg Leu  
115 120 125

Asp Lys Val Leu Lys Asn Ala Glu Val Gln Ala Ile Ile Thr Ala Leu  
130 135 140

Gly Thr Gly Ile His Asp Glu Phe Asp Ile Asn Lys Leu Arg Tyr His  
145 150 155 160

Lys Ile Val Leu Met Ala Asp Ala Asp Val Asp Gly Gln His Ile Ala  
165 170 175

Thr Leu Leu Leu Thr Leu Leu Phe Arg Phe Met Pro  
180 185

<210> 119  
<211> 1239  
<212> DNA  
<213> Corynebacterium glutamicum

<220>  
<221> CDS  
<222> (101)..(1216)  
<223> RXN01689

<400> 119  
ttttgccgtt tctcgcggtg tgcgtggtac tacgtgggga cctaagcgtg taagatggaa 60

acgtctgtat cggataagta gcgaggagtg ttcgtaaaaa gtg gca aac act gaa 115  
Val Ala Asn Thr Glu  
1 5

cac aat tat gac gct tca tgg atc acc atc ctt gaa ggt ctt gag gcg 163  
His Asn Tyr Asp Ala Ser Ser Ile Thr Ile Leu Glu Gly Leu Glu Ala  
10 15 20

gta cgt aag cgc ccg gcc atg tac atc ggt tca act gga ccg cgt gga 211  
Val Arg Lys Arg Pro Gly Met Tyr Ile Gly Ser Thr Gly Pro Arg Gly  
25 30 35

ctg cac cac ctg att tgg gaa gtc gtt gac aac tca gtg gat gag gcc 259  
Leu His His Leu Ile Trp Glu Val Val Asp Asn Ser Val Asp Glu Ala  
40 45 50

atg gct gcc cac gcc acc aag gtt gaa gtg acc ctt ctg gaa gat ggt 307  
Met Ala Gly His Ala Thr Lys Val Glu Val Thr Leu Leu Glu Asp Gly  
55 60 65

ggc gtt caa gtt gtc gat gac ggt cga gga att ccc gtc gat atg cac 355

Gly Val Gln Val Val Asp Asp Gly Arg Gly Ile Pro Val Asp Met His  
 70 75 80 85  
 cca tcc ggt gca cca acc gtg cag gtt gtt atg acc cag ctg cac gcc 403  
 Pro Ser Gly Ala Pro Thr Val Gln Val Val Met Thr Gln Leu His Ala  
 90 95 100  
 ggc ggt aag ttt gac tcc gat tct tac gcc gtt tcc ggt ggt ctg cat 451  
 Gly Gly Lys Phe Asp Ser Asp Ser Tyr Ala Val Ser Gly Gly Leu His  
 105 110 115  
 ggt gtt ggt att tct gtg gtg aac gcc ctg tcc acc cgc gtg gaa gcc 499  
 Gly Val Gly Ile Ser Val Val Asn Ala Leu Ser Thr Arg Val Glu Ala  
 120 125 130  
 gac atc aag ttg cac ggc aag cac tgg tac caa aac ttt gaa aag tct 547  
 Asp Ile Lys Leu His Gly Lys His Trp Tyr Gln Asn Phe Glu Lys Ser  
 135 140 145  
 gtt cca gac gag ttg atc gaa ggc ggc aac gct cgc ggc acc ggt acc 595  
 Val Pro Asp Glu Leu Ile Glu Gly Gly Asn Ala Arg Gly Thr Gly Thr  
 150 155 160 165  
 acc att cgt ttt tgg cca gac gct gaa att ttc gaa acc acc gag ttt 643  
 Thr Ile Arg Phe Trp Pro Asp Ala Glu Ile Phe Glu Thr Thr Glu Phe  
 170 175 180  
 gat ttc gaa acg att tct cga cgt ctg cag gaa atg gca ttc ctt aac 691  
 Asp Phe Glu Thr Ile Ser Arg Arg Leu Gln Glu Met Ala Phe Leu Asn  
 185 190 195  
 aag ggt ctg acc atc acc ttg acg gac aac cgc gcc acc gac gag gaa 739  
 Lys Gly Leu Thr Ile Thr Leu Thr Asp Asn Arg Ala Thr Asp Glu Glu  
 200 205 210  
 ctc gag ctc gaa gca ctc gct gag cag gcc gaa acc gca acg gaa cta 787  
 Leu Glu Leu Glu Ala Leu Ala Glu Gln Gly Glu Thr Ala Thr Glu Leu  
 215 220 225  
 tcc ctc gat gag atc gac aac gaa acc gaa ctc gtt gaa gag acc acc 835  
 Ser Leu Asp Glu Ile Asp Asn Glu Thr Glu Leu Val Glu Glu Thr Thr  
 230 235 240 245  
 gat gct cca aag aag cca aaa aag cgt gag aag aag aaa atc ttc cac 883  
 Asp Ala Pro Lys Lys Pro Lys Lys Arg Glu Lys Lys Lys Ile Phe His  
 250 255 260  
 tac ccc aat ggc ctc gag gac tac gtt cac tac ctc aac cgc agc aag 931  
 Tyr Pro Asn Gly Leu Glu Asp Tyr Val His Tyr Leu Asn Arg Ser Lys  
 265 270 275  
 acc aac atc cac cct tca atc gtg tca ttc gag gca aag gga gat gac 979  
 Thr Asn Ile His Pro Ser Ile Val Ser Phe Glu Ala Lys Gly Asp Asp  
 280 285 290  
 cac gag gtt gag gtg gca atg cag tgg aac tcc tcc tac aag gaa tcc 1027  
 His Glu Val Glu Val Ala Met Gln Trp Asn Ser Ser Tyr Lys Glu Ser  
 295 300 305  
 gtc cac acc ttc gcc aac acc att aac acc cgc gaa ggc ggc acc cac 1075  
 Val His Thr Phe Ala Asn Thr Ile Asn Thr Arg Glu Gly Gly Thr His

310                      315                      320                      325

gag gaa ggt ttc cgc tct gcg ctg acc tcc ctg atg aac cgc tac gca 1123  
 Glu Glu Gly Phe Arg Ser Ala Leu Thr Ser Leu Met Asn Arg Tyr Ala  
                     330                      335                      340

cgt gag cac aag ctt ctg aaa gaa aag gaa gca aac ctt acc ggt gac 1171  
 Arg Glu His Lys Leu Leu Lys Glu Lys Glu Ala Asn Leu Thr Gly Asp  
                     345                      350                      355

gac tgt cgt gaa ggc ctg tcc gcg gtt att ttc cgt gcg cgt tgg 1216  
 Asp Cys Arg Glu Gly Leu Ser Ala Val Ile Phe Arg Ala Arg Trp  
                     360                      365                      370

tgacccacag ttggaaggcc aga 1239

<210> 120  
 <211> 372  
 <212> PRT  
 <213> *Corynebacterium glutamicum*

<400> 120  
 Val Ala Asn Thr Glu His Asn Tyr Asp Ala Ser Ser Ile Thr Ile Leu  
   1                    5                    10                    15

Glu Gly Leu Glu Ala Val Arg Lys Arg Pro Gly Met Tyr Ile Gly Ser  
                     20                    25                    30

Thr Gly Pro Arg Gly Leu His His Leu Ile Trp Glu Val Val Asp Asn  
                     35                    40                    45

Ser Val Asp Glu Ala Met Ala Gly His Ala Thr Lys Val Glu Val Thr  
   50                    55                    60

Leu Leu Glu Asp Gly Gly Val Gln Val Val Asp Asp Gly Arg Gly Ile  
   65                    70                    75                    80

Pro Val Asp Met His Pro Ser Gly Ala Pro Thr Val Gln Val Val Met  
                     85                    90                    95

Thr Gln Leu His Ala Gly Gly Lys Phe Asp Ser Asp Ser Tyr Ala Val  
                     100                    105                    110

Ser Gly Gly Leu His Gly Val Gly Ile Ser Val Val Asn Ala Leu Ser  
                     115                    120                    125

Thr Arg Val Glu Ala Asp Ile Lys Leu His Gly Lys His Trp Tyr Gln  
                     130                    135                    140

Asn Phe Glu Lys Ser Val Pro Asp Glu Leu Ile Glu Gly Gly Asn Ala  
   145                    150                    155                    160

Arg Gly Thr Gly Thr Thr Ile Arg Phe Trp Pro Asp Ala Glu Ile Phe  
                     165                    170                    175

Glu Thr Thr Glu Phe Asp Phe Glu Thr Ile Ser Arg Arg Leu Gln Glu  
                     180                    185                    190

Met Ala Phe Leu Asn Lys Gly Leu Thr Ile Thr Leu Thr Asp Asn Arg  
                     195                    200                    205



Ala Thr Asp Glu Glu Leu Glu Leu Glu Ala Leu Ala Glu Gln Gly Glu  
210 215 220

Thr Ala Thr Glu Leu Ser Leu Asp Glu Ile Asp Asn Glu Thr Glu Leu  
225 230 235 240

Val Glu Glu Thr Thr Asp Ala Pro Lys Lys Pro Lys Lys Arg Glu Lys  
245 250 255

Lys Lys Ile Phe His Tyr Pro Asn Gly Leu Glu Asp Tyr Val His Tyr  
260 265 270

Leu Asn Arg Ser Lys Thr Asn Ile His Pro Ser Ile Val Ser Phe Glu  
275 280 285

Ala Lys Gly Asp Asp His Glu Val Glu Val Ala Met Gln Trp Asn Ser  
290 295 300

Ser Tyr Lys Glu Ser Val His Thr Phe Ala Asn Thr Ile Asn Thr Arg  
305 310 315 320

Glu Gly Gly Thr His Glu Glu Gly Phe Arg Ser Ala Leu Thr Ser Leu  
325 330 335

Met Asn Arg Tyr Ala Arg Glu His Lys Leu Leu Lys Glu Lys Glu Ala  
340 345 350

Asn Leu Thr Gly Asp Asp Cys Arg Glu Gly Leu Ser Ala Val Ile Phe  
355 360 365

Arg Ala Arg Trp  
370

<210> 121

<211> 726

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(726)

<223> FRXA01689

<400> 121

ttt gac tcc gat tct tac gcc gtt tcc ggt ggt ctg cat ggt gtt ggt 48  
Phe Asp Ser Asp Ser Tyr Ala Val Ser Gly Gly Leu His Gly Val Gly  
1 5 10 15

att tct gtg gtg aac gcc ctg tcc acc cgc gtg gaa gcc gac atc aag 96  
Ile Ser Val Val Asn Ala Leu Ser Thr Arg Val Glu Ala Asp Ile Lys  
20 25 30

ttg cac ggc aag cac tgg tac caa aac ttt gaa aag tct gtt cca gac 144  
Leu His Gly Lys His Trp Tyr Gln Asn Phe Glu Lys Ser Val Pro Asp  
35 40 45

gag ttg atc gaa ggc ggc aac gct cgc ggc acc ggt acc acc att cgt 192  
Glu Leu Ile Glu Gly Gly Asn Ala Arg Gly Thr Gly Thr Thr Ile Arg  
50 55 60

ttt tgg cca gac gct gaa att ttc gaa acc acc gag ttt gat ttc gaa 240  
 Phe Trp Pro Asp Ala Glu Ile Phe Glu Thr Thr Glu Phe Asp Phe Glu  
 65 70 75 80  
 acg att tct cga cgt ctg cag gaa atg gca ttc ctt aac aag ggt ctg 288  
 Thr Ile Ser Arg Arg Leu Gln Glu Met Ala Phe Leu Asn Lys Gly Leu  
 85 90 95  
 acc atc acc ttg acg gac aac cgc gcc acc gac gag gaa ctc gag ctc 336  
 Thr Ile Thr Leu Thr Asp Asn Arg Ala Thr Asp Glu Glu Leu Glu Leu  
 100 105 110  
 gaa gca ctc gct gag cag gcc gaa acc gca acg gaa cta tcc ctc gat 384  
 Glu Ala Leu Ala Glu Gln Gly Glu Thr Ala Thr Glu Leu Ser Leu Asp  
 115 120 125  
 gag atc gac aac gaa acc gaa ctc gtt gaa gag acc acc gat gct cca 432  
 Glu Ile Asp Asn Glu Thr Glu Leu Val Glu Glu Thr Thr Asp Ala Pro  
 130 135 140  
 aag aag cca aaa aag cgt gag aag aag aaa atc ttc cac tac ccc aat 480  
 Lys Lys Pro Lys Lys Arg Glu Lys Lys Lys Ile Phe His Tyr Pro Asn  
 145 150 155 160  
 gcc ctc gag gac tac gtt cac tac ctc aac cgc agc aag acc aac atc 528  
 Gly Leu Glu Asp Tyr Val His Tyr Leu Asn Arg Ser Lys Thr Asn Ile  
 165 170 175  
 cac cct tca atc gtg tca ttc gag gca aag gga gat gac cac gag gtt 576  
 His Pro Ser Ile Val Ser Phe Glu Ala Lys Gly Asp Asp His Glu Val  
 180 185 190  
 gag gtg gca atg cag tgg aac tcc tcc tac aag gaa tcc gtc cac acc 624  
 Glu Val Ala Met Gln Trp Asn Ser Ser Tyr Lys Glu Ser Val His Thr  
 195 200 205  
 ttc gcc aac acc att aac acc cgc gaa gcc gcc acc cac gag gaa ggt 672  
 Phe Ala Asn Thr Ile Asn Thr Arg Glu Gly Gly Thr His Glu Glu Gly  
 210 215 220  
 ttc cgc tct gcg ctg acc tcc ctg atg aac cgc tac gca cgt gag cac 720  
 Phe Arg Ser Ala Leu Thr Ser Leu Met Asn Arg Tyr Ala Arg Glu His  
 225 230 235 240  
 aag ctt 726  
 Lys Leu

&lt;210&gt; 122

&lt;211&gt; 242

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 122

Phe Asp Ser Asp Ser Tyr Ala Val Ser Gly Gly Leu His Gly Val Gly  
 1 5 10 15

Ile Ser Val Val Asn Ala Leu Ser Thr Arg Val Glu Ala Asp Ile Lys  
 20 25 30

Leu His Gly Lys His Trp Tyr Gln Asn Phe Glu Lys Ser Val Pro Asp  
35 40 45

Glu Leu Ile Glu Gly Gly Asn Ala Arg Gly Thr Gly Thr Thr Ile Arg  
50 55 60

Phe Trp Pro Asp Ala Glu Ile Phe Glu Thr Thr Glu Phe Asp Phe Glu  
65 70 75 80

Thr Ile Ser Arg Arg Leu Gln Glu Met Ala Phe Leu Asn Lys Gly Leu  
85 90 95

Thr Ile Thr Leu Thr Asp Asn Arg Ala Thr Asp Glu Glu Leu Glu Leu  
100 105 110

Glu Ala Leu Ala Glu Gln Gly Glu Thr Ala Thr Glu Leu Ser Leu Asp  
115 120 125

Glu Ile Asp Asn Glu Thr Glu Leu Val Glu Glu Thr Thr Asp Ala Pro  
130 135 140

Lys Lys Pro Lys Lys Arg Glu Lys Lys Lys Ile Phe His Tyr Pro Asn  
145 150 155 160

Gly Leu Glu Asp Tyr Val His Tyr Leu Asn Arg Ser Lys Thr Asn Ile  
165 170 175

His Pro Ser Ile Val Ser Phe Glu Ala Lys Gly Asp Asp His Glu Val  
180 185 190

Glu Val Ala Met Gln Trp Asn Ser Ser Tyr Lys Glu Ser Val His Thr  
195 200 205

Phe Ala Asn Thr Ile Asn Thr Arg Glu Gly Gly Thr His Glu Glu Gly  
210 215 220

Phe Arg Ser Ala Leu Thr Ser Leu Met Asn Arg Tyr Ala Arg Glu His  
225 230 235 240

Lys Leu

<210> 123

<211> 382

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(382)

<223> FRXA01735

<400> 123

ttttgccgtt tctcgcggtt tgcgtggtac tacgtgggga cctaagcgtg taagatggaa 60

acgtctgtat cggataagta gcgaggagtg ttcgttaaaa gtg gca aac act gaa 115  
Val Ala Asn Thr Glu  
1 5

cac aat tat gac gct tca tgc atc acc atc ctt gaa ggt ctt gag gcg 163  
 His Asn Tyr Asp Ala Ser Ser Ile Thr Ile Leu Glu Gly Leu Glu Ala  
                   10                  15                  20

gta cgt aag cgc ccg ggc atg tac atc ggt tca act gga ccg cgt gga 211  
 Val Arg Lys Arg Pro Gly Met Tyr Ile Gly Ser Thr Gly Pro Arg Gly  
                   25                  30                  35

ctg cac cac ctg att tgg gaa gtc gtt gac aac tca gtg gat gag gcc 259  
 Leu His His Leu Ile Trp Glu Val Val Asp Asn Ser Val Asp Glu Ala  
                   40                  45                  50

atg gct ggc cac gcc acc aag gtt gaa gtg acc ctt ctg gaa gat ggt 307  
 Met Ala Gly His Ala Thr Lys Val Glu Val Thr Leu Leu Glu Asp Gly  
                   55                  60                  65

ggc gtt caa gtt gtc gat gac ggt cga gga att ccc gtc gat atg cac 355  
 Gly Val Gln Val Val Asp Asp Gly Arg Gly Ile Pro Val Asp Met His  
                   70                  75                  80                  85

cca tcc ggt gca cca acc gtg cag gtt 382  
 Pro Ser Gly Ala Pro Thr Val Gln Val  
                   90

&lt;210&gt; 124

&lt;211&gt; 94

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 124

Val Ala Asn Thr Glu His Asn Tyr Asp Ala Ser Ser Ile Thr Ile Leu  
                   1                  5                  10                  15

Glu Gly Leu Glu Ala Val Arg Lys Arg Pro Gly Met Tyr Ile Gly Ser  
                   20                  25                  30

Thr Gly Pro Arg Gly Leu His His Leu Ile Trp Glu Val Val Asp Asn  
                   35                  40                  45

Ser Val Asp Glu Ala Met Ala Gly His Ala Thr Lys Val Glu Val Thr  
                   50                  55                  60

Leu Leu Glu Asp Gly Gly Val Gln Val Val Asp Asp Gly Arg Gly Ile  
                   65                  70                  75                  80

Pro Val Asp Met His Pro Ser Gly Ala Pro Thr Val Gln Val  
                   85                  90

&lt;210&gt; 125

&lt;211&gt; 1962

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101) ..(1939)

&lt;223&gt; RXN03093

&lt;400&gt; 125

ctcagtgggc	acagacacgc	aataagaaca	gtggctttct	gaagtgttct	aaaaggaaca	60
tgaagggggg	caaggcagtt	aacgagaggg	atgcattccc	gtg	gca gat acc gca	115
				Val	Ala Asp Thr Ala	
				1	5	
ggc acc aca gga	tcg aaa aag aag	tac ttg gtg	atc gtc gag	tcg gcg		163
Gly Thr Thr Gly	Ser Lys Lys Lys	Tyr Leu Val	Ile Val Glu	Ser Ala		
	10	15	20			
acc aag gct	aaa aag att	cag cct tac	ctt ggc aac	gac tac	atc gtc	211
Thr Lys Ala Lys	Lys Ile Gln Pro	Tyr Leu Gly	Asn Asp Tyr	Ile Val		
	25	30	35			
gag gcc tcc	ggt cat att	cgt gat	ctg cca cgt	ggc gct	gct gac	259
Glu Ala Ser Val	Gly His Ile Arg	Asp Leu Pro	Arg Gly Ala Ala	Asp		
	40	45	50			
atc cct gca	aag tac aag	aag gag	cct tgg gct	cgt ctt	ggt gtg gac	307
Ile Pro Ala Lys	Tyr Lys Lys	Glu Glu Pro	Trp Ala Arg	Leu Gly Val	Asp	
	55	60	65			
acc gat cgc	ggt ttc gcg	ccg ctt tat	gtg gtg agc	ccc gat	aaa aag	355
Thr Asp Arg Gly	Phe Ala Pro	Leu Tyr Val	Val Val Ser	Pro Asp Lys	Lys	
	70	75	80		85	
aag aag gtc	gct gac ctc	aag gcg	aag ctc	ctc gtt	gat gag ttg	403
Lys Lys Val Ala	Asp Leu Lys	Ala Lys	Leu Lys	Val Asp	Glu Leu	
	90	95	100			
ctg ctg gca	aca gac ccc	gac cgt	gag ggc	gag gcg	att gcg	451
Leu Leu Ala Thr	Asp Pro Asp	Arg Glu Gly	Glu Glu Ala	Ile Ala	Trp His	
	105	110	115			
ttg ctt gag	gtg ttg aag	ccg act gtt	cct gtg cgt	cgc atg	gtg ttc	499
Leu Leu Glu Val	Leu Lys Pro	Thr Val Pro	Val Val Arg	Arg Met	Val Phe	
	120	125	130			
aat gag atc	acg aag cct	gcc att ttg	gct gcg gcg	gaa aac	act cgt	547
Asn Glu Ile Thr	Lys Pro Ala Ile	Leu Ala Ala	Ala Ala Glu	Asn Thr	Arg	
	135	140	145			
gag ctg gat	gag aac ctg	gtg gat gcg	cag gaa act	cgt cgt	att ctg	595
Glu Leu Asp Glu	Asn Leu Val	Asp Ala Gln	Glu Thr Arg	Arg Ile	Leu	
	150	155	160		165	
gac cgt ttg	tac ggc tat	gaa gtc tct	cct gtg cgt	tgg aaa	aag gtc	643
Asp Arg Leu Tyr	Gly Tyr Glu	Val Ser Pro	Val Val Leu	Trp Lys	Lys Val	
	170	175	180			
atg ccg agg	ttg tcg gcg	ggc cgt gtg	cag tcg gtg	gca acc	cgt gtg	691
Met Pro Arg Leu	Ser Ala Gly Arg	Val Gln Ser	Val Ala Thr	Arg Val		
	185	190	195			
att gtt gag	cgg gag cgc	gag cgc atg	gcg ttc gtg	tcg gcg	gat tat	739
Ile Val Glu Arg	Glu Arg Glu	Arg Met Ala	Phe Val Ser	Ala Asp	Tyr	
	200	205	210			
tggtgat	ctg tcg gcg	gag ttt aat	gcg cgt gaa	aac ggc	aag gcg	787
Trp Asp Leu Ser	Ala Glu Phe	Asn Ala Arg	Glu Asn Gly	Lys Ala	Asp	
	215	220	225			

tcg gat aac ccg tcg tcg ttt act gcg cgt ttg tcc acg att gat gga 835  
 Ser Asp Asn Pro Ser Ser Phe Thr Ala Arg Leu Ser Thr Ile Asp Gly 245  
 230 235 240

aac cgt gtt gct caa ggc cgt gat ttt aat gat cgg gga gag ctg acc 883  
 Asn Arg Val Ala Gln Gly Arg Asp Phe Asn Asp Arg Gly Glu Leu Thr 260  
 250 255

tcg gag gct gtc gtc gtc gat aag cag cgt gct gag cgc tta gcc gag 931  
 Ser Glu Ala Val Val Val Asp Lys Gln Arg Ala Glu Ala Leu Ala Glu 275  
 265 270

gct ttg gaa ggc cag gaa atg gcc gtc gtt ggg gtc gag gaa aag ccg 979  
 Ala Leu Glu Gly Gln Glu Met Ala Val Val Gly Val Glu Glu Lys Pro 290  
 280 285

tac acc cgt cgc cct tat gcg ccg ttt atg acc tct acg ctg cag caa 1027  
 Tyr Thr Arg Arg Pro Tyr Ala Pro Phe Met Thr Ser Thr Leu Gln Gln 305  
 295 300

gag tct ggc cgc aag ctg cat tac act tct gag cgc acg atg cgt att 1075  
 Glu Ser Gly Arg Lys Leu His Tyr Thr Ser Glu Arg Thr Met Arg Ile 325  
 310 315 320

gcg cag cgc ttg tat gaa aac ggc cat atc act tat atg cgt act gac 1123  
 Ala Gln Arg Leu Tyr Glu Asn Gly His Ile Thr Tyr Met Arg Thr Asp 340  
 330 335

tcg acc tcg ttg tcg gag cag ggc atg aag gct gcg cgc gat cag gcg 1171  
 Ser Thr Ser Leu Ser Glu Gln Gly Met Lys Ala Ala Arg Asp Gln Ala 355  
 345 350

ttg gag ctg tac ggt gcg gaa tat gtt tcg ccg agc cca cgt acc tat 1219  
 Leu Glu Leu Tyr Gly Ala Glu Tyr Val Ser Pro Ser Pro Arg Thr Tyr 370  
 360 365

gac cgc aag gtg aag aac tcc cag gag gcc cac gag gcg att cgc cca 1267  
 Asp Arg Lys Val Lys Asn Ser Gln Glu Ala His Glu Ala Ile Arg Pro 385  
 375 380

gct ggt gaa act ttt gcg acc ccg ggc cag ctg cat ggc cag ttg gat 1315  
 Ala Gly Glu Thr Phe Ala Thr Pro Gly Gln Leu His Gly Gln Leu Asp 405  
 390 395 400

gcg gaa gaa ttt aag ctc tat gag ctg att tgg cag cgc act gtg gcc 1363  
 Ala Glu Glu Phe Lys Leu Tyr Glu Leu Ile Trp Gln Arg Thr Val Ala 420  
 410 415

tcc cag atg gcc gat gcc aag ggc acg tcc atg aag gtc acc atc ggt 1411  
 Ser Gln Met Ala Asp Ala Lys Gly Thr Ser Met Lys Val Thr Ile Gly 435  
 425 430

ggc acc gcg aag acc ggc gag aag act gag ttc aac gcg acc ggc ccg 1459  
 Gly Thr Ala Lys Thr Gly Glu Lys Thr Glu Phe Asn Ala Thr Gly Arg 450  
 440 445

acg ctg act ttc cct ggc ttc ctg cgc gct tac gtg gaa acc acc ccg 1507  
 Thr Leu Thr Phe Pro Gly Phe Leu Arg Ala Tyr Val Glu Thr Thr Arg 465  
 455 460

Ser Pro Asp Lys Lys Lys Lys Val Ala Asp Leu Lys Ala Lys Leu Lys

85	90	95
Leu Val Asp Glu Leu Leu Leu Ala Thr Asp Pro Asp Arg Glu Gly Leu 100 105 110		
Ala Ile Ala Trp His Leu Leu Glu Val Leu Lys Pro Thr Val Pro Val 115 120 125		
Arg Arg Met Val Phe Asn Glu Ile Thr Lys Pro Ala Ile Leu Ala Ala 130 135 140		
Ala Glu Asn Thr Arg Glu Leu Asp Glu Asn Leu Val Asp Ala Gln Glu 145 150 155 160		
Thr Arg Arg Ile Leu Asp Arg Leu Tyr Gly Tyr Glu Val Ser Pro Val 165 170 175		
Leu Trp Lys Lys Val Met Pro Arg Leu Ser Ala Gly Arg Val Gln Ser 180 185 190		
Val Ala Thr Arg Val Ile Val Glu Arg Glu Arg Glu Arg Met Ala Phe 195 200 205		
Val Ser Ala Asp Tyr Trp Asp Leu Ser Ala Glu Phe Asn Ala Arg Glu 210 215 220		
Asn Gly Lys Ala Asp Ser Asp Asn Pro Ser Ser Phe Thr Ala Arg Leu 225 230 235 240		
Ser Thr Ile Asp Gly Asn Arg Val Ala Gln Gly Arg Asp Phe Asn Asp 245 250 255		
Arg Gly Glu Leu Thr Ser Glu Ala Val Val Val Asp Lys Gln Arg Ala 260 265 270		
Glu Ala Leu Ala Glu Ala Leu Glu Gly Gln Glu Met Ala Val Val Gly 275 280 285		
Val Glu Glu Lys Pro Tyr Thr Arg Arg Pro Tyr Ala Pro Phe Met Thr 290 295 300		
Ser Thr Leu Gln Gln Glu Ser Gly Arg Lys Leu His Tyr Thr Ser Glu 305 310 315 320		
Arg Thr Met Arg Ile Ala Gln Arg Leu Tyr Glu Asn Gly His Ile Thr 325 330 335		
Tyr Met Arg Thr Asp Ser Thr Ser Leu Ser Glu Gln Gly Met Lys Ala 340 345 350		
Ala Arg Asp Gln Ala Leu Glu Leu Tyr Gly Ala Glu Tyr Val Ser Pro 355 360 365		
Ser Pro Arg Thr Tyr Asp Arg Lys Val Lys Asn Ser Gln Glu Ala His 370 375 380		
Glu Ala Ile Arg Pro Ala Gly Glu Thr Phe Ala Thr Pro Gly Gln Leu 385 390 395 400		
His Gly Gln Leu Asp Ala Glu Glu Phe Lys Leu Tyr Glu Leu Ile Trp 405 410 415		



Gln Arg Thr Val Ala Ser Gln Met Ala Asp Ala Lys Gly Thr Ser Met  
420 425

Lys Val Thr Ile Gly Gly Thr Ala Lys Thr Gly Glu Lys Thr Glu Phe  
435 440 445

Asn Ala Thr Gly Arg Thr Leu Thr Phe Pro Gly Phe Leu Arg Ala Tyr  
450 455 460

Val Glu Thr Thr Arg Thr Ala Asp Gly Arg Asp Val Ala Asp Asn Ala  
465 470 475 480

Glu Lys Arg Leu Pro Leu Leu Ser Glu Gly Asp Leu Leu Lys Val Leu  
485 490 495

Ser Ile Glu Ala Asp Gly His Ser Thr Asn Pro Pro Ala Arg Tyr Thr  
500 505 510

Glu Ala Ser Leu Val Lys Lys Met Glu Asp Leu Gly Ile Gly Arg Pro  
515 520 525

Ser Thr Tyr Ala Ser Ile Ile Lys Thr Ile Gln Asp Arg Gly Tyr Val  
530 535 540

Tyr Ser Arg Gly Asn Ala Leu Val Pro Ser Trp Val Ala Phe Ala Val  
545 550 555 560

Val Gly Leu Leu Glu Ala Asn Phe Thr Ser Leu Val Asp Tyr Asp Phe  
565 570 575

Thr Ser Ser Met Glu Asp Glu Leu Asp Asn Ile Ala Ala Gly Arg Glu  
580 585 590

Gly Arg Thr Glu Trp Leu Asn Gly Phe Tyr Phe Gly Arg Cys Arg Ser  
595 600 605

Gly Ser Val His Gly  
610

<210> 127

<211> 2378

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(2355)

<223> FRXA00798

<400> 127

gat tat tgg gat ctg tcg gcg gag ttt aat gcg cgt gaa aac ggc aag 48  
Asp Tyr Trp Asp Leu Ser Ala Glu Phe Asn Ala Arg Glu Asn Gly Lys  
1 5 10 15

gcg gat tcg gat aac ccg tcg tcg ttt act gcg cgt ttg tcc acg att 96  
Ala Asp Ser Asp Asn Pro Ser Ser Phe Thr Ala Arg Leu Ser Thr Ile  
20 25 30

gat gga aac cgt gtt gct caa ggc cgt gat ttt aat gat cgg gga gag 144

ctg cca ctg ctg tct gag ggc gat ctg ctc aag gtt ttg agc atc gaa 864  
Leu Pro Leu Leu Ser Glu Gly Asp Leu Leu Lys Val Leu Ser Ile Glu

275	280	285	
gcc gat ggt cac agc acc aat cca cct gcg cgc tac aca gag gcg tcg Ala Asp Gly His Ser Thr Asn Pro Pro Ala Arg Tyr Thr Glu Ala Ser 290 295 300			912
ctg gtg aag aag atg gaa gat ctg ggc atc ggc cgt cct act tat Leu Val Lys Lys Met Glu Asp Leu Gly Ile Gly Arg Pro Ser Thr Tyr 305 310 315 320			960
gca tcg atc att aag acg att cag gat cga ggc tac gtt tat tcg cgt Ala Ser Ile Ile Lys Thr Ile Gln Asp Arg Gly Tyr Val Tyr Ser Arg 325 330 335			1008
ggc aat gcg ctg gtg ccg tcc tgg gtc gcg ttc gcc gtg gtc gga ttg Gly Asn Ala Leu Val Pro Ser Trp Val Ala Phe Ala Val Gly Leu 340 345 350			1056
ctt gaa gcc aac ttc acc tcg ctg gtg gat tac gat ttc acc tcc tcc Leu Glu Ala Asn Phe Thr Ser Ser Val Asp Tyr Asp Phe Thr Ser Ser 355 360 365			1104
atg gaa gat gag ctg gac aac atc gcc gca ggt cgc gag gcc cgc acg Met Glu Asp Glu Leu Asp Asn Ile Ala Ala Gly Arg Glu Gly Arg Thr 370 375 380			1152
gag tgg ctc aac ggt ttc tac ttc ggc gat gcc gaa gcg gat cag tcc Glu Trp Leu Asn Gly Phe Tyr Phe Gly Asp Ala Glu Ala Asp Gln Ser 385 390 395 400			1200
atg gct gaa tca gtt gcc cgc cag gcc ggt ttg aag gcg ctt gtc gac Met Ala Glu Ser Val Ala Arg Gln Gly Gly Leu Lys Ala Leu Val Asp 405 410 415			1248
gcg aac ctg gag cac atc gac gcg cgt tca gta aac tca ctc aag ctt Ala Asn Leu Glu His Ile Asp Ala Arg Ser Val Asn Ser Leu Lys Leu 420 425 430			1296
ttc gac gac gcc gaa gcc cgt gcc gtg aac gtt cga gtc gga cgc tac Phe Asp Asp Ala Glu Gly Arg Ala Val Asn Val Arg Val Gly Arg Tyr 435 440 445			1344
ggt cgc tac atc gag cgc atc gtg gcc acc acc gcg gaa gcc gag cca Gly Pro Tyr Ile Glu Arg Ile Val Gly Thr Thr Ala Glu Gly Glu Pro 450 455 460			1392
gaa ttt cag cgc gcc aac cta cct gag gaa acc acg cct gat gag ctg Glu Phe Gln Arg Ala Asn Leu Pro Glu Glu Thr Thr Pro Asp Glu Leu 465 470 475 480			1440
acc ctc gag gtc gct gag aag ctt ttc gct acc cca caa ggt gga cgt Thr Leu Glu Val Ala Glu Lys Leu Phe Ala Thr Pro Gln Gly Gly Arg 485 490 495			1488
gaa ctg gcc att aac cca gca aac ggt cgc atg gtg gtg gct aag gaa Glu Leu Gly Ile Asn Pro Ala Asn Gly Arg Met Val Val Ala Lys Glu 500 505 510			1536
ggc cgc ttt ggt cca tac gtg atc gag cag gtc acg gac tca gag cgc Gly Arg Phe Gly Pro Tyr Val Ile Glu Gln Val Thr Asp Ser Glu Arg 515 520 525			1584

gct ggc gcc gaa gcc caa gca gaa gaa gtc gtt gca gcg gaa cga aaa 1632  
 Ala Gly Ala Glu Ala Gln Ala Glu Glu Val Val Ala Ala Glu Arg Lys  
 530 535 540

gct gaa gac gaa caa cgt gcc acc gat gga atg cga ccc aag aac tgg 1680  
 Ala Glu Asp Glu Gln Arg Ala Thr Asp Gly Met Arg Pro Lys Asn Trp  
 545 550 555 560

gaa acc aag act gcc gca aac cag aag gaa aag cgc atc aac cag ctg 1728  
 Glu Thr Lys Thr Ala Ala Asn Gln Lys Glu Lys Arg Ile Asn Gln Leu  
 565 570 575

gtt gag gaa aac ctc aag cca gcg acc gca tcc ctg ttc agc ggc atg 1776  
 Val Glu Glu Asn Leu Lys Pro Ala Thr Ala Ser Leu Phe Ser Gly Met  
 580 585 590

gaa cct gca gcc gtg acc ctg gaa gaa gcc ctc aag ctg ctg tcc ctg 1824  
 Glu Pro Ala Ala Val Thr Leu Glu Glu Ala Leu Lys Leu Leu Ser Leu  
 595 600 605

cca cgc gaa gta ggt gtc gat cct tcc gac aac gaa gtg atc acc gct 1872  
 Pro Arg Glu Val Gly Val Asp Pro Ser Asp Asn Glu Val Ile Thr Ala  
 610 615 620

caa aac gga cga tac ggc cct tat ctg aag aag ggt agc gac tcc cgt 1920  
 Gln Asn Gly Arg Tyr Gly Pro Tyr Leu Lys Lys Gly Ser Asp Ser Arg  
 625 630 635 640

tcc ctc aac agc gaa gag cag atc ttc acc gtc act ttg gat gag gct 1968  
 Ser Leu Asn Ser Glu Glu Gln Ile Phe Thr Val Thr Leu Asp Gly Ala  
 645 650 655

cgc cgc atc tac gcc gaa cca aag cgt cgt gga cgc gcc gct gct cag 2016  
 Arg Arg Ile Tyr Ala Glu Pro Lys Arg Arg Gly Arg Ala Ala Ala Gln  
 660 665 670

cca cca ctg aag caa ctt ggc gac aat gac gtt tcc ggc aaa cca atg 2064  
 Pro Pro Leu Lys Gln Leu Gly Asp Asn Asp Val Ser Gly Lys Pro Met  
 675 680 685

acc gtc aag gac gga cgt ttc ggc cca tac gtc acc gac ggc acc acc 2112  
 Thr Val Lys Asp Gly Arg Phe Gly Pro Tyr Val Thr Asp Gly Thr Thr  
 690 695 700

aac gcg tca ctg cgc aag ggc gat gtt cca gag tcc ctg acc gat gcg 2160  
 Asn Ala Ser Leu Arg Lys Gly Asp Val Pro Glu Ser Leu Thr Asp Ala  
 705 710 715 720

cgt gcc aac gag tta ctt tcc gag cgt cgt gcc aag gaa gca gca gat 2208  
 Arg Ala Asn Glu Leu Ser Glu Arg Arg Ala Lys Glu Ala Ala Asp  
 725 730 735

ggc gga gct cct gcg aag aag acg tcc act aaa aag act gca gcc aag 2256  
 Gly Gly Ala Pro Ala Lys Lys Thr Ser Thr Lys Lys Thr Ala Ala Lys  
 740 745 750

aag acc acg gct aaa aag aca aca gct aag aaa acc gtg agg aag gct 2304  
 Lys Thr Thr Ala Lys Lys Thr Thr Ala Lys Lys Thr Val Arg Lys Ala  
 755 760 765

ccg ccg aaa acc acc aaa aac gtg gtg aag gcc gcc gct aag aag aag 2352  
 Pro Pro Lys Thr Thr Lys Asn Val Val Lys Ala Gly Ala Lys Lys Lys  
 770 775 780

tcc taaaacatgc tgaacgggtt cgt 2378  
 Ser  
 785

<210> 128

<211> 785

<212> PRT

<213> Corynebacterium glutamicum

<400> 128

Asp Tyr Trp Asp Leu Ser Ala Glu Phe Asn Ala Arg Glu Asn Gly Lys  
 1 5 10 15

Ala Asp Ser Asp Asn Pro Ser Ser Phe Thr Ala Arg Leu Ser Thr Ile  
 20 25 30

Asp Gly Asn Arg Val Ala Gln Gly Arg Asp Phe Asn Asp Arg Gly Glu  
 35 40 45

Leu Thr Ser Glu Ala Val Val Val Asp Lys Gln Arg Ala Glu Ala Leu  
 50 55 60

Ala Glu Ala Leu Glu Gly Gln Glu Met Ala Val Val Gly Val Glu Glu  
 65 70 75 80

Lys Pro Tyr Thr Arg Arg Pro Tyr Ala Pro Phe Met Thr Ser Thr Leu  
 85 90 95

Gln Gln Glu Ser Gly Arg Lys Leu His Tyr Thr Ser Glu Arg Thr Met  
 100 105 110

Arg Ile Ala Gln Arg Leu Tyr Glu Asn Gly His Ile Thr Tyr Met Arg  
 115 120 125

Thr Asp Ser Thr Ser Leu Ser Glu Gln Gly Met Lys Ala Ala Arg Asp  
 130 135 140

Gln Ala Leu Glu Leu Tyr Gly Ala Glu Tyr Val Ser Pro Ser Pro Arg  
 145 150 155 160

Thr Tyr Asp Arg Lys Val Lys Asn Ser Gln Glu Ala His Glu Ala Ile  
 165 170 175

Arg Pro Ala Gly Glu Thr Phe Ala Thr Pro Gly Gln Leu His Gly Gln  
 180 185 190

Leu Asp Ala Glu Glu Phe Lys Leu Tyr Glu Leu Ile Trp Gln Arg Thr  
 195 200 205

Val Ala Ser Gln Met Ala Asp Ala Lys Gly Thr Ser Met Lys Val Thr  
 210 215 220

Ile Gly Gly Thr Ala Lys Thr Gly Glu Lys Thr Glu Phe Asn Ala Thr  
 225 230 235 240

Gly Arg Thr Leu Thr Phe Pro Gly Phe Leu Arg Ala Tyr Val Glu Thr

	245		250		255
Thr Arg Thr	Ala Asp Gly Arg Asp Val Ala Asp Asn Ala Glu Lys Arg				
	260		265		270
Leu Pro Leu Leu Ser	Glu Gly Asp Leu Leu Lys Val Leu Ser Ile Glu				
	275		280		285
Ala Asp Gly His Ser	Thr Asn Pro Pro Ala Arg Tyr Thr Glu Ala Ser				
	290		295		300
Leu Val Lys Lys Met	Glu Asp Leu Gly Ile Gly Arg Pro Ser Thr Tyr				
	305		310		315
Ala Ser Ile Ile Lys	Thr Ile Gln Asp Arg Gly Tyr Val Tyr Ser Arg				
	325		330		335
Gly Asn Ala Leu Val	Pro Ser Trp Val Ala Phe Ala Val Val Gly Leu				
	340		345		350
Leu Glu Ala Asn Phe	Thr Ser Leu Val Asp Tyr Asp Phe Thr Ser Ser				
	355		360		365
Met Glu Asp Glu Leu	Asp Asn Ile Ala Ala Gly Arg Glu Gly Arg Thr				
	370		375		380
Glu Trp Leu Asn Gly	Phe Tyr Phe Gly Asp Ala Glu Ala Asp Gln Ser				
	385		390		395
Met Ala Glu Ser Val	Ala Arg Gln Gly Gly Leu Lys Ala Leu Val Asp				
	405		410		415
Ala Asn Leu Glu His	Ile Asp Ala Arg Ser Val Asn Ser Leu Lys Leu				
	420		425		430
Phe Asp Asp Ala Glu	Gly Arg Ala Val Asn Val Arg Val Gly Arg Tyr				
	435		440		445
Gly Pro Tyr Ile Glu	Arg Ile Val Gly Thr Thr Ala Glu Gly Glu Pro				
	450		455		460
Glu Phe Gln Arg Ala	Asn Leu Pro Glu Glu Thr Thr Pro Asp Glu Leu				
	465		470		475
Thr Leu Glu Val Ala	Glu Lys Leu Phe Ala Thr Pro Gln Gly Gly Arg				
	485		490		495
Glu Leu Gly Ile Asn	Pro Ala Asn Gly Arg Met Val Val Ala Lys Glu				
	500		505		510
Gly Arg Phe Gly Pro	Tyr Val Ile Glu Gln Val Thr Asp Ser Glu Arg				
	515		520		525
Ala Gly Ala Glu Ala	Gln Ala Glu Glu Val Val Ala Ala Glu Arg Lys				
	530		535		540
Ala Glu Asp Glu Gln	Arg Ala Thr Asp Gly Met Arg Pro Lys Asn Trp				
	545		550		555
Glu Thr Lys Thr Ala	Ala Asn Gln Lys Glu Lys Arg Ile Asn Gln Leu				
	565		570		575

Val Glu Glu Asn Leu Lys Pro Ala Thr Ala Ser Leu Phe Ser Gly Met  
580 585 590

Glu Pro Ala Ala Val Thr Leu Glu Glu Ala Leu Lys Leu Leu Ser Leu  
595 600 605

Pro Arg Glu Val Gly Val Asp Pro Ser Asp Asn Glu Val Ile Thr Ala  
610 615 620

Gln Asn Gly Arg Tyr Gly Pro Tyr Leu Lys Lys Gly Ser Asp Ser Arg  
625 630 635 640

Ser Leu Asn Ser Glu Glu Gln Ile Phe Thr Val Thr Leu Asp Glu Ala  
645 650 655

Arg Arg Ile Tyr Ala Glu Pro Lys Arg Arg Gly Arg Ala Ala Ala Gln  
660 665 670

Pro Pro Leu Lys Gln Leu Gly Asp Asn Asp Val Ser Gly Lys Pro Met  
675 680 685

Thr Val Lys Asp Gly Arg Phe Gly Pro Tyr Val Thr Asp Gly Thr Thr  
690 695 700

Asn Ala Ser Leu Arg Lys Gly Asp Val Pro Glu Ser Leu Thr Asp Ala  
705 710 715 720

Arg Ala Asn Glu Leu Leu Ser Glu Arg Arg Ala Lys Glu Ala Ala Asp  
725 730 735

Gly Gly Ala Pro Ala Lys Lys Thr Ser Thr Lys Lys Thr Ala Ala Lys  
740 745 750

Lys Thr Thr Ala Lys Lys Thr Thr Ala Lys Lys Thr Val Arg Lys Ala  
755 760 765

Pro Pro Lys Thr Thr Lys Asn Val Val Lys Ala Gly Ala Lys Lys Lys  
770 775 780

Ser  
785

&lt;210&gt; 129

&lt;211&gt; 488

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(465)

&lt;223&gt; RXN00990

&lt;400&gt; 129

atc ccc gtc ttg gtg gcc acc gat atc gcc gcc cgt ggc att gac gtg 48  
ile Pro Val Leu Val Ala Thr Asp Ile Ala Ala Arg Gly Ile Asp Val  
1 5 10 15

gat gac gtc tcg ctt gtt gtg cac gtt gat ccc cca gca gaa cac aaa 96  
Asp Asp Val Ser Leu Val Val His Val Asp Pro Pro Ala Glu His Lys

	20	25	30	
gcg tat ttg cac cgc gct ggt cgt act gca cga gcc gga act tcc ggt				144
Ala Tyr Leu His Arg Ala Gly Arg Thr Ala Arg Ala Gly Thr Ser Gly				
	35	40	45	
aca gtt gtg act cta gta atg gac gaa caa atc aag gaa gtc cgt gaa				192
Thr Val Val Thr Leu Val Met Asp Glu Gln Ile Lys Glu Val Arg Glu				
	50	55	60	
ctt ttc caa aaa gca ggc gtg aca gcc gct gag gta aaa gtc aac gaa				240
Leu Phe Gln Lys Ala Gly Val Thr Ala Ala Glu Val Lys Val Asn Glu				
	65	70	75	80
aac tca cct gaa ttg gct aaa att act ggt gca cga cgc ccg tca ggc				288
Asn Ser Pro Glu Leu Ala Lys Ile Thr Gly Ala Arg Arg Pro Ser Gly				
	85	90	95	
gtt gct ctt cca gca cct gga cag cag cag cca aag cgg gaa caa aaa				336
Val Ala Leu Pro Ala Pro Gly Gln Gln Gln Pro Lys Arg Glu Gln Lys				
	100	105	110	
aat acc cat aat cgt tct gat tcc aga ggt tcc agc cgg aat cca cgc				384
Asn Thr His Asn Arg Ser Asp Ser Arg Gly Ser Ser Arg Asn Pro Arg				
	115	120	125	
agg cgc gga caa agc gga tcc aga tca acg gcc cgc tcc aac ccg agg				432
Arg Arg Gly Gln Ser Gly Ser Arg Ser Thr Gly Arg Ser Asn Pro Arg				
	130	135	140	
cgt cag act tca agg aaa gac ggt ccc aag agc taaaactccc ccacggcacg				485
Arg Gln Thr Ser Arg Lys Asp Gly Pro Lys Ser				
	145	150	155	
cga				488
 <210> 130				
<211> 155				
<212> PRT				
<213> Corynebacterium glutamicum				
 <400> 130				
Ile Pro Val Leu Val Ala Thr Asp Ile Ala Ala Arg Gly Ile Asp Val				
	1	5	10	15
Asp Asp Val Ser Leu Val Val His Val Asp Pro Pro Ala Glu His Lys				
	20	25	30	
Ala Tyr Leu His Arg Ala Gly Arg Thr Ala Arg Ala Gly Thr Ser Gly				
	35	40	45	
Thr Val Val Thr Leu Val Met Asp Glu Gln Ile Lys Glu Val Arg Glu				
	50	55	60	
Leu Phe Gln Lys Ala Gly Val Thr Ala Ala Glu Val Lys Val Asn Glu				
	65	70	75	80
Asn Ser Pro Glu Leu Ala Lys Ile Thr Gly Ala Arg Arg Pro Ser Gly				
	85	90	95	



Val Ala Leu Pro Ala Pro Gly Gln Gln Gln Pro Lys Arg Glu Gln Lys  
100 105 110

Asn Thr His Asn Arg Ser Asp Ser Arg Gly Ser Ser Arg Asn Pro Arg  
115 120 125

Arg Arg Gly Gln Ser Gly Ser Arg Ser Thr Gly Arg Ser Asn Pro Arg  
130 135 140

Arg Gln Thr Ser Arg Lys Asp Gly Pro Lys Ser  
145 150 155

<210> 131

<211> 476

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(453)

<223> FRXA00990

<400> 131

gtg gcc acc gat atc gcc gcc cgt ggc att gac gtg gat gac gtc tgc 48  
Val Ala Thr Asp Ile Ala Ala Arg Gly Ile Asp Val Asp Val Ser  
1 5 10 15

ctt gtt gtg cac gtt gat ccc cca gca gaa cac aaa gcg tat ttg cac 96  
Leu Val Val His Val Asp Pro Pro Ala Glu His Lys Ala Tyr Leu His  
20 25 30

cgc gct ggt cgt act gca cga gcc gga act tcc ggt aca gtt gtg act 144  
Arg Ala Gly Arg Thr Ala Arg Ala Gly Thr Ser Gly Thr Val Val Thr  
35 40 45

cta gta atg gac gaa caa atc aag gaa gtc cgt gaa ctt ttc caa aaa 192  
Leu Val Met Asp Glu Gln Ile Lys Glu Val Arg Glu Leu Phe Gln Lys  
50 55 60

gca ggc gtg aca gcc gct gag gta aaa gtc aac gaa aac tca cct gaa 240  
Ala Gly Val Thr Ala Ala Glu Val Lys Val Asn Glu Asn Ser Pro Glu  
65 70 75 80

ttg gct aaa att act ggt gca cga cgc ccg tca ggc gtt gct ctt cca 288  
Leu Ala Lys Ile Thr Gly Ala Arg Arg Pro Ser Gly Val Ala Leu Pro  
85 90 95

gca cct gga cag cag cag cca aag cgg gaa caa aaa aat acc cat aat 336  
Ala Pro Gly Gln Gln Pro Lys Arg Glu Gln Lys Asn Thr His Asn  
100 105 110

cgt tct gat tcc aga ggt tcc agc cgg aat cca cgc agg cgc gga caa 384  
Arg Ser Asp Ser Arg Gly Ser Ser Arg Asn Pro Arg Arg Arg Gly Gln  
115 120 125

agc gga tcc aga tca acg ggc cgc tcc aac ccg agg cgt cag act tca 432  
Ser Gly Ser Arg Ser Thr Gly Arg Ser Asn Pro Arg Arg Gln Thr Ser  
130 135 140

agg aaa gac ggt ccc aag agc taaaactccc ccacggcacy cga 476

Arg Lys Asp Gly Pro Lys Ser  
145 150

<210> 132

<211> 151

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 132

Val Ala Thr Asp Ile Ala Ala Arg Gly Ile Asp Val Asp Asp Val Ser  
1 5 10 15

Leu Val Val His Val Asp Pro Pro Ala Glu His Lys Ala Tyr Leu His  
20 25 30

Arg Ala Gly Arg Thr Ala Arg Ala Gly Thr Ser Gly Thr Val Val Thr  
35 40 45

Leu Val Met Asp Glu Gln Ile Lys Glu Val Arg Glu Leu Phe Gln Lys  
50 55 60

Ala Gly Val Thr Ala Ala Glu Val Lys Val Asn Glu Asn Ser Pro Glu  
65 70 75 80

Leu Ala Lys Ile Thr Gly Ala Arg Arg Pro Ser Gly Val Ala Leu Pro  
85 90 95

Ala Pro Gly Gln Gln Gln Pro Lys Arg Glu Gln Lys Asn Thr His Asn  
100 105 110

Arg Ser Asp Ser Arg Gly Ser Ser Arg Asn Pro Arg Arg Arg Gly Gln  
115 120 125

Ser Gly Ser Arg Ser Thr Gly Arg Ser Asn Pro Arg Arg Gln Thr Ser  
130 135 140

Arg Lys Asp Gly Pro Lys Ser  
145 150

<210> 133

<211> 451

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(451)

<223> RXN00994

<400> 133

taatcaacat tcgcaagagg tgtgtcgcaa aagcactagc tcagcgatta aaagttccca 60

tgatcacttt tcaaccagca ccgactagag ttagtgggca atg act acc ttt cta 115  
Met Thr Thr Phe Leu  
1 5

gaa ctc aag ctt ccc gac gag att gtg cgc gaa ctt cgc agt cag gga 163  
Glu Leu Lys Leu Pro Asp Glu Ile Val Arg Glu Leu Arg Ser Gln Gly  
10 15 20

atc acc gag gca ttc ccc atc caa gaa gca gcc atc ccc gat gcg ctc 211  
 Ile Thr Glu Ala Phe Pro Ile Gln Glu Ala Ala Ile Pro Asp Ala Leu  
 25 30 35  
 gct ggc aaa gat gtc ctc ggc cgt gga ccc acc ggc tct ggt aaa acc 259  
 Ala Gly Lys Asp Val Leu Gly Arg Gly Pro Thr Gly Ser Gly Lys Thr  
 40 45 50  
 ttc acc ttt ggg ctt ccc atg atc acc cga ctc gcg cgc tcg ggc gcc 307  
 Phe Thr Phe Gly Leu Pro Met Ile Thr Arg Leu Ala Arg Ser Gly Ala  
 55 60 65  
 tcc aaa cca ggt cgc ccc cgc ggg ctt gtc ctg gtt ccc acc cgt gaa 355  
 Ser Lys Pro Gly Arg Pro Arg Gly Leu Val Leu Val Pro Thr Arg Glu  
 70 75 80 85  
 cta gca gct cag gtg cgt gaa cgc ctc gac gat ccc gcc cgc gtt atg 403  
 Leu Ala Ala Gln Val Arg Glu Arg Leu Asp Asp Pro Ala Arg Val Met  
 90 95 100  
 ggt ctg cgc gtc ctc gag gtg gtc ggt ggc gtc aac atc aac cgc aac 451  
 Gly Leu Arg Val Leu Glu Val Val Gly Gly Val Asn Ile Asn Arg Asn  
 105 110 115  
 <210> 134  
 <211> 117  
 <212> PRT  
 <213> *Corynebacterium glutamicum*  
 <400> 134  
 Met Thr Thr Phe Leu Glu Leu Lys Leu Pro Asp Glu Ile Val Arg Glu  
 1 5 10 15  
 Leu Arg Ser Gln Gly Ile Thr Glu Ala Phe Pro Ile Gln Glu Ala Ala  
 20 25 30  
 Ile Pro Asp Ala Leu Ala Gly Lys Asp Val Leu Gly Arg Gly Pro Thr  
 35 40 45  
 Gly Ser Gly Lys Thr Phe Thr Phe Gly Leu Pro Met Ile Thr Arg Leu  
 50 55 60  
 Ala Arg Ser Gly Ala Ser Lys Pro Gly Arg Pro Arg Gly Leu Val Leu  
 65 70 75 80  
 Val Pro Thr Arg Glu Leu Ala Ala Gln Val Arg Glu Arg Leu Asp Asp  
 85 90 95  
 Pro Ala Arg Val Met Gly Leu Arg Val Leu Glu Val Val Gly Gly Val  
 100 105 110  
 Asn Ile Asn Arg Asn  
 115  
 <210> 135  
 <211> 442  
 <212> DNA  
 <213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(442)

&lt;223&gt; FRXA00994

&lt;400&gt; 135

taatcaacat tcgcaagagg tgtgtcgcaa aagcactagc tcagcgatta aaagttccca 60

tgatcacttt tcaaccagca cgcactagag ttagtgggca atg act acc ttt cta 115  
Met Thr Thr Phe Leu  
1 5

gaa ctc aag ctt ccc gac gag att gtg cgc gaa ctt cgc agt cag gga 163  
Glu Leu Lys Leu Pro Asp Glu Ile Val Arg Glu Leu Arg Ser Gln Gly  
10 15 20

atc acc gag gca ttc ccc atc caa gaa gca gcc atc ccc gat gcg ctc 211  
Ile Thr Glu Ala Phe Pro Ile Gln Glu Ala Ala Ile Pro Asp Ala Leu  
25 30 35

gct ggc aaa gat gtc ctc ggc cgt gga ccc acc ggc tct ggt aaa acc 259  
Ala Gly Lys Asp Val Leu Gly Arg Gly Pro Thr Gly Ser Gly Lys Thr  
40 45 50

ttc acc ttt ggg ctt ccc atg atc acc cga ctc gcg cgc tcg ggc gcc 307  
Phe Thr Phe Gly Leu Pro Met Ile Thr Arg Leu Ala Arg Ser Gly Ala  
55 60 65

tcc aaa cca ggt cgc ccc cgc ggg ctt gtc ctg gtt ccc acc cgt gaa 355  
Ser Lys Pro Gly Arg Pro Arg Gly Leu Val Leu Val Pro Thr Arg Glu  
70 75 80 85

cta gca gct cag gtg cgt gaa cgc ctc gac gat ccc gcc cgc gtt atg 403  
Leu Ala Ala Gln Val Arg Glu Arg Leu Asp Asp Pro Ala Arg Val Met  
90 95 100

ggc ctg cgc gtc ctc gag gtg gtc ggt ggc gtc aac atc 442  
Gly Leu Arg Val Leu Glu Val Val Gly Gly Val Asn Ile  
105 110

&lt;210&gt; 136

&lt;211&gt; 114

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 136

Met Thr Thr Phe Leu Glu Leu Lys Leu Pro Asp Glu Ile Val Arg Glu  
1 5 10 15

Leu Arg Ser Gln Gly Ile Thr Glu Ala Phe Pro Ile Gln Glu Ala Ala  
20 25 30

Ile Pro Asp Ala Leu Ala Gly Lys Asp Val Leu Gly Arg Gly Pro Thr  
35 40 45

Gly Ser Gly Lys Thr Phe Thr Phe Gly Leu Pro Met Ile Thr Arg Leu  
50 55 60

Ala Arg Ser Gly Ala Ser Lys Pro Gly Arg Pro Arg Gly Leu Val Leu

[illegible]

ggc gcg cta tgc ctc gac aaa gta gcg atc tta gtc ctc gat gaa gcc 547  
 Gly Ala Leu Ser Leu Asp Lys Val Ala Ile Leu Val Leu Asp Glu Ala  
 135 140 145

gac gaa atg ctc gat ctg ggc ttt ctg ccc gac atc gaa aaa atc ctc 595  
 Asp Glu Met Leu Asp Leu Gly Phe Leu Pro Asp Ile Glu Lys Ile Leu  
 150 155 160 165

cgt gcc ctc acc cac cag cat caa acc atg ctg ttc tct gcc acg atg 643  
 Arg Ala Leu Thr His Gln His Gln Thr Met Leu Phe Ser Ala Thr Met  
 170 175 180

ccc ggc gcg atc ctc aca ctc gca cgc agc ttc ctg aac aaa cca gtg 691  
 Pro Gly Ala Ile Leu Thr Leu Ala Arg Ser Phe Leu Asn Lys Pro Val  
 185 190 195

cac atc cga gcc gag aca tgc gac gcc tca gca aca cac aaa acc acc 739  
 His Ile Arg Ala Glu Thr Ser Asp Ala Ser Ala Thr His Lys Thr Thr  
 200 205 210

aga caa gtg gtt ttt cag gca cac aaa atg gac aag gaa gcc atc acc 787  
 Arg Gln Val Val Phe Gln Ala His Lys Met Asp Lys Glu Ala Ile Thr  
 215 220 225

gcg aaa att ctg cag tgc aaa gat cgc ggc aaa acg atc atc ttc gcc 835  
 Ala Lys Ile Leu Gln Ser Lys Asp Arg Gly Lys Thr Ile Ile Phe Ala  
 230 235 240 245

cgc acg aaa cgc acc gca gcg caa gtt gcc gaa gac cta gcc tcc aga 883  
 Arg Thr Lys Arg Thr Ala Ala Gln Val Ala Glu Asp Leu Ala Ser Arg  
 250 255 260

gga ttc tcc gtc gga tca gtg cac ggc gac atg ggc caa cca gcc cgc 931  
 Gly Phe Ser Val Gly Ser Val His Gly Asp Met Gly Gln Pro Ala Arg  
 265 270 275

gag aaa tca ctc aac gca ttc cgc aca gga aaa att gac atc ctt gta 979  
 Glu Lys Ser Leu Asn Ala Phe Arg Thr Gly Lys Ile Asp Ile Leu Val  
 280 285 290

gcc aca gac gta gcc gcc cga ggc atc gat gtt gat gac gtc acc cac 1027  
 Ala Thr Asp Val Ala Ala Arg Gly Ile Asp Val Asp Asp Val Thr His  
 295 300 305

gtg atc aac tac caa acc ccc gac gat cct atg acc tac gtc cat cgt 1075  
 Val Ile Asn Tyr Gln Thr Pro Asp Asp Pro Met Thr Tyr Val His Arg  
 310 315 320 325

atc gga cgc acg gga cgc gca ggg cac aac gga aca gcc gtc act ctt 1123  
 Ile Gly Arg Thr Gly Arg Ala Gly His Asn Gly Thr Ala Val Thr Leu  
 330 335 340

gtc ggg tac gac gaa acc ctc aaa tgg act gtc atc gac aac gaa ctc 1171  
 Val Gly Tyr Asp Glu Thr Leu Lys Trp Thr Val Ile Asp Asn Glu Leu  
 345 350 355

gaa ctc ggc caa cca aac cca cca caa tgg ttc tcc acc tca cca gag 1219  
 Glu Leu Gly Gln Pro Asn Pro Pro Gln Trp Phe Ser Thr Ser Pro Glu  
 360 365 370

ctg ctt gaa aca ctc gac atc cca gaa ggt gtc acc gaa cga gtc gga 1267

Leu Leu Glu Thr Leu Asp Ile Pro Glu Gly Val Thr Glu Arg Val Gly  
 375 380 385  
 cca cca acc aaa gtt cta ggc gga aca gcc cca cga cca cca cgc cgc 1315  
 Pro Pro Thr Lys Val Leu Gly Gly Thr Ala Pro Arg Pro Pro Arg Arg 405  
 390 395 400  
 acc cgg aaa taacttatgg cagcaaagct tca 1347  
 Thr Arg Lys

<210> 138  
 <211> 408  
 <212> PRT  
 <213> *Corynebacterium glutamicum*

<400> 138  
 Val Glu Ile Thr Asp Ala Leu Glu Ala Leu Gly Ile Asn Arg Thr Phe  
 1 5 10 15  
 Ala Ile Gln Glu Tyr Thr Leu Pro Ile Ala Leu Asp Gly His Asp Phe  
 20 25 30  
 Ile Gly Gln Ala Arg Thr Gly Met Gly Lys Thr Tyr Gly Phe Gly Val  
 35 40 45  
 Pro Leu Leu Asp Arg Val Phe Asp Ser Ala Asp Val Ala Glu Thr Asp  
 50 55 60  
 Gly Thr Pro Arg Ala Leu Val Ile Val Pro Thr Arg Glu Leu Ala Val  
 65 70 75 80  
 Gln Val Gly Asp Asp Leu Gln Arg Ala Ala Thr Asn Leu Pro Leu Lys  
 85 90 95  
 Ile Phe Thr Phe Tyr Gly Gly Thr Pro Tyr Glu Glu Gln Ile Asp Ala  
 100 105 110  
 Leu Lys Val Gly Val Asp Val Val Val Gly Thr Pro Gly Arg Leu Leu  
 115 120 125  
 Asp Leu His Lys Arg Gly Ala Leu Ser Leu Asp Lys Val Ala Ile Leu  
 130 135 140  
 Val Leu Asp Glu Ala Asp Glu Met Leu Asp Leu Gly Phe Leu Pro Asp  
 145 150 155 160  
 Ile Glu Lys Ile Leu Arg Ala Leu Thr His Gln His Gln Thr Met Leu  
 165 170 175  
 Phe Ser Ala Thr Met Pro Gly Ala Ile Leu Thr Leu Ala Arg Ser Phe  
 180 185 190  
 Leu Asn Lys Pro Val His Ile Arg Ala Glu Thr Ser Asp Ala Ser Ala  
 195 200 205  
 Thr His Lys Thr Thr Arg Gln Val Val Phe Gln Ala His Lys Met Asp  
 210 215 220  
 Lys Glu Ala Ile Thr Ala Lys Ile Leu Gln Ser Lys Asp Arg Gly Lys

[illegible]

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<210> 139
<211> 237
<212> DNA
<213> Corynebacterium glutamicum
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<220>
<221> CDS
<222> (101)..(214)
<223> FRXA02463
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<400> 139  
nnnnnaaant gacatccttg tagccacaga cgtagccgcc cnaggnntnt atnttnatna 60

cnttaccac gtnattaaat accaaanccc cgnccatcct atg acc tac gtt cat 115  
Met Thr Tyr Val His  
1 5

tgt atn gga cgc acg gga cgc gca ggg cac aac gga aca gcc gtc act 163  
Cys Xaa Gly Arg Thr Gly Arg Ala Gly His Asn Gly Thr Ala Val Thr  
10 15 20

ctt gtc ggg ttc nac gaa acc ctn aaa tgg act gnc atn gac aac gaa 211  
 Leu Val Gly Phe Xaa Glu Thr Leu Lys Trp Thr Xaa Xaa Asp Asn Glu  
                   25                                  30  35



ctn naactcgggc aaccaaacc acc  
Leu

237

<210> 140  
<211> 38  
<212> PRT  
<213> Corynebacterium glutamicum

<400> 140  
Met Thr Tyr Val His Cys Xaa Gly Arg Thr Gly Arg Ala Gly His Asn  
1 5 10 15

Gly Thr Ala Val Thr Leu Val Gly Phe Xaa Glu Thr Leu Lys Trp Thr  
20 25 30

Xaa Xaa Asp Asn Glu Leu  
35

<210> 141  
<211> 631  
<212> DNA  
<213> Corynebacterium glutamicum

<220>  
<221> CDS  
<222> (101)..(631)  
<223> FRXA02468

<400> 141  
tcgtgtgatt ggaatgaccc tattgtaacc gtgcaacgat agtatctaag ttgtgtcttc 60  
tgaaagcccc agacctacgt tcacagagct cggcgttgcg gtg gaa atc acc gac 115  
Val Glu Ile Thr Asp  
1 5

gca ctc gaa gcc ctc gcc atc aac cga act ttc gcg atc cag gag tac 163  
Ala Leu Glu Ala Leu Gly Ile Asn Arg Thr Phe Ala Ile Gln Glu Tyr  
10 15 20

aca ctt ccc atc gcg ctc gac gcc cac gac ttc atc gcc caa gcc cgc 211  
Thr Leu Pro Ile Ala Leu Asp Gly His Asp Phe Ile Gly Gln Ala Arg  
25 30 35

acc gcc atg gcc aaa acc tac gga ttc ggt gtc cca ctc ctc gat aga 259  
Thr Gly Met Gly Lys Thr Tyr Gly Phe Gly Val Pro Leu Leu Asp Arg  
40 45 50

gtc ttc gac tca gcc gac gtc gca gaa acc gac ggt acc ccc cga gcc 307  
Val Phe Asp Ser Ala Asp Val Ala Glu Thr Asp Gly Thr Pro Arg Ala  
55 60 65

ctc gtc atc gtg ccc acc cga gaa ctc gca gtc caa gtc gcc gac gac 355  
Leu Val Ile Val Pro Thr Arg Glu Leu Ala Val Gln Val Gly Asp Asp  
70 75 80 85

ctc caa cgc gca gca acc aac ctg cgg cta aag atc ttc acc ttc tac 403  
Leu Gln Arg Ala Ala Thr Asn Leu Pro Leu Lys Ile Phe Thr Phe Tyr  
90 95 100

ggc ggc acc ccc tac gaa gaa cag atc gac gca ctc aaa gtc ggc gtc 451  
 Gly Gly Thr Pro Tyr Glu Glu Gln Ile Asp Ala Leu Lys Val Gly Val  
 105 110 115

gac gtt gtc gta ggc aca ccc gga cga tta ctc gac ctg cac aaa cga 499  
 Asp Val Val Val Gly Thr Pro Gly Arg Leu Leu Asp Leu His Lys Arg  
 120 125 130

ggc gcg cta tcg ctc gac aaa gta gcg atc tta gtc ctc gat gaa gcc 547  
 Gly Ala Leu Ser Leu Asp Lys Val Ala Ile Leu Val Leu Asp Glu Ala  
 135 140 145

gac gaa atg ctc gat ctg ggc ttt ctg ccc gac atc gaa aaa atc ctc 595  
 Asp Glu Met Leu Asp Leu Gly Phe Leu Pro Asp Ile Glu Lys Ile Leu  
 150 155 160 165

cgt gcc ctc acc cac cag cat caa acc atg ctg ttc 631  
 Arg Ala Leu Thr His Gln His Gln Thr Met Leu Phe  
 170 175

<210> 142

<211> 177

<212> PRT

<213> Corynebacterium glutamicum

<400> 142

Val Glu Ile Thr Asp Ala Leu Glu Ala Leu Gly Ile Asn Arg Thr Phe  
 1 5 10 15

Ala Ile Gln Glu Tyr Thr Leu Pro Ile Ala Leu Asp Gly His Asp Phe  
 20 25 30

Ile Gly Gln Ala Arg Thr Gly Met Gly Lys Thr Tyr Gly Phe Gly Val  
 35 40 45

Pro Leu Leu Asp Arg Val Phe Asp Ser Ala Asp Val Ala Glu Thr Asp  
 50 55 60

Gly Thr Pro Arg Ala Leu Val Ile Val Pro Thr Arg Glu Leu Ala Val  
 65 70 75 80

Gln Val Gly Asp Asp Leu Gln Arg Ala Ala Thr Asn Leu Pro Leu Lys  
 85 90 95

Ile Phe Thr Phe Tyr Gly Gly Thr Pro Tyr Glu Glu Gln Ile Asp Ala  
 100 105 110

Leu Lys Val Gly Val Asp Val Val Val Gly Thr Pro Gly Arg Leu Leu  
 115 120 125

Asp Leu His Lys Arg Gly Ala Leu Ser Leu Asp Lys Val Ala Ile Leu  
 130 135 140

Val Leu Asp Glu Ala Asp Glu Met Leu Asp Leu Gly Phe Leu Pro Asp  
 145 150 155 160

Ile Glu Lys Ile Leu Arg Ala Leu Thr His Gln His Gln Thr Met Leu  
 165 170 175

Phe

<210> 143  
 <211> 2319  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(2296)  
 <223> RXA00050

<400> 143  
 agcaatgtcc cattttccct gctcacctgt atgggcaccc gcggcggaag tggattgca 60  
 tatggagttt tgatgatatt tagcgtaact taaaggaaca atg agt aat acc gag 115  
 Met Ser Asn Thr Glu  
 1 5  
 aac gtc aac ggc gac gta gaa cag ccg aat aac gtc att tcg tcg gaa 163  
 Asn Val Asn Gly Asp Val Glu Gln Pro Asn Asn Val Ile Ser Ser Glu  
 10 15 20  
 tct cag gaa acc ccg cag ggt gac tca gca tca gct gac ttc gct ctc 211  
 Ser Gln Glu Thr Pro Gln Gly Asp Ser Ala Ser Ala Asp Phe Ala Leu  
 25 30 35  
 gaa acc cca acc aac act gtt gaa gat gca cca gca tct gag ggt agc 259  
 Glu Thr Pro Thr Asn Thr Val Glu Asp Ala Pro Ala Ser Glu Gly Ser  
 40 45 50  
 gaa gag atc acc agg gtt gcg gat act tct gag gac gcc gac tct gca 307  
 Glu Glu Ile Thr Arg Val Ala Asp Thr Ser Glu Asp Ala Asp Ser Ala  
 55 60 65  
 gat gca gac aac gcg agc aat gta atc aat gag aat gag gac tcc tcg 355  
 Asp Ala Asp Asn Ala Ser Asn Val Ile Asn Glu Asn Glu Asp Ser Ser  
 70 75 80 85  
 gaa ggt gct aac cag cct tca aac gag tca tcc tct acg gaa gcc aaa 403  
 Glu Gly Ala Asn Gln Pro Ser Asn Glu Ser Ser Ser Thr Glu Ala Lys  
 90 95 100  
 tcc ggc ttc gat gca ctc gga ctg cca gag cgt gtt ctt gac gct gtg 451  
 Ser Gly Phe Asp Ala Leu Gly Leu Pro Glu Arg Val Leu Asp Ala Val  
 105 110 115  
 cgc aag gtg ggt tac gaa act cct tcc cca att cag gca caa acc atc 499  
 Arg Lys Val Gly Tyr Glu Thr Pro Ser Pro Ile Gln Ala Gln Thr Ile  
 120 125 130  
 cca atc ctc atg gag ggc cag gat gtt gtt ggt cta gca cag acc ggt 547  
 Pro Ile Leu Met Glu Gly Gln Asp Val Val Gly Leu Ala Gln Thr Gly  
 135 140 145  
 acc ggt aag act gca gct ttc gcg ctg cca atc ctt gcc cgt att gac 595  
 Thr Gly Lys Thr Ala Ala Phe Ala Leu Pro Ile Leu Ala Arg Ile Asp  
 150 155 160 165

aag tcc gtg cgc agc cca cag gca ctt gtg ctt gcc cct acc cgt gag	643
Lys Ser Val Arg Ser Pro Gln Ala Leu Val Leu Ala Pro Thr Arg Glu	
170 175 180	
ctg gca ctt cag gtt gct gac tcc ttc caa tcc ttc gct gac cac gtc	691
Leu Ala Leu Gln Val Ala Asp Ser Phe Gln Ser Phe Ala Asp His Val	
185 190 195	
ggc ggc ctg aac gtt ctg cca atc tat ggt gga cag gct tac ggc att	739
Gly Gly Leu Asn Val Leu Pro Ile Tyr Gly Gly Gln Ala Tyr Gly Ile	
200 205 210	
cag ctg tct ggc ctg cgt cgt ggc gct cac atc gtc gtg ggt acc cca	787
Gln Leu Ser Gly Leu Arg Arg Gly Ala His Val Val Gly Thr Pro	
215 220 225	
ggc cga atc atc gat cac ctg gaa aag ggc tcc ctg gat atc tcc gga	835
Gly Arg Ile Ile Asp His Leu Glu Lys Gly Ser Leu Asp Ile Ser Gly	
230 235 240 245	
ctg cgc ttc ctg gtg ctg gat gaa gca gac gag atg ctg aac atg ggc	883
Leu Arg Phe Leu Val Leu Asp Glu Ala Asp Glu Met Leu Asn Met Gly	
250 255 260	
ttc cag gaa gat gtc gag cgc atc ctg gag gac acc cca gac gag aag	931
Phe Gln Glu Asp Val Glu Arg Ile Leu Glu Asp Thr Pro Asp Glu Lys	
265 270 275	
cag gtt gca cta ttc tcc gca acg atg cca aac ggc att cgt cgc ctg	979
Gln Val Ala Leu Phe Ser Ala Thr Met Pro Asn Gly Ile Arg Arg Leu	
280 285 290	
tcc aag cag tac ctg aac aac cct gct gaa atc acc gtt aag tcc gag	1027
Ser Lys Gln Tyr Leu Asn Asn Pro Ala Glu Ile Thr Val Lys Ser Glu	
295 300 305	
acc agg act aac acc aac atc acc cag cgc ttc ctg aac gtt gca cac	1075
Thr Arg Thr Asn Thr Asn Ile Thr Gln Arg Phe Leu Asn Val Ala His	
310 315 320 325	
cgc aac aag atg gat gca ctg acc cgt att ctg gag gtc acc gag ttt	1123
Arg Asn Lys Met Asp Ala Leu Thr Arg Ile Leu Glu Val Thr Glu Phe	
330 335 340	
gaa gca atg atc atg ttc gtg cgc acc aag cac gaa act gaa gaa gtt	1171
Glu Ala Met Ile Met Phe Val Arg Thr Lys His Glu Thr Glu Val	
345 350 355	
gct gaa aag ctg cgt gca cgc gga ttc tcc gca gca gcc atc aac ggc	1219
Ala Glu Lys Leu Arg Ala Arg Gly Phe Ser Ala Ala Ala Ile Asn Gly	
360 365 370	
gac att gct cag gca cag cgt gag cgc acc gtc gac cag ctg aag gac	1267
Asp Ile Ala Gln Ala Gln Arg Glu Arg Thr Val Asp Gln Leu Lys Asp	
375 380 385	
ggc cgc ctg gac atc ctg gtt gca acc gac gtt gca gcc cgt ggt ctt	1315
Gly Arg Leu Asp Ile Leu Val Ala Thr Asp Val Ala Ala Arg Gly Leu	
390 395 400 405	
gac gtt gag cgc atc tcc cac gtg ctt aac ttc gac att cca aac gac	1363

Asp Val Glu Arg Ile Ser His Val Leu Asn Phe Asp Ile Pro Asn Asp	410	415	420	
acc gag tcc tac gtt cac cgc atc ggc cgc acc ggc cgt gca gga cgt				1411
Thr Glu Ser Tyr Val His Arg Ile Gly Arg Thr Gly Arg Ala Gly Arg	425	430	435	
acc ggc gag gca atc ctg ttc gtg acc cca cgt gag cgt cgt atg ctt				1459
Thr Gly Glu Ala Ile Leu Phe Val Thr Pro Arg Glu Arg Arg Met Leu	440	445	450	
cgc tcc atc gag cgc gca acc aac gca cca ctg cac gaa atg gaa ctg				1507
Arg Ser Ile Glu Arg Ala Thr Asn Ala Pro Leu His Glu Met Glu Leu	455	460	465	
cca acc gtc gat cag gtc aac gac ttc cgc aag gtc aag ttc gct gac				1555
Pro Thr Val Asp Gln Val Asn Asp Phe Arg Lys Val Lys Phe Ala Asp	470	475	480	485
tcc atc acc aag tcc ctg gag gac aag cag atg gac ctg ttc cgc acc				1603
Ser Ile Thr Lys Ser Leu Glu Asp Lys Gln Met Asp Leu Phe Arg Thr	490	495	500	
ctg gtc aag gaa tac tcc cag gcc aac gac gtt cct cta gag gac atc				1651
Leu Val Lys Glu Tyr Ser Gln Ala Asn Asp Val Pro Leu Glu Asp Ile	505	510	515	
gca gcg gca ctg gca acc cag gca cag tcc ggc gac ttc ctg ctg aag				1699
Ala Ala Ala Leu Ala Thr Gln Ala Gln Ser Gly Asp Phe Leu Leu Lys	520	525	530	
gag ctg cca cca gag cgc cgt gag cgc aac gac cgc cgt cgt gac cgt				1747
Glu Leu Pro Pro Glu Arg Arg Glu Arg Asn Asp Arg Arg Arg Asp Arg	535	540	545	
gac ttc gac gac cgt ggt gga cgt gga cgc gac cgt gac cgt ggc gac				1795
Asp Phe Asp Asp Arg Gly Gly Arg Gly Arg Asp Arg Asp Arg Gly Asp	550	555	560	565
cgc gga gat cgt ggc tca cgc ttc gac cgc gac gac gag aac ctg gca				1843
Arg Gly Asp Arg Gly Ser Arg Phe Asp Arg Asp Asp Glu Asn Leu Ala	570	575	580	
acc tac cgc ctg gca gtg ggc aag cgc cag cac atc cgc cca ggc gca				1891
Thr Tyr Arg Leu Ala Val Gly Lys Arg Gln His Ile Arg Pro Gly Ala	585	590	595	
atc gtt ggt gca ctt gcc aac gaa ggt ggc ctg aac tcc aag gac ttc				1939
Ile Val Gly Ala Leu Ala Asn Glu Gly Gly Leu Asn Ser Lys Asp Phe	600	605	610	
ggc cgc atc acc atc gca gcc gac cac acc ctg gtt gaa ctg cca aag				1987
Gly Arg Ile Thr Ile Ala Ala Asp His Thr Leu Val Glu Leu Pro Lys	615	620	625	
gat ctg cca cag agc gtt ctt gac aac ctg cgc gac acc cgc atc tcc				2035
Asp Leu Pro Gln Ser Val Leu Asp Asn Leu Arg Asp Thr Arg Ile Ser	630	635	640	645
ggc cag ctg atc aac ata gaa cgc gac tcc ggt gga cgc cca cca cgc				2083
Gly Gln Leu Ile Asn Ile Glu Arg Asp Ser Gly Gly Arg Pro Pro Arg				

650	655	660	
cgc ttc gag cgc gat gac cgt ggc gga cgc ggc gga ttc cgc ggc gac			2131
Arg Phe Glu Arg Asp Asp Arg Gly	Gly Arg Gly Gly Phe Arg Gly Asp		
665	670	675	
cgt gat gac cgc ggt gga cgt gga cgt gac cgt gac gat cgt gga agc			2179
Arg Asp Asp Arg Gly Gly Arg Gly Arg Asp Arg Asp Arg Gly Ser			
680	685	690	
cgt gga ggt ttc cgc ggt gga cgt gac cgt gat gat cgt ggc gga cgc			2227
Arg Gly Gly Phe Arg Gly Gly Arg Asp Arg Asp Arg Gly Gly Arg			
695	700	705	
ggt gga ttc cgc gga cgc gac gac cgc gga gac cgt ggt ggc cgt ggc			2275
Gly Gly Phe Arg Gly Arg Asp Asp Arg Gly Asp Arg Gly Gly Arg Gly			
710	715	720	725
ggt tac cgt ggc gga cgc gac taagagttcg ttttagcttc agc			2319
Gly Tyr Arg Gly Gly Arg Asp			
730			

&lt;210&gt; 144

&lt;211&gt; 732

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 144

Met Ser Asn Thr Glu Asn Val Asn Gly Asp Val Glu Gln Pro Asn Asn	
1 5 10 15	

Val Ile Ser Ser Glu Ser Gln Glu Thr Pro Gln Gly Asp Ser Ala Ser	
20 25 30	

Ala Asp Phe Ala Leu Glu Thr Pro Thr Asn Thr Val Glu Asp Ala Pro	
35 40 45	

Ala Ser Glu Gly Ser Glu Glu Ile Thr Arg Val Ala Asp Thr Ser Glu	
50 55 60	

Asp Ala Asp Ser Ala Asp Ala Asp Asn Ala Ser Asn Val Ile Asn Glu	
65 70 75 80	

Asn Glu Asp Ser Ser Glu Gly Ala Asn Gln Pro Ser Asn Glu Ser Ser	
85 90 95	

Ser Thr Glu Ala Lys Ser Gly Phe Asp Ala Leu Gly Leu Pro Glu Arg	
100 105 110	

Val Leu Asp Ala Val Arg Lys Val Gly Tyr Glu Thr Pro Ser Pro Ile	
115 120 125	

Gln Ala Gln Thr Ile Pro Ile Leu Met Glu Gly Gln Asp Val Val Gly	
130 135 140	

Leu Ala Gln Thr Gly Thr Gly Lys Thr Ala Ala Phe Ala Leu Pro Ile	
145 150 155 160	

Leu Ala Arg Ile Asp Lys Ser Val Arg Ser Pro Gln Ala Leu Val Leu	
165 170 175	

Ala Pro Thr Arg Glu Leu Ala Leu Gln Val Ala Asp Ser Phe Gln Ser  
180 185 190

Phe Ala Asp His Val Gly Gly Leu Asn Val Leu Pro Ile Tyr Gly Gly  
195 200 205

Gln Ala Tyr Gly Ile Gln Leu Ser Gly Leu Arg Arg Gly Ala His Ile  
210 215 220

Val Val Gly Thr Pro Gly Arg Ile Ile Asp His Leu Glu Lys Gly Ser  
225 230 235 240

Leu Asp Ile Ser Gly Leu Arg Phe Leu Val Leu Asp Glu Ala Asp Glu  
245 250 255

Met Leu Asn Met Gly Phe Gln Glu Asp Val Glu Arg Ile Leu Glu Asp  
260 265 270

Thr Pro Asp Glu Lys Gln Val Ala Leu Phe Ser Ala Thr Met Pro Asn  
275 280 285

Gly Ile Arg Arg Leu Ser Lys Gln Tyr Leu Asn Asn Pro Ala Glu Ile  
290 295 300

Thr Val Lys Ser Glu Thr Arg Thr Asn Thr Asn Ile Thr Gln Arg Phe  
305 310 315 320

Leu Asn Val Ala His Arg Asn Lys Met Asp Ala Leu Thr Arg Ile Leu  
325 330 335

Glu Val Thr Glu Phe Glu Ala Met Ile Met Phe Val Arg Thr Lys His  
340 345 350

Glu Thr Glu Glu Val Ala Glu Lys Leu Arg Ala Arg Gly Phe Ser Ala  
355 360 365

Ala Ala Ile Asn Gly Asp Ile Ala Gln Ala Gln Arg Glu Arg Thr Val  
370 375 380

Asp Gln Leu Lys Asp Gly Arg Leu Asp Ile Leu Val Ala Thr Asp Val  
385 390 395 400

Ala Ala Arg Gly Leu Asp Val Glu Arg Ile Ser His Val Leu Asn Phe  
405 410 415

Asp Ile Pro Asn Asp Thr Glu Ser Tyr Val His Arg Ile Gly Arg Thr  
420 425 430

Gly Arg Ala Gly Arg Thr Gly Glu Ala Ile Leu Phe Val Thr Pro Arg  
435 440 445

Glu Arg Arg Met Leu Arg Ser Ile Glu Arg Ala Thr Asn Ala Pro Leu  
450 455 460

His Glu Met Glu Leu Pro Thr Val Asp Gln Val Asn Asp Phe Arg Lys  
465 470 475 480

Val Lys Phe Ala Asp Ser Ile Thr Lys Ser Leu Glu Asp Lys Gln Met  
485 490 495

Asp Leu Phe Arg Thr Leu Val Lys Glu Tyr Ser Gln Ala Asn Asp Val  
 500 505 510  
 Pro Leu Glu Asp Ile Ala Ala Ala Leu Ala Thr Gln Ala Gln Ser Gly  
 515 520 525  
 Asp Phe Leu Leu Lys Glu Leu Pro Pro Glu Arg Arg Glu Arg Asn Asp  
 530 535 540  
 Arg Arg Arg Asp Arg Asp Phe Asp Asp Arg Gly Gly Arg Gly Arg Asp  
 545 550 555 560  
 Arg Asp Arg Gly Asp Arg Gly Asp Arg Gly Ser Arg Phe Asp Arg Asp  
 565 570 575  
 Asp Glu Asn Leu Ala Thr Tyr Arg Leu Ala Val Gly Lys Arg Gln His  
 580 585 590  
 Ile Arg Pro Gly Ala Ile Val Gly Ala Leu Ala Asn Glu Gly Gly Leu  
 595 600 605  
 Asn Ser Lys Asp Phe Gly Arg Ile Thr Ile Ala Ala Asp His Thr Leu  
 610 615 620  
 Val Glu Leu Pro Lys Asp Leu Pro Gln Ser Val Leu Asp Asn Leu Arg  
 625 630 635 640  
 Asp Thr Arg Ile Ser Gly Gln Leu Ile Asn Ile Glu Arg Asp Ser Gly  
 645 650 655  
 Gly Arg Pro Pro Arg Arg Phe Glu Arg Asp Asp Arg Gly Gly Arg Gly  
 660 665 670  
 Gly Phe Arg Gly Asp Arg Asp Asp Arg Gly Gly Arg Gly Arg Asp Arg  
 675 680 685  
 Asp Asp Arg Gly Ser Arg Gly Gly Phe Arg Gly Gly Arg Asp Arg Asp  
 690 695 700  
 Asp Arg Gly Gly Arg Gly Gly Phe Arg Gly Arg Asp Asp Arg Gly Asp  
 705 710 715 720  
 Arg Gly Gly Arg Gly Gly Tyr Arg Gly Gly Arg Asp  
 725 730

<210> 145  
 <211> 450  
 <212> DNA  
 <213> *Corynebacterium glutamicum*

<220>  
 <221> CDS  
 <222> (101)..(427)  
 <223> RXA02682

<400> 145  
 tcccgatgct gctaggttgc tgtaaagcaa ccacaagttg caccaccatt cttccatcca 60  
 gagaatacga attcgtttac ctctagaaag gcactttccc atg tct tac cac gat 115  
 Met Ser Tyr His Asp



1

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cac agc gac atc gaa tac ctc aag aag atc ggc gcc aac tcc cct gac 163  
 His Ser Asp Ile Glu Tyr Leu Lys Lys Ile Gly Ala Asn Ser Pro Asp  
                   10                                  15                                  20

gcc ttc aaa gct ttt gtc cat ttt gat gag gca gct ctc cgc ggc ccg 211  
 Ala Phe Lys Ala Phe Val His Phe Asp Glu Ala Ala Leu Arg Gly Pro  
                   25                                  30                                  35

aac aag aaa atc cca cgc aac tac acc gaa atg atc gca ctt cgc gtc 259  
 Asn Lys Lys Ile Pro Arg Asn Tyr Thr Glu Met Ile Ala Leu Ala Val  
                   40                                  45                                  50

gca ttc aca acc caa tgc gcc tac tgc atc gac atc cac act gcc gct 307  
 Ala Phe Thr Thr Gln Cys Ala Tyr Cys Ile Asp Ile His Thr Ala Ala  
                   55                                  60                                  65

gcg aag aag gaa ggt gtc acc acc gag gag ctc gct gag gtt cgc ctc 355  
 Ala Lys Lys Glu Gly Val Thr Thr Glu Glu Leu Ala Glu Val Ala Leu  
                   70                                  75                                  80                                  85

atc gcc gca gca ctt cgg gca ggc ggc gcc atg acg cac ggc gca ctt 403  
 Ile Ala Ala Ala Leu Arg Ala Gly Gly Ala Met Thr His Gly Ala Leu  
                   90                                  95                                  100

gcc atg aag ctt tac gac gaa aac tagaagcgat tctgcacatt ttt 450  
 Ala Met Lys Leu Tyr Asp Glu Asn  
                   105

&lt;210&gt; 146

&lt;211&gt; 109

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 146

Met Ser Tyr His Asp His Ser Asp Ile Glu Tyr Leu Lys Lys Ile Gly  
                   1                  5                  10                  15

Ala Asn Ser Pro Asp Ala Phe Lys Ala Phe Val His Phe Asp Glu Ala  
                   20                  25                  30

Ala Leu Arg Gly Pro Asn Lys Lys Ile Pro Arg Asn Tyr Thr Glu Met  
                   35                  40                  45

Ile Ala Leu Ala Val Ala Phe Thr Thr Gln Cys Ala Tyr Cys Ile Asp  
                   50                  55                  60

Ile His Thr Ala Ala Ala Lys Lys Glu Gly Val Thr Thr Glu Glu Leu  
                   65                  70                  75                  80

Ala Glu Val Ala Leu Ile Ala Ala Ala Leu Arg Ala Gly Gly Ala Met  
                   85                  90                  95

Thr His Gly Ala Leu Ala Met Lys Leu Tyr Asp Glu Asn  
                   100                  105

&lt;210&gt; 147

&lt;211&gt; 798

<213> *Corynebacterium glutamicum*

<221> CDS

<223> RXN00542

&lt;400&gt; 147

gtaaagaact ttaaggctct agagaggtag ttgaaggatt atg gca atc gga gat 115  
Met Ala Ile Gly Asp  
1 5

act aac atc acc gtc gtt ggc aac att gtt gct gac ccg gaa ctc cgc 163  
Thr Asn Ile Thr Val Val Gly Asn Ile Val Ala Asp Pro Glu Leu Arg  
10 15 20

ttc acc cca tgc ggt gca gca gtg gct aac ttc cgc att gca tca act 211  
Phe Thr Pro Ser Gly Ala Ala Val Asn Phe Arg Ile Ala Ser Thr  
25 30 35

ccc cgc tgc ttc aac cgc caa acc aac cag tgg gaa gac ggc gaa gcc 259  
Pro Arg Ser Phe Asn Arg Gln Thr Asn Gln Trp Glu Asp Gly Glu Ala  
40 45 50

ctc ttt ctc acc gtt aac gtt tgg cgt cag gca gct gaa aac gtt gca 307  
Leu Phe Leu Thr Val Asn Val Trp Arg Gln Ala Ala Glu Asn Val Ala  
55 60 65

gag tcc ctg tcc aag ggt atg cgc gtt atc gtc acc ggt cgc ctc aag 355  
Glu Ser Leu Ser Lys Gly Met Arg Val Ile Val Thr Gly Arg Leu Lys  
70 75 80 85

cag cgc tcc tat gaa acc cgt gag ggc gaa aag cgc agc gtt ttt gag 403  
Gln Arg Ser Tyr Glu Thr Arg Glu Gly Glu Lys Arg Ser Val Phe Glu  
90 95 100

gtc gaa gcg gat gaa gtc gga cca tca cta aca ttt gcc aag gca gat 451  
Val Glu Ala Asp Glu Val Gly Pro Ser Leu Thr Phe Ala Lys Ala Asp  
105 110 115

gtc cag cgc aca ccg cgc ggt gga aac tct ggc gga aac tac ggt ggc 499  
Val Gln Arg Thr Pro Arg Gly Gly Asn Ser Gly Gly Asn Tyr Gly Gly  
120 125 130

ggc aac caa ggt ggt ggc ctc ggt gga aac caa ggc aac cag caa ggt 547  
Gly Asn Gln Gly Gly Gly Leu Gly Gly Asn Gln Gly Asn Gln Gln Gly  
135 140 145

gga ttc agc aac cag aac tct ggc ggc ttc ggt gga aac caa ggc aac 595  
Gly Phe Ser Asn Gln Asn Ser Gly Gly Phe Gly Gly Asn Gln Gly Asn  
150 155 160 165

cag cag caa agc aac cag ggc gga ttt ggt gga aac caa aac cag tcc 643  
Gln Gln Gln Ser Asn Gln Gly Gly Phe Gly Gly Asn Gln Asn Gln Ser  
170 175 180

cag ggt aac aac ttc aac caa ggt gga ttt ggc gga ggc agc cca cag 691  
Gln Gly Asn Asn Phe Asn Gln Gly Gly Phe Gly Gly Gly Ser Pro Gln

185	190	195	
gca gca ccg gac aat gac cct tgg aat tct gca cca cca gct ggc tcc			739
Ala Ala Pro Asp Asn Asp Pro Trp Asn Ser Ala Pro Pro Ala Gly Ser			
200	205	210	
ggc ggc ttc ggc ggc gca gac gat gag cca ccg ttc taaagctttt			785
Gly Gly Phe Gly Gly Ala Asp Asp Glu Pro Pro Phe			
215	220	225	
cttttctaaa aca			798
 <210> 148			
<211> 225			
<212> PRT			
<213> Corynebacterium glutamicum			
 <400> 148			
Met Ala Ile Gly Asp Thr Asn Ile Thr Val Val Gly Asn Ile Val Ala			
1	5	10	15
Asp Pro Glu Leu Arg Phe Thr Pro Ser Gly Ala Ala Val Ala Asn Phe			
20	25	30	
Arg Ile Ala Ser Thr Pro Arg Ser Phe Asn Arg Gln Thr Asn Gln Trp			
35	40	45	
Glu Asp Gly Glu Ala Leu Phe Leu Thr Val Asn Val Trp Arg Gln Ala			
50	55	60	
Ala Glu Asn Val Ala Glu Ser Leu Ser Lys Gly Met Arg Val Ile Val			
65	70	75	80
Thr Gly Arg Leu Lys Gln Arg Ser Tyr Glu Thr Arg Glu Gly Glu Lys			
85	90	95	
Arg Ser Val Phe Glu Val Glu Ala Asp Glu Val Gly Pro Ser Leu Thr			
100	105	110	
Phe Ala Lys Ala Asp Val Gln Arg Thr Pro Arg Gly Gly Asn Ser Gly			
115	120	125	
Gly Asn Tyr Gly Gly Asn Gln Gly Gly Gly Leu Gly Gly Asn Gln			
130	135	140	
Gly Asn Gln Gln Gly Gly Phe Ser Asn Gln Asn Ser Gly Gly Phe Gly			
145	150	155	160
Gly Asn Gln Gly Asn Gln Gln Ser Asn Gln Gly Gly Phe Gly Gly			
165	170	175	
Asn Gln Asn Gln Ser Gln Gly Asn Asn Phe Asn Gln Gly Gly Phe Gly			
180	185	190	
Gly Gly Ser Pro Gln Ala Ala Pro Asp Asn Asp Pro Trp Asn Ser Ala			
195	200	205	
Pro Pro Ala Gly Ser Gly Gly Phe Gly Gly Ala Asp Asp Glu Pro Pro			
210	215	220	

Phe  
225

<210> 149  
<211> 542  
<212> DNA  
<213> *Corynebacterium glutamicum*

<220>  
<221> CDS  
<222> (1)..(519)  
<223> FRXA00542

<400> 149  
gcc ctc ttt ctc acc gtt aac gtt tgg cgt cag gca gct gaa aac gtt 48  
Ala Leu Phe Leu Thr Val Asn Val Trp Arg Gln Ala Ala Glu Asn Val  
1 5 10 15

gca gag tcc ctg tcc aag ggt atg cgc gtt atc gtc acc ggt cgc ctc 96  
Ala Glu Ser Leu Ser Lys Gly Met Arg Val Ile Val Thr Gly Arg Leu  
20 25 30

aag cag cgc tcc tat gaa acc cgt gag ggc gaa aag cgc agc gtt ttt 144  
Lys Gln Arg Ser Tyr Glu Thr Arg Glu Gly Glu Lys Arg Ser Val Phe  
35 40 45

gag gtc gaa gcg gat gaa gtc gga cca tca cta aca ttt gcc aag gca 192  
Glu Val Glu Ala Asp Glu Val Gly Pro Ser Leu Thr Phe Ala Lys Ala  
50 55 60

gat gtc cag cgc aca ccg cgc ggt gga aac tct ggc gga aac tac ggt 240  
Asp Val Gln Arg Thr Pro Arg Gly Gly Asn Ser Gly Gly Asn Tyr Gly  
65 70 75 80

ggc ggc aac caa ggt ggt ggc ctc ggt gga aac caa ggc aac cag caa 288  
Gly Gly Asn Gln Gly Gly Gly Leu Gly Gly Asn Gln Gly Asn Gln Gln  
85 90 95

ggt gga ttc agc aac cag aac tct ggc ggc ttc ggt gga aac caa ggc 336  
Gly Gly Phe Ser Asn Gln Asn Ser Gly Gly Phe Gly Gly Asn Gln Gly  
100 105 110

aac cag cag caa agc aac cag ggc gga ttt ggt gga aac caa aac cag 384  
Asn Gln Gln Gln Ser Asn Gln Gly Gly Phe Gly Gly Asn Gln Asn Gln  
115 120 125

tcc cag ggt aac aac ttc aac caa ggt gga ttt ggc gga ggc agc cca 432  
Ser Gln Gly Asn Asn Phe Asn Gln Gly Gly Phe Gly Gly Gly Ser Pro  
130 135 140

cag gca gca ccg gac aat gac cct tgg aat tct gca cca cca gct ggc 480  
Gln Ala Ala Pro Asp Asn Asp Pro Trp Asn Ser Ala Pro Pro Ala Gly  
145 150 155 160

tcc ggc ggg ttc ggc ggc gca gac gat gag cca ccg ttc taaagctttt 529  
Ser Gly Gly Phe Gly Gly Ala Asp Asp Glu Pro Pro Phe  
165 170

cttttctaaa aca 542

<210> 150  
 <211> 173  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 150  
 Ala Leu Phe Leu Thr Val Asn Val Trp Arg Gln Ala Ala Glu Asn Val  
   1                  5                  10                  15  
 Ala Glu Ser Leu Ser Lys Gly Met Arg Val Ile Val Thr Gly Arg Leu  
           20                  25                  30  
 Lys Gln Arg Ser Tyr Glu Thr Arg Glu Gly Glu Lys Arg Ser Val Phe  
           35                  40                  45  
 Glu Val Glu Ala Asp Glu Val Gly Pro Ser Leu Thr Phe Ala Lys Ala  
           50                  55                  60  
 Asp Val Gln Arg Thr Pro Arg Gly Gly Asn Ser Gly Gly Asn Tyr Gly  
           65                  70                  75                  80  
 Gly Gly Asn Gln Gly Gly Gly Leu Gly Gly Asn Gln Gly Asn Gln Gln  
                   85                  90                  95  
 Gly Gly Phe Ser Asn Gln Asn Ser Gly Gly Phe Gly Gly Asn Gln Gly  
           100                  105                  110  
 Asn Gln Gln Gln Ser Asn Gln Gly Gly Phe Gly Gly Asn Gln Asn Gln  
           115                  120                  125  
 Ser Gln Gly Asn Asn Phe Asn Gln Gly Gly Phe Gly Gly Gly Ser Pro  
           130                  135                  140  
 Gln Ala Ala Pro Asp Asn Asp Pro Trp Asn Ser Ala Pro Pro Ala Gly  
           145                  150                  155                  160  
 Ser Gly Gly Phe Gly Gly Ala Asp Asp Glu Pro Pro Phe  
                   165                  170

<210> 151  
 <211> 906  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(883)  
 <223> RXN02833

<400> 151  
 tagcttctcc gccacccttc atccacggct gaataaaaatt atttttcgat agtttcgcga 60  
 aaaggagata cctaacatag tgagccagaa ctcacattct ttg ctc gaa acc tgg 115  
                                   Leu Leu Glu Thr Trp  
                                   1                  5  
 cgc caa gtt gtt gcc gat ctc aca act ttg agc cag caa gcg gac agt 163  
 Arg Gln Val Val Ala Asp Leu Thr Thr Leu Ser Gln Gln Ala Asp Ser  
                   10                  15                  20

gga ttc gac cca ttg acg cca act caa cgt gca tat ttg aac ctg acg 211  
 Gly Phe Asp Pro Leu Thr Pro Thr Gln Arg Ala Tyr Leu Asn Leu Thr  
 25 30 35

aag ccg att gcc atc gtc gat ggc tac gcc gtg ctg tcc aca ccc aac 259  
 Lys Pro Ile Ala Ile Val Asp Gly Tyr Ala Val Leu Ser Thr Pro Asn  
 40 45 50

gcg atg gca aaa aat gtc att gaa aac gat ttg ggc gat gct ttg acc 307  
 Ala Met Ala Lys Asn Val Ile Glu Asn Asp Leu Gly Asp Ala Leu Thr  
 55 60 65

cgt gtg ttg tgg ctg cgc atg ggc cga tca ttc agc ttg gct gtc agt 355  
 Arg Val Leu Ser Leu Arg Met Gly Arg Ser Phe Ser Leu Ala Val Ser  
 70 75 80 85

gtg gag cct gag cag gaa att cca gaa acc cca gct cag cag gag ttt 403  
 Val Glu Pro Glu Gln Glu Ile Pro Glu Thr Pro Ala Gln Gln Glu Phe  
 90 95 100

aaa tat cag cct gac gca cct gtg atc tct tcc aac aag cgc cca aag 451  
 Lys Tyr Gln Pro Asp Ala Pro Val Ile Ser Ser Asn Lys Ala Pro Lys  
 105 110 115

cag tat gaa gtt ggt ggt cgg gga gag cgc tgg aca agc gac gcc tgg 499  
 Gln Tyr Glu Val Gly Gly Arg Gly Glu Ala Ser Thr Ser Asp Gly Trp  
 120 125 130

gaa cgt acc cac tct gca cgg gct ccc gag ccg cac ccg gca cct atc 547  
 Glu Arg Thr His Ser Ala Pro Ala Pro Glu Pro His Pro Ala Pro Ile  
 135 140 145

gcc gat cgt gag cca gag ctg gcc acc ccg cag cgc att ccg cgc gaa 595  
 Ala Asp Arg Glu Pro Glu Leu Ala Thr Pro Gln Arg Ile Pro Arg Glu  
 150 155 160 165

acc cca gct cac aac cct aat cgg gaa gtg tcc ctc aac ccg aaa tac 643  
 Thr Pro Ala His Asn Pro Asn Arg Glu Val Ser Leu Asn Pro Lys Tyr  
 170 175 180

act ttt gaa agc ttc gtg atc ggg ccg ttc aac cgt ttc gcc aat gca 691  
 Thr Phe Glu Ser Phe Val Ile Gly Pro Phe Asn Arg Phe Ala Asn Ala  
 185 190 195

gcc gca gtt gct gtg cgc gaa agc cca cgc aaa gct ttc aac ccg ctg 739  
 Ala Ala Val Ala Val Ala Glu Ser Pro Ala Lys Ala Phe Asn Pro Leu  
 200 205 210

ttt att tcc ggc ggt tcc ggc ttg ggc aaa act cac ctg ctg cac gca 787  
 Phe Ile Ser Gly Gly Ser Gly Leu Gly Lys Thr His Leu Leu His Ala  
 215 220 225

gta gga aat tat gct caa gaa ttg cag cct ggc ccg cgg att aag tac 835  
 Val Gly Asn Tyr Ala Gln Glu Leu Gln Pro Gly Pro Arg Ile Lys Tyr  
 230 235 240 245

gtc tca agt gag gaa tat cac caa cga cta cat caa ctc cgt cgc aga 883  
 Val Ser Ser Glu Glu Tyr His Gln Arg Leu His Gln Leu Arg Ala Arg  
 250 255 260

906

tgaccgccag gaaaccttca agc

&lt;210&gt; 152

&lt;211&gt; 261

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 152

Leu Leu Glu Thr Trp Arg Gln Val Val Ala Asp Leu Thr Thr Leu Ser  
 1 5 10 15

Gln Gln Ala Asp Ser Gly Phe Asp Pro Leu Thr Pro Thr Gln Arg Ala  
 20 25 30

Tyr Leu Asn Leu Thr Lys Pro Ile Ala Ile Val Asp Gly Tyr Ala Val  
 35 40 45

Leu Ser Thr Pro Asn Ala Met Ala Lys Asn Val Ile Glu Asn Asp Leu  
 50 55 60

Gly Asp Ala Leu Thr Arg Val Leu Ser Leu Arg Met Gly Arg Ser Phe  
 65 70 75 80

Ser Leu Ala Val Ser Val Glu Pro Glu Gln Glu Ile Pro Glu Thr Pro  
 85 90 95

Ala Gln Gln Glu Phe Lys Tyr Gln Pro Asp Ala Pro Val Ile Ser Ser  
 100 105 110

Asn Lys Ala Pro Lys Gln Tyr Glu Val Gly Gly Arg Gly Glu Ala Ser  
 115 120 125

Thr Ser Asp Gly Trp Glu Arg Thr His Ser Ala Pro Ala Pro Glu Pro  
 130 135 140

His Pro Ala Pro Ile Ala Asp Arg Glu Pro Glu Leu Ala Thr Pro Gln  
 145 150 155 160

Arg Ile Pro Arg Glu Thr Pro Ala His Asn Pro Asn Arg Glu Val Ser  
 165 170 175

Leu Asn Pro Lys Tyr Thr Phe Glu Ser Phe Val Ile Gly Pro Phe Asn  
 180 185 190

Arg Phe Ala Asn Ala Ala Val Ala Val Ala Glu Ser Pro Ala Lys  
 195 200 205

Ala Phe Asn Pro Leu Phe Ile Ser Gly Gly Ser Gly Leu Gly Lys Thr  
 210 215 220

His Leu Leu His Ala Val Gly Asn Tyr Ala Gln Glu Leu Gln Pro Gly  
 225 230 235 240

Pro Arg Ile Lys Tyr Val Ser Ser Glu Glu Tyr His Gln Arg Leu His  
 245 250 255

Gln Leu Arg Ala Arg  
 260

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 <223> FRXA02833

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 Thr Arg Val Leu Ser Leu Arg Met Gly Arg Ser Phe Ser Leu Ala Val  
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 agt gtg gag cct gag cag gaa att cca aaa ccc cag ctc aag cag gag 96  
 Ser Val Glu Pro Glu Gln Glu Ile Pro Lys Pro Gln Leu Lys Gln Glu  
 20 25 30  
 ttt aaa tat cag cct gac gca ctt gtg ttt tct tcc aac aag cgc cca 144  
 Phe Lys Tyr Gln Pro Asp Ala Leu Val Phe Ser Ser Asn Lys Ala Pro  
 35 40 45  
 aag cag tat gaa gtt ggt ggt cgg gga gag cgc tgc aca agc gac ggt 192  
 Lys Gln Tyr Glu Val Gly Gly Arg Gly Glu Ala Ser Thr Ser Asp Gly  
 50 55 60  
 tgg gaa ggt acc cac tct gca ccg gct ccc gag cgc cac cgc gca cct 240  
 Trp Glu Gly Thr His Ser Ala Pro Ala Pro Glu Pro His Pro Ala Pro  
 65 70 75 80  
 atc gcc gat cgt gag cca gag ctg gcc acc cgc cag cgc att ccg cgc 288  
 Ile Ala Asp Arg Glu Pro Glu Leu Ala Thr Pro Gln Arg Ile Pro Arg  
 85 90 95  
 gaa acc cca gct cac aac cct aat cgg gaa gtg tcc ctc aac ccg aaa 336  
 Glu Thr Pro Ala His Asn Pro Asn Arg Glu Val Ser Leu Asn Pro Lys  
 100 105 110  
 tac act ttt gaa agc ttc gtg atc ggg cgc ttc aac cgt ttc gcc aat 384  
 Tyr Thr Phe Glu Ser Phe Val Ile Gly Pro Phe Asn Arg Phe Ala Asn  
 115 120 125  
 gca gcc gca gtt gct gtg cgc gaa agc cca cgc aaa gct ttc aac ccg 432  
 Ala Ala Ala Val Ala Val Ala Glu Ser Pro Ala Lys Ala Phe Asn Pro  
 130 135 140  
 ctg ttt att tcc ggc ggt tcc ggc ttg ggc aaa act cac ctg ctg cac 480  
 Leu Phe Ile Ser Gly Gly Ser Gly Leu Gly Lys Thr His Leu Leu His  
 145 150 155 160  
 gca gta gga aat tat gct caa gaa ttg cag cct ggc ccg cgg att aag 528  
 Ala Val Gly Asn Tyr Ala Gln Glu Leu Gln Pro Gly Pro Arg Ile Lys  
 165 170 175  
 tac gtc tca agt gag gaa tat cac caa cga cta cat caa ctc cgt gcg 576  
 Tyr Val Ser Ser Glu Glu Tyr His Gln Arg Leu His Gln Leu Arg Ala  
 180 185 190  
 aga tgaccgccag gaaaccttca agc 602  
 Arg



<210> 154  
 <211> 193  
 <212> PRT  
 <213> *Corynebacterium glutamicum*

<400> 154  
 Thr Arg Val Leu Ser Leu Arg Met Gly Arg Ser Phe Ser Leu Ala Val  
 1 5 10 15  
 Ser Val Glu Pro Glu Gln Glu Ile Pro Lys Pro Gln Leu Lys Gln Glu  
 20 25 30  
 Phe Lys Tyr Gln Pro Asp Ala Leu Val Phe Ser Ser Asn Lys Ala Pro  
 35 40 45  
 Lys Gln Tyr Glu Val Gly Gly Arg Gly Glu Ala Ser Thr Ser Asp Gly  
 50 55 60  
 Trp Glu Gly Thr His Ser Ala Pro Ala Pro Glu Pro His Pro Ala Pro  
 65 70 75 80  
 Ile Ala Asp Arg Glu Pro Glu Leu Ala Thr Pro Gln Arg Ile Pro Arg  
 85 90 95  
 Glu Thr Pro Ala His Asn Pro Asn Arg Glu Val Ser Leu Asn Pro Lys  
 100 105 110  
 Tyr Thr Phe Glu Ser Phe Val Ile Gly Pro Phe Asn Arg Phe Ala Asn  
 115 120 125  
 Ala Ala Ala Val Ala Val Ala Glu Ser Pro Ala Lys Ala Phe Asn Pro  
 130 135 140  
 Leu Phe Ile Ser Gly Gly Ser Gly Leu Gly Lys Thr His Leu Leu His  
 145 150 155 160  
 Ala Val Gly Asn Tyr Ala Gln Glu Leu Gln Pro Gly Pro Arg Ile Lys  
 165 170 175  
 Tyr Val Ser Ser Glu Glu Tyr His Gln Arg Leu His Gln Leu Arg Ala  
 180 185 190  
 Arg

<210> 155  
 <211> 2016  
 <212> DNA  
 <213> *Corynebacterium glutamicum*

<220>  
 <221> CDS  
 <222> (101)..(1993)  
 <223> RXA01480

<400> 155  
 cgaggacaac gatgactccg agcactccgc cgagggtctt cttgctgttt tgcatacaac 60

caatataggc acactaaagg gacgggctaa agtgatggtc atg gca aag gga cgt Met Ala Lys Gly Arg 1 5	115
att ccg gaa agt gac att cag gca atc cgc gag cgc acc ccg atc gag Ile Pro Glu Ser Asp Ile Gln Ala Ile Arg Glu Arg Thr Pro Ile Glu 10 15 20	163
gag atc gtg ggt gat tat gtg cag ctg aaa tcg gca ggt gct gat tcg Glu Ile Val Gly Asp Tyr Val Gln Leu Lys Ser Ala Gly Ala Asp Ser 25 30 35	211
ctc aag ggg ctt tct ccc ttt aaa gat gaa aaa aca cca tcg ttc cat Leu Lys Gly Leu Ser Pro Phe Lys Asp Glu Lys Thr Pro Ser Phe His 40 45 50	259
gtg cgc ccc aac cgt ggt tac tac cac tgt ttc tcc acc ggc aaa ggt Val Arg Pro Asn Arg Gly Tyr Tyr His Cys Phe Ser Thr Gly Lys Gly 55 60 65	307
gga gat gtg ttc tcc ttc ctc atg gag atg gaa cac atc tct ttc cct Gly Asp Val Phe Ser Phe Leu Met Glu Met Glu His Ile Ser Phe Pro 70 75 80 85	355
gag gct gtg gaa gtg gct ggc gag aaa att ggt tat cag atc aat tac Glu Ala Val Glu Val Cys Ala Glu Lys Ile Gly Tyr Gln Ile Asn Tyr 90 95 100	403
caa ggt ggt ggc ccg ggg cgc cgt gag gaa cct gga act cgc cag cgc Gln Gly Gly Gly Pro Gly Arg Arg Glu Glu Pro Gly Thr Arg Gln Arg 105 110 115	451
ctt att ttg gct aat aag gct cgc cac cag ttt tat cgc gag caa tta Leu Ile Leu Ala Asn Lys Ala Ala His Gln Phe Tyr Arg Glu Gln Leu 120 125 130	499
gaa acc ccc gaa gca caa cct ggc agg gag ttt ttg ctg cag cgt gga Glu Thr Pro Glu Ala Gln Pro Gly Arg Glu Phe Leu Leu Gln Arg Gly 135 140 145	547
ttc gga cag cag cac att tat cat ttc gaa tgt ggc tat cgc cct gcc Phe Gly Gln Gln His Ile Tyr His Phe Glu Cys Gly Tyr Ala Pro Ala 150 155 160 165	595
ggc tgg gat acc ttg acc aag cat ttg ctg aag aag ggc ttt gag ttc Gly Trp Asp Thr Leu Thr Lys His Leu Leu Lys Lys Gly Phe Glu Phe 170 175 180	643
aag gaa tta gaa gct gcc ggt cta agc aag atg ggt aag cgc ggt ccg Lys Glu Leu Glu Ala Ala Gly Leu Ser Lys Met Gly Lys Arg Gly Pro 185 190 195	691
att gat cag ttc cag cgc agg ttg ctg tgg ccg atc aag aac ctg tct Ile Asp Gln Phe Gln Arg Arg Leu Leu Trp Pro Ile Lys Asn Leu Ser 200 205 210	739
ggt gat gtc att ggt ttt ggc gcc cgc aag ctt ttc gat gac gac aaa Gly Asp Val Ile Gly Phe Gly Ala Arg Lys Leu Phe Asp Asp Asp Lys 215 220 225	787

atg ggc aag tac atg aat acg cct gag acg ttg ttg tac aaa aag tcc	835
Met Gly Lys Tyr Met Asn Thr Pro Glu Thr Leu Tyr Lys Lys Ser	
230 235 240 245	
aag gtg ctc ttt ggt cta gat tct gca aag aag gcc att gca gct ggc	883
Lys Val Leu Phe Gly Leu Asp Ser Ala Lys Lys Ala Ile Ala Ala Gly	
250 255 260	
cac caa gca gta gtg gtg gaa ggc tac acc gat gtg atg gcc atg cat	931
His Gln Ala Val Val Val Glu Gly Tyr Thr Asp Val Met Ala Met His	
265 270 275	
gcc gcg gcc att gat aca gcc gtg gca tgg tgt gcc act ttt ggt	979
Ala Ala Gly Ile Asp Thr Ala Val Ala Ser Cys Gly Thr Ala Phe Gly	
280 285 290	
gaa gaa cac ttg cag atg ctt cgt cga ctc atg ctg gat gat aac tac	1027
Glu Glu His Leu Gln Met Leu Arg Arg Leu Met Leu Asp Asp Asn Tyr	
295 300 305	
ttc cgc ggt gaa ctg att tac acc ttc gat ggt gat gag gcc ggc cag	1075
Phe Arg Gly Glu Leu Ile Tyr Thr Phe Asp Gly Asp Glu Ala Gly Gln	
310 315 320 325	
aag gcc gcc atg cgt gcc ttt gag ggc gat cag aag ttc aca gga caa	1123
Lys Ala Ala Met Arg Ala Phe Glu Gly Asp Gln Lys Phe Thr Gly Gln	
330 335 340	
tca ttt gtg tct gtg gca ccc aac ggc atg gat ccg tgt gat ctg cgc	1171
Ser Phe Val Ser Val Ala Pro Asn Gly Met Asp Pro Cys Asp Leu Arg	
345 350 355	
ctt gag cgt gcc gat gcg gcg gtg cgt gat ctt gtg gca cga cgc atc	1219
Leu Glu Arg Gly Asp Ala Ala Val Arg Asp Leu Val Ala Arg Arg Ile	
360 365 370	
ccg atg ttt gag ttc gtc atc caa tgc atc atc agc gaa tac acc ctc	1267
Pro Met Phe Glu Phe Val Ile Gln Ser Ile Ile Ser Glu Tyr Thr Leu	
375 380 385	
gac acc gtg gaa ggc cgt ctg gct gcg ctt cgt cgg gca gtc ccc atc	1315
Asp Thr Val Glu Gly Arg Leu Ala Ala Leu Arg Arg Ala Val Pro Ile	
390 395 400 405	
gtg gcg gat att cgc gat aag acg ctg cag tct gaa tac gcc cgc ctg	1363
Val Ala Asp Ile Arg Asp Lys Thr Leu Gln Ser Glu Tyr Ala Arg Leu	
410 415 420	
ctg tct ggt tgg gtc gcc tgg tct gat cct tca gag gtg ctg cgt cag	1411
Leu Ser Gly Trp Val Gly Trp Ser Asp Pro Ser Glu Val Leu Arg Gln	
425 430 435	
gtt cac gag gaa gca cgt gcg ccc aag cgc gat aag aag cct gtg cgt	1459
Val His Glu Glu Ala Arg Arg Pro Lys Arg Asp Lys Lys Pro Val Arg	
440 445 450	
gca aag cgt ttc gat caa ccg ctc gag gat caa agc ctg cga ccc acc	1507
Ala Lys Arg Phe Asp Gln Pro Leu Glu Asp Gln Ser Leu Arg Pro Thr	
455 460 465	
atg gcg ctg cct aat ccg cgg aac cct gtg ctg tgg cag gaa cgg gaa	1555

Met Ala Leu Pro Asn Pro Arg Asn Pro Val Leu Trp Gln Glu Arg Glu  
470 475 480 485

tca ctc aag atc gcc ctg caa tat ccg gag ctc gcg gga tcg tac ttt 1603  
Ser Leu Lys Ile Ala Leu Gln Tyr Pro Glu Leu Ala Gly Ser Tyr Phe  
490 495 500

gat gga ctg cca acc gat agc ttc acc aac cct gcc tac cgc atg gta 1651  
Asp Gly Leu Pro Thr Asp Ser Phe Thr Asn Pro Ala Tyr Arg Met Val  
505 510 515

cgc gat gcc att tcg gct gct ggg gga tgt gaa cgt gcc ctc gat ggc 1699  
Arg Asp Ala Ile Ser Ala Ala Gly Gly Cys Glu Arg Ala Leu Asp Gly  
520 525 530

act gat tgg ttg cct gcc gta tcg gaa aat atg act gat att ttg ggc 1747  
Thr Asp Trp Leu Pro Ala Val Ser Glu Asn Met Thr Asp Ile Leu Gly  
535 540 545

acg tcg ttg gtg tca gag ctg gcg atg gaa ccc atc gag gtg gaa gcg 1795  
Thr Ser Leu Val Ser Glu Leu Ala Met Glu Pro Ile Glu Val Glu Ala  
550 555 560 565

caa gac ctg gaa tca tat acc gat ggt gtg ttg tcc agg ctg cag gaa 1843  
Gln Asp Leu Glu Ser Tyr Thr Asp Gly Val Leu Ser Arg Leu Gln Glu  
570 575 580

aca cga gtg gcc aac cag atc gcc atc ttg aaa gga cag ctg caa aga 1891  
Thr Arg Val Gly Asn Gln Ile Ala Ile Leu Lys Gly Gln Leu Gln Arg  
585 590 595

atg cgt ccg tct gaa gat gag caa gcc tac aac tcg ctg ttt tcc gat 1939  
Met Arg Pro Ser Glu Asp Glu Gln Ala Tyr Asn Ser Leu Phe Ser Asp  
600 605 610

ctg gtt gcc ctg gaa cag gcg cgc cgg gag ctg ttg gcc cgg gcg ttt 1987  
Leu Val Ala Leu Glu Gln Ala Arg Arg Glu Leu Leu Ala Arg Ala Phe  
615 620 625

aga ggg taatttagtc ctggtcttgc tcg 2016  
Arg Gly  
630

<210> 156  
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<212> PRT  
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<400> 156  
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Arg Thr Pro Ile Glu Glu Ile Val Gly Asp Tyr Val Gln Leu Lys Ser  
20 25 30  
Ala Gly Ala Asp Ser Leu Lys Gly Leu Ser Pro Phe Lys Asp Glu Lys  
35 40 45  
Thr Pro Ser Phe His Val Arg Pro Asn Arg Gly Tyr His Cys Phe  
50 55 60

Ser Thr Gly Lys Gly Gly Asp Val Phe Ser Phe Leu Met Glu Met Glu  
 65 70 75 80  
 His Ile Ser Phe Pro Glu Ala Val Glu Val Cys Ala Glu Lys Ile Gly  
 85 90 95  
 Tyr Gln Ile Asn Tyr Gln Gly Gly Gly Pro Gly Arg Arg Glu Glu Pro  
 100 105 110  
 Gly Thr Arg Gln Arg Leu Ile Leu Ala Asn Lys Ala Ala His Gln Phe  
 115 120 125  
 Tyr Arg Glu Gln Leu Glu Thr Pro Glu Ala Gln Pro Gly Arg Glu Phe  
 130 135 140  
 Leu Leu Gln Arg Gly Phe Gly Gln Gln His Ile Tyr His Phe Glu Cys  
 145 150 155 160  
 Gly Tyr Ala Pro Ala Gly Trp Asp Thr Leu Thr Lys His Leu Leu Lys  
 165 170 175  
 Lys Gly Phe Glu Phe Lys Glu Leu Glu Ala Ala Gly Leu Ser Lys Met  
 180 185 190  
 Gly Lys Arg Gly Pro Ile Asp Gln Phe Gln Arg Arg Leu Trp Pro  
 195 200 205  
 Ile Lys Asn Leu Ser Gly Asp Val Ile Gly Phe Gly Ala Arg Lys Leu  
 210 215 220  
 Phe Asp Asp Asp Lys Met Gly Lys Tyr Met Asn Thr Pro Glu Thr Leu  
 225 230 235 240  
 Leu Tyr Lys Lys Ser Lys Val Leu Phe Gly Leu Asp Ser Ala Lys Lys  
 245 250 255  
 Ala Ile Ala Ala Gly His Gln Ala Val Val Val Glu Gly Tyr Thr Asp  
 260 265 270  
 Val Met Ala Met His Ala Ala Gly Ile Asp Thr Ala Val Ala Ser Cys  
 275 280 285  
 Gly Thr Ala Phe Gly Glu Glu His Leu Gln Met Leu Arg Arg Leu Met  
 290 295 300  
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 305 310 315 320  
 Asp Glu Ala Gly Gln Lys Ala Ala Met Arg Ala Phe Glu Gly Asp Gln  
 325 330 335  
 Lys Phe Thr Gly Gln Ser Phe Val Ser Val Ala Pro Asn Gly Met Asp  
 340 345 350  
 Pro Cys Asp Leu Arg Leu Glu Arg Gly Asp Ala Ala Val Arg Asp Leu  
 355 360 365  
 Val Ala Arg Arg Ile Pro Met Phe Glu Phe Val Ile Gln Ser Ile Ile  
 370 375 380

Ser Glu Tyr Thr Leu Asp Thr Val Glu Gly Arg Leu Ala Ala Leu Arg  
385 390 395 400

Arg Ala Val Pro Ile Val Ala Asp Ile Arg Asp Lys Thr Leu Gln Ser  
405 410 415

Glu Tyr Ala Arg Leu Leu Ser Gly Trp Val Gly Trp Ser Asp Pro Ser  
420 425 430

Glu Val Leu Arg Gln Val His Glu Glu Ala Arg Arg Pro Lys Arg Asp  
435 440 445

Lys Lys Pro Val Arg Ala Lys Arg Phe Asp Gln Pro Leu Glu Asp Gln  
450 455 460

Ser Leu Arg Pro Thr Met Ala Leu Pro Asn Pro Arg Asn Pro Val Leu  
465 470 475 480

Trp Gln Glu Arg Glu Ser Leu Lys Ile Ala Leu Gln Tyr Pro Glu Leu  
485 490 495

Ala Gly Ser Tyr Phe Asp Gly Leu Pro Thr Asp Ser Phe Thr Asn Pro  
500 505 510

Ala Tyr Arg Met Val Arg Asp Ala Ile Ser Ala Ala Gly Gly Cys Glu  
515 520 525

Arg Ala Leu Asp Gly Thr Asp Trp Leu Pro Ala Val Ser Glu Asn Met  
530 535 540

Thr Asp Ile Leu Gly Thr Ser Leu Val Ser Glu Leu Ala Met Glu Pro  
545 550 555 560

Ile Glu Val Glu Ala Gln Asp Leu Glu Ser Tyr Thr Asp Gly Val Leu  
565 570 575

Ser Arg Leu Gln Glu Thr Arg Val Gly Asn Gln Ile Ala Ile Leu Lys  
580 585 590

Gly Gln Leu Gln Arg Met Arg Pro Ser Glu Asp Glu Gln Ala Tyr Asn  
595 600 605

Ser Leu Phe Ser Asp Leu Val Ala Leu Glu Gln Ala Arg Arg Glu Leu  
610 615 620

Leu Ala Arg Ala Phe Arg Gly  
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<210> 157

<211> 1597

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1597)

<223> RXN03163

<400> 157

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tcaagttggc ctaaaaatct gatgtagtat cttcggattc atg gca aaa acc cgc 115  
Met Ala Lys Thr Arg  
1 5

gtc ccc gct cct gaa aag tgc gtg gcg cgg gtt tta cct ctt ttg ggg 163  
Val Pro Ala Pro Glu Lys Ser Val Ala Arg Val Leu Pro Leu Leu Gly  
10 15 20

tta cct cac ctg gat cga ctg ttt gat tac cgc atc agc gaa gac caa 211  
Leu Pro His Leu Asp Arg Leu Phe Asp Tyr Arg Ile Ser Glu Asp Gln  
25 30 35

cac gat gat gtg caa cct ggc gtg cgg gtg cgc gtg cgt ttt ggt gga 259  
His Asp Asp Val Gln Pro Gly Val Arg Val Arg Val Arg Phe Gly Gly  
40 45 50

cgt tta gtt gat gcc atc gtg atg tca cgc acc gcg caa acc tgc cac 307  
Arg Leu Val Asp Ala Ile Val Met Ser Arg Thr Ala Gln Thr Ser His  
55 60 65

gag gga aag ctg atg tgg ctg gat cgg gtg att tgc ccg atc gtg gtg 355  
Glu Gly Lys Leu Met Trp Leu Asp Arg Val Ile Ser Pro Ile Val Val  
70 75 80 85

tat cca cct caa aca gca aag cta att gag caa ctc agt gat cgc tat 403  
Tyr Pro Pro Gln Thr Ala Lys Leu Ile Glu Gln Leu Ser Asp Arg Tyr  
90 95 100

ggc ggg gta cgt tgc gat ctc atc cgt tgc gcg cta ccg gcg cgg cat 451  
Gly Gly Val Arg Ser Asp Leu Ile Arg Ser Ala Leu Pro Ala Arg His  
105 110 115

gct ggg gca gaa gag gca gat acc tcc acg tgc tgg gag tca ttg ggt 499  
Ala Gly Ala Glu Glu Ala Asp Thr Ser Thr Ser Trp Glu Ser Leu Gly  
120 125 130

gag gtt aaa gaa ccc gat tta tgc tgc tgg tct gcg tat cag cat ggt 547  
Glu Val Lys Glu Pro Asp Leu Ser Ser Trp Ser Ala Tyr Gln His Gly  
135 140 145

caa tca ttt gtt gac gcc gtc ttg gcg gga aca act gcg cgg gcg tca 595  
Gln Ser Phe Val Asp Ala Val Leu Ala Gly Thr Thr Ala Arg Ala Ser  
150 155 160 165

tgg cag att gct ccc gga gat gat tgg gcg ctg gct ttg gct tct ttg 643  
Trp Gln Ile Ala Pro Gly Asp Asp Trp Ala Leu Ala Leu Ala Ser Leu  
170 175 180

gcg gtc aag gtt gtc aaa gac ggc ggc gga gcg ctt ctc gta gtg cct 691  
Ala Val Lys Val Val Lys Asp Gly Gly Gly Ala Leu Leu Val Val Pro  
185 190 195

gat cag cgc gat ctc gac cgc ttg gaa gct gcg ctt cga ggt ttg gtt 739  
Asp Gln Arg Asp Leu Asp Arg Leu Glu Ala Ala Leu Arg Gly Leu Val  
200 205 210

gcg gcg aaa caa atc act gtg ctt aat tca ggt ctt ggt ccg cag gca 787  
Ala Ala Lys Gln Ile Thr Val Leu Asn Ser Gly Leu Gly Pro Gln Ala  
215 220 225

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cga tat cgg cgt ttc cta tgc gta ctc agt ggg cag gga cga ctg att 835  
 Arg Tyr Arg Arg Phe Leu Ser Val Leu Ser Gly Gln Gly Arg Leu Ile 245  
 230 235 240

att gga acc aga agt gcc gct ttt gca ccc gtg aag gat ctg aaa ctg 883  
 Ile Gly Thr Arg Ser Ala Ala Phe Ala Pro Val Lys Asp Leu Lys Leu 260  
 250 255

gcc gtc att tta aat gat gcc gac gac aac ctc gtt gat cct aga cgc 931  
 Ala Val Ile Leu Asn Asp Gly Asp Asn Leu Val Asp Pro Arg Ala 275  
 265 270

ccc tat gcc cac gcc agg gaa gtg ctg acc acg cgt tcc agt ttg gaa 979  
 Pro Tyr Ala His Ala Arg Glu Val Leu Thr Thr Arg Ser Ser Leu Glu 290  
 280 285

gca gca tcc ttg att att gcg gga cat gcg cgg acc gcg gaa acc caa 1027  
 Ala Ser Ser Leu Ile Ile Ala Gly His Ala Arg Thr Ala Glu Thr Gln 305  
 295 300

ttg ctg gtg gaa tgc gga tgg atg cac aat ctc atc gca cgg agg gat 1075  
 Leu Leu Val Glu Ser Gly Trp Met His Asn Leu Ile Ala Pro Arg Asp 325  
 310 315 320

acc att cgc act agg atg ccg cgt att cag gca gtg gcc gat tcc gat 1123  
 Thr Ile Arg Thr Arg Met Pro Arg Ile Gln Ala Val Gly Asp Ser Asp 340  
 330 335

ttc cag atg gaa cgc gat cca atg gcc cga tca gcg cgg ctg cct gcc 1171  
 Phe Gln Met Glu Arg Asp Pro Met Ala Arg Ser Ala Arg Leu Pro Gly 355  
 345 350

att gcg ttt cat gcg gtg cgc agc gcc tta gaa cgt gat caa cca gcg 1219  
 Ile Ala Phe His Ala Val Arg Ser Ala Leu Glu Arg Asp Gln Pro Ala 370  
 360 365

ctt atc cag gta cca agg aaa gcc tac gtg cca acc ttg gcg tgt gga 1267  
 Leu Ile Gln Val Pro Arg Lys Gly Tyr Val Pro Thr Leu Ala Cys Gly 385  
 375 380

aac tgc cgc acc cca gcg cgg tgc cgg cac tgt aat ggg cct gtg gga 1315  
 Asn Cys Arg Thr Pro Ala Arg Cys Arg His Cys Asn Gly Pro Val Gly 405  
 390 395 400

ctt ccc cag gga agc tct gat cta gcg gga gtg ccc act tgc cga tgg 1363  
 Leu Pro Gln Gly Ser Ser Asp Leu Ala Gly Val Pro Thr Cys Arg Trp 420  
 410 415

tgc gga cgc cct gat tgc cgg ttt aag tgc caa aac tgc gcc tct cca 1411  
 Cys Gly Arg Pro Asp Ser Arg Phe Lys Cys Gln Asn Cys Gly Ser Pro 435  
 425 430

aaa ctg cgt gct gtg gtg ctg gga acg gaa cgc aca gca gaa gaa ctg 1459  
 Lys Leu Arg Ala Val Val Leu Gly Thr Glu Arg Thr Ala Glu Glu Leu 450  
 440 445

gcc cgc gcg ttc ccg tct gtg cgg gta att acc tct ggt gcc aac aag 1507  
 Gly Arg Ala Phe Pro Ser Val Arg Val Ile Thr Ser Gly Gly Asn Lys 465  
 455 460

gtg gtg gat tgc gtg gaa aac cga gcc agc att gtg gtg tcc acg cca 1555



Val Val Asp Ser Val Glu Asn Arg Ala Ser Ile Val Val Ser Thr Pro  
 470 475 480 485

ggt gca gaa cct ttt gtg gcc aac tcg ccg gag aga cca gag 1597  
 Gly Ala Glu Pro Phe Val Ala Asn Ser Pro Glu Arg Pro Glu  
 490 495

&lt;210&gt; 158

&lt;211&gt; 499

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 158

Met Ala Lys Thr Arg Val Pro Ala Pro Glu Lys Ser Val Ala Arg Val  
 1 5 10 15

Leu Pro Leu Leu Gly Leu Pro His Leu Asp Arg Leu Phe Asp Tyr Arg  
 20 25 30

Ile Ser Glu Asp Gln His Asp Val Gln Pro Gly Val Arg Val Arg  
 35 40 45

Val Arg Phe Gly Gly Arg Leu Val Asp Ala Ile Val Met Ser Arg Thr  
 50 55 60

Ala Gln Thr Ser His Glu Gly Lys Leu Met Trp Leu Asp Arg Val Ile  
 65 70 75 80

Ser Pro Ile Val Val Tyr Pro Pro Gln Thr Ala Lys Leu Ile Glu Gln  
 85 90 95

Leu Ser Asp Arg Tyr Gly Gly Val Arg Ser Asp Leu Ile Arg Ser Ala  
 100 105 110

Leu Pro Ala Arg His Ala Gly Ala Glu Glu Ala Asp Thr Ser Thr Ser  
 115 120 125

Trp Glu Ser Leu Gly Glu Val Lys Glu Pro Asp Leu Ser Ser Trp Ser  
 130 135 140

Ala Tyr Gln His Gly Gln Ser Phe Val Asp Ala Val Leu Ala Gly Thr  
 145 150 155 160

Thr Ala Arg Ala Ser Trp Gln Ile Ala Pro Gly Asp Asp Trp Ala Leu  
 165 170 175

Ala Leu Ala Ser Leu Ala Val Lys Val Val Lys Asp Gly Gly Gly Ala  
 180 185 190

Leu Leu Val Val Pro Asp Gln Arg Asp Leu Asp Arg Leu Glu Ala Ala  
 195 200 205

Leu Arg Gly Leu Val Ala Ala Lys Gln Ile Thr Val Leu Asn Ser Gly  
 210 215 220

Leu Gly Pro Gln Ala Arg Tyr Arg Arg Phe Leu Ser Val Leu Ser Gly  
 225 230 235 240

Gln Gly Arg Leu Ile Ile Gly Thr Arg Ser Ala Ala Phe Ala Pro Val  
 245 250 255

Lys Asp Leu Lys Leu Ala Val Ile Leu Asn Asp Gly Asp Asp Asn Leu  
 260 265 270  
 Val Asp Pro Arg Ala Pro Tyr Ala His Ala Arg Glu Val Leu Thr Thr  
 275 280 285  
 Arg Ser Ser Leu Glu Ala Ser Ser Leu Ile Ile Ala Gly His Ala Arg  
 290 295 300  
 Thr Ala Glu Thr Gln Leu Leu Val Glu Ser Gly Trp Met His Asn Leu  
 305 310 315 320  
 Ile Ala Pro Arg Asp Thr Ile Arg Thr Arg Met Pro Arg Ile Gln Ala  
 325 330 335  
 Val Gly Asp Ser Asp Phe Gln Met Glu Arg Asp Pro Met Ala Arg Ser  
 340 345 350  
 Ala Arg Leu Pro Gly Ile Ala Phe His Ala Val Arg Ser Ala Leu Glu  
 355 360 365  
 Arg Asp Gln Pro Ala Leu Ile Gln Val Pro Arg Lys Gly Tyr Val Pro  
 370 375 380  
 Thr Leu Ala Cys Gly Asn Cys Arg Thr Pro Ala Arg Cys Arg His Cys  
 385 390 395 400  
 Asn Gly Pro Val Gly Leu Pro Gln Gly Ser Ser Asp Leu Ala Gly Val  
 405 410 415  
 Pro Thr Cys Arg Trp Cys Gly Arg Pro Asp Ser Arg Phe Lys Cys Gln  
 420 425 430  
 Asn Cys Gly Ser Pro Lys Leu Arg Ala Val Val Leu Gly Thr Glu Arg  
 435 440 445  
 Thr Ala Glu Glu Leu Gly Arg Ala Phe Pro Ser Val Arg Val Ile Thr  
 450 455 460  
 Ser Gly Gly Asn Lys Val Val Asp Ser Val Glu Asn Arg Ala Ser Ile  
 465 470 475 480  
 Val Val Ser Thr Pro Gly Ala Glu Pro Phe Val Ala Asn Ser Pro Glu  
 485 490 495  
 Arg Pro Glu

<210> 159  
 <211> 2151  
 <212> DNA  
 <213> Corynebacterium glutamicum  
 <220>  
 <221> CDS  
 <222> (101)..(2128)  
 <223> FRXA02241  
 <400> 159



gga cga ctg att att gga acc aga agt gcc gct ttt gca ccc gtg aag 835  
 Gly Arg Leu Ile Ile Gly Thr Arg Ser Ala Ala Phe Ala Pro Val Lys  
 230 235 240 245

gat ctg aaa ctg gcc gtc att tta aat gat ggc gac gac aac ctc gtt 883  
 Asp Leu Lys Leu Ala Val Ile Leu Asn Asp Gly Asp Asp Asn Leu Val  
 250 255 260

gat cct aga gcg ccc tat gcc cac gcc agg gaa gtg ctg acc acg cgt 931  
 Asp Pro Arg Ala Pro Tyr Ala His Ala Arg Glu Val Leu Thr Thr Arg  
 265 270 275

tcc agt ttg gaa gca agc tcc ttg att att gcg gga cat gcg cgg acc 979  
 Ser Ser Leu Glu Ala Ser Ser Leu Ile Ile Ala Gly His Ala Arg Thr  
 280 285 290

gcg gaa acc caa ttg ctg gtg gaa tcg gga tgg atg cac aat ctc atc 1027  
 Ala Glu Thr Gln Leu Leu Val Glu Ser Gly Trp Met His Asn Leu Ile  
 295 300 305

gca ccg agg gat acc att cgc act agg atg ccg cgt att cag gca gtg 1075  
 Ala Pro Arg Asp Thr Ile Arg Thr Arg Met Pro Arg Ile Gln Ala Val  
 310 315 320 325

ggc gat tcc gat ttc cag atg gaa cgc gat cca atg gcc cga tca gcg 1123  
 Gly Asp Ser Asp Phe Gln Met Glu Arg Asp Pro Met Ala Arg Ser Ala  
 330 335 340

cgg ctg cct ggc att gcg ttt cat gcg gtg cgc agc gcc tta gaa cgt 1171  
 Arg Leu Pro Gly Ile Ala Phe His Ala Val Arg Ser Ala Leu Glu Arg  
 345 350 355

gat caa cca gcg ctt atc cag gta cca agg aaa gcc tac gtg cca acc 1219  
 Asp Gln Pro Ala Leu Ile Gln Val Pro Arg Lys Gly Tyr Val Pro Thr  
 360 365 370

ttg gcg tgt gga aac tgc cgc acc cca gcg cgg tgc cgg cac tgt aat 1267  
 Leu Ala Cys Gly Asn Cys Arg Thr Pro Ala Arg Cys Arg His Cys Asn  
 375 380 385

ggg cct gtg gga ctt ccc cag gga agc tct gat cta gcg gga gtg ccc 1315  
 Gly Pro Val Gly Leu Pro Gln Gly Ser Ser Asp Leu Ala Gly Val Pro  
 390 395 400 405

act tgc cga tgg tgc gga cgc cct gat tcg cgg ttt aag tgc caa aac 1363  
 Thr Cys Arg Trp Cys Gly Arg Pro Asp Ser Arg Phe Lys Cys Gln Asn  
 410 415 420

tgc ggc tct cca aaa ctg cgt gct gtg gtg ctg gga acg gaa cgc aca 1411  
 Cys Gly Ser Pro Lys Leu Arg Ala Val Val Leu Gly Thr Glu Arg Thr  
 425 430 435

gca gaa gaa ctg ggc cgc gcg ttc ccg tct gtg cgg gta att acc tct 1459  
 Ala Glu Glu Leu Gly Arg Ala Phe Pro Ser Val Arg Val Ile Thr Ser  
 440 445 450

ggt ggc aac aag gtg gtg gat tcg gtg gaa aac cga gcc agc att gtg 1507  
 Gly Gly Asn Lys Val Val Asp Ser Val Glu Asn Arg Ala Ser Ile Val  
 455 460 465

gtg tcc acg cca ggt gca gaa cct ttt gtg gcc aac tcg ccg gag aga 1555  
 Val Ser Thr Pro Gly Ala Glu Pro Phe Val Ala Asn Ser Pro Glu Arg 485  
 470 475 480

cca gag aaa tcg gag aaa cca gag cac aag gcc gct tac ggt gcc ttg 1603  
 Pro Glu Lys Ser Glu Lys Pro Glu His Lys Gly Ala Tyr Gly Ala Leu 500  
 490 495

tta ttg ctg gat acc tgg gcg ttg atg ggt cgg caa gat ctg cgc gcc 1651  
 Leu Leu Leu Asp Thr Trp Ala Leu Met Gly Arg Gln Asp Leu Arg Ala 515  
 505 510

atg gag gac gcg ctg cac aag tgg gca gcg gcg gcc acg ctg gtg cat 1699  
 Met Glu Asp Ala Leu His Lys Trp Ala Ala Ala Ala Thr Leu Val His 520 525 530

tct cat ctg cac cag ggt caa gtc atc gtg gtt gca gat cca tcg ttt 1747  
 Ser His Leu His Gln Gly Gln Val Ile Val Val Ala Asp Pro Ser Phe 535 540 545

cct gct gtg caa tcg ttg att cgg tgg gat atg gca ggt gct gca gcg 1795  
 Pro Ala Val Gln Ser Leu Ile Arg Trp Asp Met Ala Gly Ala Ala 550 555 560 565

caa gag ttg gct agc cga gcg gag gtt atg ttc ccg cct tct gta cac 1843  
 Gln Glu Leu Ala Ser Arg Arg Glu Val Met Phe Pro Pro Ser Val His 570 575 580

atg gca gca atc gat ggg gct acc gct gca ttg gaa agt ttc ttg gat 1891  
 Met Ala Ala Ile Asp Gly Ala Thr Ala Ala Leu Glu Ser Phe Leu Asp 585 590 595

ttg gcg gag ctt ccc gat cat gct gaa gtc ctc gcc cct gtt gat ctg 1939  
 Leu Ala Glu Leu Pro Asp His Ala Glu Val Leu Gly Pro Val Asp Leu 600 605 610

cca ccg ggt gtg agt ttg cct ggt gaa tat gat gag cag cgc ttt ggt 1987  
 Pro Pro Gly Val Ser Leu Pro Gly Glu Tyr Asp Glu Gln Arg Phe Gly 615 620 625

ccg ccg cag cgc ctt ctc atc aga act cca ttg gga ccg ccg tct gag 2035  
 Pro Pro Gln Arg Leu Leu Ile Arg Thr Pro Leu Gly Pro Arg Ser Glu 630 635 640 645

ttg ggt aga gcg ctg cgc tca gcc cag gtg gcg cgt gcg gtg agg aag 2083  
 Leu Gly Arg Ala Leu Arg Ser Ala Gln Val Ala Arg Ala Val Arg Lys 650 655 660

aat gat ttg ccg ttg cgt att cag atg gat ccg att cac atc gga 2128  
 Asn Asp Leu Pro Leu Arg Ile Gln Met Asp Pro Ile His Ile Gly 665 670 675

taaaactgct ggtgaaaggc cta 2151

&lt;210&gt; 160

&lt;211&gt; 676

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 160

Val Ala Arg Val Leu Pro Leu Leu Gly Leu Pro His Leu Asp Arg Leu  
 1 5 10 15  
 Phe Asp Tyr Arg Ile Ser Glu Asp Gln His Asp Asp Val Gln Pro Gly  
 20 25 30  
 Val Arg Val Arg Val Arg Phe Gly Gly Arg Leu Val Asp Ala Ile Val  
 35 40 45  
 Met Ser Arg Thr Ala Gln Thr Ser His Glu Gly Lys Leu Met Trp Leu  
 50 55 60  
 Asp Arg Val Ile Ser Pro Ile Val Val Tyr Pro Pro Gln Thr Ala Lys  
 65 70 75 80  
 Leu Ile Glu Gln Leu Ser Asp Arg Tyr Gly Gly Val Arg Ser Asp Leu  
 85 90 95  
 Ile Arg Ser Ala Leu Pro Ala Arg His Ala Gly Ala Glu Glu Ala Asp  
 100 105 110  
 Thr Ser Thr Ser Trp Glu Ser Leu Gly Glu Val Lys Glu Pro Asp Leu  
 115 120 125  
 Ser Ser Trp Ser Ala Tyr Gln His Gly Gln Ser Phe Val Asp Ala Val  
 130 135 140  
 Leu Ala Gly Thr Thr Ala Arg Ala Ser Trp Gln Ile Ala Pro Gly Asp  
 145 150 155 160  
 Asp Trp Ala Leu Ala Leu Ala Ser Leu Ala Val Lys Val Val Lys Asp  
 165 170 175  
 Gly Gly Gly Ala Leu Leu Val Val Pro Asp Gln Arg Asp Leu Asp Arg  
 180 185 190  
 Leu Glu Ala Ala Leu Arg Gly Leu Val Ala Ala Lys Gln Ile Thr Val  
 195 200 205  
 Leu Asn Ser Gly Leu Gly Pro Gln Ala Arg Tyr Arg Arg Phe Leu Ser  
 210 215 220  
 Val Leu Ser Gly Gln Gly Arg Leu Ile Ile Gly Thr Arg Ser Ala Ala  
 225 230 235 240  
 Phe Ala Pro Val Lys Asp Leu Lys Leu Ala Val Ile Leu Asn Asp Gly  
 245 250 255  
 Asp Asp Asn Leu Val Asp Pro Arg Ala Pro Tyr Ala His Ala Arg Glu  
 260 265 270  
 Val Leu Thr Thr Arg Ser Ser Leu Glu Ala Ser Ser Leu Ile Ile Ala  
 275 280 285  
 Gly His Ala Arg Thr Ala Glu Thr Gln Leu Leu Val Glu Ser Gly Trp  
 290 295 300  
 Met His Asn Leu Ile Ala Pro Arg Asp Thr Ile Arg Thr Arg Met Pro  
 305 310 315 320  
 Arg Ile Gln Ala Val Gly Asp Ser Asp Phe Gln Met Glu Arg Asp Pro

[illegible]

Arg Ala Val Arg Lys Asn Asp Leu Pro Leu Arg Ile Gln Met Asp Pro  
660 665 670

Ile His Ile Gly  
675

<210> 161  
<211> 2790  
<212> DNA  
<213> Corynebacterium glutamicum

<220>  
<221> CDS  
<222> (101)..(2767)  
<223> RXN00061

<400> 161  
tgaaagcaat attagaccat caatgattag gaatggaaaat taggggtctg gtttgggtga 60  
atgtgtcgcct aattttttcca ctgccttaca ctcgaggagc gtg act gag aag act 115  
Val Thr Glu Lys Thr 5  
1  
gac cag acc tta atg ctt atc gac ggc cac tcg atg gct ttc cgc gca 163  
Asp Gln Thr Leu Met Leu Ile Asp Gly His Ser Met Ala Phe Arg Ala 20  
10 15  
ttc ttt gct ttg ccg gct gag aat ttc tcc acg tcg ggc ggg cag gcc 211  
Phe Phe Ala Leu Pro Ala Glu Asn Phe Ser Thr Ser Gly Gly Gln Ala 35  
25 30  
acc aat gct gtc tat ggc ttt ctc tcg atg ctg tcc acg ttg ttg aag 259  
Thr Asn Ala Val Tyr Gly Phe Leu Ser Met Leu Ser Thr Leu Leu Lys 50  
40 45  
gat gag cag cct act cat gtg gcg gtg gct ttc gat gtg ggg cgt aag 307  
Asp Glu Gln Pro Thr His Val Ala Val Ala Phe Asp Val Gly Arg Lys 60  
55 65  
acg ttc cgt acc gat atg ttc ccg gcg tat aag gcg cag cgt gaa gca 355  
Thr Phe Arg Thr Asp Met Phe Pro Ala Tyr Lys Ala Gln Arg Glu Ala 85  
70 75 80  
acg cca cct gag ttt aag ggc cag gtg gaa atc ctc aag gag gtg ttg 403  
Thr Pro Pro Glu Phe Lys Gly Gln Val Glu Ile Leu Lys Glu Val Leu 100  
90 95  
tcc act ttg gga att acg act att gag aaa atc gat ttt gag gct gat 451  
Ser Thr Leu Gly Ile Thr Thr Ile Glu Lys Ile Asp Phe Glu Ala Asp 110  
105 115  
gat gtg atc gcc acg ttg tct gtg gcg gcg aaa cct tta ggc ttt aag 499  
Asp Val Ile Ala Thr Leu Ser Val Ala Ala Lys Pro Leu Gly Phe Lys 120  
120 125 130  
acg ctg att gtt acg ggt gac cgt gat tcc ttc cag ttg gtc aat gac 547  
Thr Leu Ile Val Thr Gly Asp Arg Asp Ser Phe Gln Leu Val Asn Asp 140  
135 140 145



acc acc acg gtg ttg tat ccg atg aag ggc gtg tct gtg ctg cac cgt 595  
 Thr Thr Thr Val Leu Tyr Pro Met Lys Gly Val Ser Val Leu His Arg  
 150 155 160 165

ttc acg ccg gaa gca gtg gag gag aag tat gga ctg aca ccg agg cag 643  
 Phe Thr Pro Glu Ala Val Glu Glu Lys Tyr Gly Leu Thr Pro Arg Gln  
 170 175 180

tat ccg gag ttt gca gcg ctg cgt ggt gat cct tcc gat aac ttg cct 691  
 Tyr Pro Glu Phe Ala Ala Leu Arg Gly Asp Pro Ser Asp Asn Leu Pro  
 185 190 195

aat att cct ggc gtg ggc gag aag act gct acc aag tgg att gcc cag 739  
 Asn Ile Pro Gly Val Gly Glu Lys Thr Ala Thr Lys Trp Ile Ala Gln  
 200 205 210

tat gaa act ttg gat aat ttg ctt gat cac gct gat gag atc aag ggc 787  
 Tyr Glu Thr Leu Asp Asn Leu Leu Asp His Ala Asp Glu Ile Lys Gly  
 215 220 225

aag gtt ggc gcc agc ctg cgt gag cgc att gag cag gtc ccg atg aac 835  
 Lys Val Gly Ala Ser Leu Arg Glu Arg Ile Glu Gln Val Arg Met Asn  
 230 235 240 245

cgc aag ctc acg gag atg gtg aag gat ctg gag ctg ccg ctt ggt ccg 883  
 Arg Lys Leu Thr Glu Met Val Lys Asp Leu Glu Leu Pro Leu Gly Pro  
 250 255 260

gac gat ttt gag atg aag cct gtg cag gtt gcg gag gtt gcg gcg aag 931  
 Asp Asp Phe Glu Met Lys Pro Val Gln Val Ala Glu Val Ala Ala Lys  
 265 270 275

ttt gac gat ctg gag ttt ggt acc aat ttg cgt gag ccg gtg ctg gcg 979  
 Phe Asp Asp Leu Glu Phe Gly Thr Asn Leu Arg Glu Arg Val Leu Ala  
 280 285 290

gtg gtg aag gcc gag ggt tcc gct gcc ccc gtg gag gaa gtg gaa gcg 1027  
 Val Val Lys Ala Glu Gly Ser Ala Ala Pro Val Glu Glu Val Glu Ala  
 295 300 305

gaa cag gtt gtc gtc gat acg caa tct ttg gcg caa tgg ctg cct gct 1075  
 Glu Gln Val Val Val Asp Thr Gln Ser Leu Ala Gln Trp Leu Pro Ala  
 310 315 320 325

agg gct ggc cag gcg ctt gct tta gcg ctg gct gga gtg gct aaa cct 1123  
 Arg Ala Gly Gln Ala Leu Ala Leu Ala Gly Val Ala Lys Pro  
 330 335 340

gct gct ggc gac acg tat gcg cta gcg att gcg gat acc aag cgc cat 1171  
 Ala Ala Gly Asp Thr Tyr Ala Leu Ala Ile Ala Asp Thr Lys Arg His  
 345 350 355

gcg gtg ttg gtt gat gtg gct gat att tca gcg gag gat gaa aag gcg 1219  
 Ala Val Leu Val Asp Val Ala Asp Ile Ser Ala Glu Asp Glu Lys Ala  
 360 365 370

ctg gcc acg tgg ttg gcg tgc gaa gat cca aag atg ctg cac ggc gct 1267  
 Leu Ala Thr Trp Leu Ala Ser Glu Asp Pro Lys Met Leu His Gly Ala  
 375 380 385

aag gcc gcc tat cat atg ctc gct ggg cgc ggt ttt gag ctg cac ggc 1315

Lys Ala Ala Tyr His Met Leu Ala Gly Arg Gly Phe Glu Leu His Gly  
 390 395 400 405  
 gtg gtg cat gac acg gcg atc gcg gca tac ttg ctg cgt ccg ggc caa 1363  
 Val Val His Asp Thr Ala Ile Ala Ala Tyr Leu Leu Arg Pro Gly Gln  
 410 415 420  
 cgc acc tat gag ctt gcc gac gtc tac cag cgg cat ctt caa cga cag 1411  
 Arg Thr Tyr Glu Leu Ala Asp Val Tyr Gln Arg His Leu Gln Arg Gln  
 425 430 435  
 ttg tct aca aac gac aat ggc ggc cag ctc acg ctg ctc gac gca gct 1459  
 Leu Ser Thr Asn Asp Asn Gly Gly Gln Leu Thr Leu Leu Asp Ala Ala  
 440 445 450  
 gat gac caa tcg ctt gtt gat gat gtc att gca atc ctt gag ctg tct 1507  
 Asp Asp Gln Ser Leu Val Asp Asp Val Ile Ala Ile Leu Glu Leu Ser  
 455 460 465  
 gaa gaa ttg acc aaa cag ctt cag gag att caa gct ttt gag ctt tac 1555  
 Glu Glu Leu Thr Lys Gln Leu Gln Glu Ile Gln Ala Phe Glu Leu Tyr  
 470 475 480 485  
 cat gac ctg gaa att ccg ctg tcg gga att ctg gcg cgc atg gag gcc 1603  
 His Asp Leu Glu Ile Pro Leu Ser Gly Ile Leu Ala Arg Met Glu Ala  
 490 495 500  
 atc ggt atc gct gtt gat gtt gcc act ttg gaa gag cag ttg aag act 1651  
 Ile Gly Ile Ala Val Asp Val Ala Thr Leu Glu Glu Gln Leu Lys Thr  
 505 510 515  
 ttc att ggt cag gtt gct cag gaa gag gaa gca gct cgc gag ctc gct 1699  
 Phe Ile Gly Gln Val Ala Gln Glu Glu Glu Ala Ala Arg Glu Leu Ala  
 520 525 530  
 gag gat cca acc ctg aat ctc tcg agc ccg aag cag ctg caa gtg gtg 1747  
 Glu Asp Pro Thr Leu Asn Leu Ser Ser Pro Lys Gln Leu Gln Val Val  
 535 540 545  
 ctt ttt gag acg ttc gga atg ccg aaa acc aag aaa acc aag acc ggc 1795  
 Leu Phe Glu Thr Phe Gly Met Pro Lys Thr Lys Lys Thr Lys Thr Gly  
 550 555 560 565  
 tac tct acg gct gcc gcg gaa att gaa gcc cta gcg atc aag aat ccg 1843  
 Tyr Ser Thr Ala Ala Ala Glu Ile Glu Ala Leu Ala Ile Lys Asn Pro  
 570 575 580  
 cac cca ttc cta gat cac ctg ttg gca cac cgt cag tac caa aag atg 1891  
 His Pro Phe Leu Asp His Leu Leu Ala His Arg Gln Tyr Gln Lys Met  
 585 590 595  
 aag acc act ctg gaa ggt ctc atc cgt gag gtg gct cct gat ggc cgt 1939  
 Lys Thr Thr Leu Glu Gly Leu Ile Arg Glu Val Ala Pro Asp Gly Arg  
 600 605 610  
 att cac acc acc ttc aac cag acg gtg gcg tct acg gga cgt ttg tca 1987  
 Ile His Thr Thr Phe Asn Gln Thr Val Ala Ser Thr Gly Arg Leu Ser  
 615 620 625  
 tcc act gat ccc aac ctg caa aac att cct gtg gcg act gag gct ggc 2035  
 Ser Thr Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Glu Ala Gly

630	635	640	645	
cga aag att cgt tgc gga ttc gtc gta ggc gag ggg tat gaa acc ttg Arg Lys Ile Arg Ser Gly Phe Val Val Gly Glu Gly Tyr Glu Thr Leu	650	655	660	2083
ctg act gcc gac tat tgc cag att gaa atg cgc gtg atg gct cac ctt Leu Thr Ala Asp Tyr Ser Gln Ile Glu Met Arg Val Met Ala His Leu	665	670	675	2131
tcc cag gac cca ggc ttg att gag cgc tac cgc gaa ggc gaa gac ctg Ser Gln Asp Pro Gly Leu Ile Glu Ala Tyr Arg Glu Gly Glu Asp Leu	680	685	690	2179
cac aat tac gtg ggt tcc aag gtg ttt aat gtg ccc atc gat ggc gtg His Asn Tyr Val Gly Ser Lys Val Phe Asn Val Pro Ile Asp Gly Val	695	700	705	2227
acc cct gag ctg cgt cgc cag gtc aag gcc atg tct tac ggt ctg gtg Thr Pro Glu Leu Arg Arg Gln Val Lys Ala Met Ser Tyr Gly Leu Val	710	715	720	2275
tac ggc ttg tcc gcg ttt ggt ttg tct cag cag ctg agc att cct gct Tyr Gly Leu Ser Ala Phe Gly Leu Ser Gln Gln Leu Ser Ile Pro Ala	730	735	740	2323
ggc gaa gcg aag cag atc atg gag tcc tac ttc gag cgc ttc ggc gga Gly Glu Ala Lys Gln Ile Met Glu Ser Tyr Phe Glu Arg Phe Gly Gly	745	750	755	2371
gta cag cgc tac ctc cgg gag atc gtg gag gag gct cga aaa gct ggc Val Gln Arg Tyr Leu Arg Glu Ile Val Glu Glu Ala Arg Lys Ala Gly	760	765	770	2419
tac acg gaa acg ctc ttt ggg cgt cgt cgc tac ctg ccg gaa ctg acc Tyr Thr Glu Thr Leu Phe Gly Arg Arg Arg Tyr Leu Pro Glu Leu Thr	775	780	785	2467
tcg gat aac cgt gtc gct cgt gaa aac gct gaa cgt gcc gca ctg aac Ser Asp Asn Arg Val Ala Arg Glu Asn Ala Glu Arg Ala Ala Leu Asn	790	795	800	2515
gcc ccg att cag gga act gcc gca gac atc atc aag gtg gcc atg atc Ala Pro Ile Gln Gly Thr Ala Ala Asp Ile Ile Lys Val Ala Met Ile	810	815	820	2563
cgg gtg gac cgt tca ctc aag gaa gct gcc gtg aaa tct cgc gtg ctg Arg Val Asp Arg Ser Leu Lys Glu Ala Ala Val Lys Ser Arg Val Leu	825	830	835	2611
ctt cag gtg cat gat gaa ttg gtc gtg gaa gta gcg gcc ggt gag ttg Leu Gln Val His Asp Glu Leu Val Val Glu Val Ala Ala Gly Glu Leu	840	845	850	2659
gaa caa gtc cgt gag att ctg gaa cgc gaa atg gat aac gcc atc aag Glu Gln Val Arg Glu Ile Leu Glu Arg Glu Met Asp Asn Ala Ile Lys	855	860	865	2707
ctg tcc gtt cct ttg gaa gtt tca gct ggt gat ggc gtt aac tgg gat Leu Ser Val Pro Leu Glu Val Ser Ala Gly Asp Gly Val Asn Trp Asp	870	875	880	2755

gct gca gcg cac taagaggtaa ctgccttttc gtc  
Ala Ala Ala His

2790

&lt;210&gt; 162

&lt;211&gt; 889

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 162

Val Thr Glu Lys Thr Asp Gln Thr Leu Met Leu Ile Asp Gly His Ser  
1 5 10 15

Met Ala Phe Arg Ala Phe Phe Ala Leu Pro Ala Glu Asn Phe Ser Thr  
20 25 30

Ser Gly Gly Gln Ala Thr Asn Ala Val Tyr Gly Phe Leu Ser Met Leu  
35 40 45

Ser Thr Leu Leu Lys Asp Glu Gln Pro Thr His Val Ala Val Ala Phe  
50 55 60

Asp Val Gly Arg Lys Thr Phe Arg Thr Asp Met Phe Pro Ala Tyr Lys  
65 70 75 80

Ala Gln Arg Glu Ala Thr Pro Pro Glu Phe Lys Gly Gln Val Glu Ile  
85 90 95

Leu Lys Glu Val Leu Ser Thr Leu Gly Ile Thr Thr Ile Glu Lys Ile  
100 105 110

Asp Phe Glu Ala Asp Asp Val Ile Ala Thr Leu Ser Val Ala Ala Lys  
115 120 125

Pro Leu Gly Phe Lys Thr Leu Ile Val Thr Gly Asp Arg Asp Ser Phe  
130 135 140

Gln Leu Val Asn Asp Thr Thr Thr Val Leu Tyr Pro Met Lys Gly Val  
145 150 155 160

Ser Val Leu His Arg Phe Thr Pro Glu Ala Val Glu Glu Lys Tyr Gly  
165 170 175

Leu Thr Pro Arg Gln Tyr Pro Glu Phe Ala Ala Leu Arg Gly Asp Pro  
180 185 190

Ser Asp Asn Leu Pro Asn Ile Pro Gly Val Gly Glu Lys Thr Ala Thr  
195 200 205

Lys Trp Ile Ala Gln Tyr Glu Thr Leu Asp Asn Leu Leu Asp His Ala  
210 215 220

Asp Glu Ile Lys Gly Lys Val Gly Ala Ser Leu Arg Glu Arg Ile Glu  
225 230 235 240

Gln Val Arg Met Asn Arg Lys Leu Thr Glu Met Val Lys Asp Leu Glu  
245 250 255

Leu Pro Leu Gly Pro Asp Asp Phe Glu Met Lys Pro Val Gln Val Ala

260	265	270
Glu Val Ala Ala Lys Phe Asp Asp Leu Glu Phe Gly Thr Asn Leu Arg 275 280 285		
Glu Arg Val Leu Ala Val Val Lys Ala Glu Gly Ser Ala Ala Pro Val 290 295 300		
Glu Glu Val Glu Ala Glu Gln Val Val Val Asp Thr Gln Ser Leu Ala 305 310 315 320		
Gln Trp Leu Pro Ala Arg Ala Gly Gln Ala Leu Ala Leu Ala Leu Ala 325 330 335		
Gly Val Ala Lys Pro Ala Ala Gly Asp Thr Tyr Ala Leu Ala Ile Ala 340 345 350		
Asp Thr Lys Arg His Ala Val Leu Val Asp Val Ala Asp Ile Ser Ala 355 360 365		
Glu Asp Glu Lys Ala Leu Ala Thr Trp Leu Ala Ser Glu Asp Pro Lys 370 375 380		
Met Leu His Gly Ala Lys Ala Ala Tyr His Met Leu Ala Gly Arg Gly 385 390 395 400		
Phe Glu Leu His Gly Val Val His Asp Thr Ala Ile Ala Ala Tyr Leu 405 410 415		
Leu Arg Pro Gly Gln Arg Thr Tyr Glu Leu Ala Asp Val Tyr Gln Arg 420 425 430		
His Leu Gln Arg Gln Leu Ser Thr Asn Asp Asn Gly Gly Gln Leu Thr 435 440 445		
Leu Leu Asp Ala Ala Asp Asp Gln Ser Leu Val Asp Asp Val Ile Ala 450 455 460		
Ile Leu Glu Leu Ser Glu Glu Leu Thr Lys Gln Leu Gln Glu Ile Gln 465 470 475 480		
Ala Phe Glu Leu Tyr His Asp Leu Glu Ile Pro Leu Ser Gly Ile Leu 485 490 495		
Ala Arg Met Glu Ala Ile Gly Ile Ala Val Asp Val Ala Thr Leu Glu 500 505 510		
Glu Gln Leu Lys Thr Phe Ile Gly Gln Val Ala Gln Glu Glu Ala 515 520 525		
Ala Arg Glu Leu Ala Glu Asp Pro Thr Leu Asn Leu Ser Ser Pro Lys 530 535 540		
Gln Leu Gln Val Val Leu Phe Glu Thr Phe Gly Met Pro Lys Thr Lys 545 550 555 560		
Lys Thr Lys Thr Gly Tyr Ser Thr Ala Ala Glu Ile Glu Ala Leu 565 570 575		
Ala Ile Lys Asn Pro His Pro Phe Leu Asp His Leu Leu Ala His Arg 580 585 590		

Gln Tyr Gln Lys Met Lys Thr Thr Leu Glu Gly Leu Ile Arg Glu Val  
 595 600 605  
 Ala Pro Asp Gly Arg Ile His Thr Thr Phe Asn Gln Thr Val Ala Ser  
 610 615 620  
 Thr Gly Arg Leu Ser Ser Thr Asp Pro Asn Leu Gln Asn Ile Pro Val  
 625 630 635 640  
 Arg Thr Glu Ala Gly Arg Lys Ile Arg Ser Gly Phe Val Val Gly Glu  
 645 650 655  
 Gly Tyr Glu Thr Leu Leu Thr Ala Asp Tyr Ser Gln Ile Glu Met Arg  
 660 665 670  
 Val Met Ala His Leu Ser Gln Asp Pro Gly Leu Ile Glu Ala Tyr Arg  
 675 680 685  
 Glu Gly Glu Asp Leu His Asn Tyr Val Gly Ser Lys Val Phe Asn Val  
 690 695 700  
 Pro Ile Asp Gly Val Thr Pro Glu Leu Arg Arg Gln Val Lys Ala Met  
 705 710 715 720  
 Ser Tyr Gly Leu Val Tyr Gly Leu Ser Ala Phe Gly Leu Ser Gln Gln  
 725 730 735  
 Leu Ser Ile Pro Ala Gly Glu Ala Lys Gln Ile Met Glu Ser Tyr Phe  
 740 745 750  
 Glu Arg Phe Gly Gly Val Gln Arg Tyr Leu Arg Glu Ile Val Glu Glu  
 755 760 765  
 Ala Arg Lys Ala Gly Tyr Thr Glu Thr Leu Phe Gly Arg Arg Arg Tyr  
 770 775 780  
 Leu Pro Glu Leu Thr Ser Asp Asn Arg Val Ala Arg Glu Asn Ala Glu  
 785 790 795 800  
 Arg Ala Ala Leu Asn Ala Pro Ile Gln Gly Thr Ala Ala Asp Ile Ile  
 805 810 815  
 Lys Val Ala Met Ile Arg Val Asp Arg Ser Leu Lys Glu Ala Ala Val  
 820 825 830  
 Lys Ser Arg Val Leu Leu Gln Val His Asp Glu Leu Val Val Glu Val  
 835 840 845  
 Ala Ala Gly Glu Leu Glu Gln Val Arg Glu Ile Leu Glu Arg Glu Met  
 850 855 860  
 Asp Asn Ala Ile Lys Leu Ser Val Pro Leu Glu Val Ser Ala Gly Asp  
 865 870 875 880  
 Gly Val Asn Trp Asp Ala Ala Ala His  
 885

&lt;210&gt; 163

&lt;211&gt; 2580

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)...(2557)

&lt;223&gt; FRXA00060

&lt;400&gt; 163

tgaaagcaat attagaccat caatgattag gaatggaaat taggggtctg gtttgggtga 60

atgtgtcgct aatttttcca ctgcctaca ctcgggagcg gtg act gag aag act 115  
 Val Thr Glu Lys Thr 5  
 1

gac cag acc tta atg ctt atc gac ggc cac tcg atg gct ttc cgc gca 163  
 Asp Gln Thr Leu Met Leu Ile Asp Gly His Ser Met Ala Phe Arg Ala 20  
 10 15

ttc ttt gct ttg ccg gct gag aat ttc tcc acg tcg ggc ggg cag gcc 211  
 Phe Phe Ala Leu Pro Ala Glu Asn Phe Ser Thr Ser Gly Gly Gln Ala 35  
 25 30

acc aat gct gtc tat ggc ttt ctc tcg atg ctg tcc acg ttg ttg aag 259  
 Thr Asn Ala Val Tyr Gly Phe Leu Ser Met Leu Ser Thr Leu Leu Lys 50  
 40 45

gat gag cag cct act cat gtg gcg gtg gct ttc gat gtg ggg cgt aag 307  
 Asp Glu Gln Pro Thr His Val Ala Val Ala Phe Asp Val Gly Arg Lys 65  
 55 60

acg ttc cgt acc gat atg ttc ccg gcg tat aag gcg cag cgt gaa gca 355  
 Thr Phe Arg Thr Asp Met Phe Pro Ala Tyr Lys Ala Gln Arg Glu Ala 85  
 70 75 80

acg cca cct gag ttt aag ggc cag gtg gaa atc ctc aag gag gtg ttg 403  
 Thr Pro Pro Glu Phe Lys Gly Gln Val Glu Ile Leu Lys Glu Val Leu 100  
 90 95

tcc act ttg gga att acg act att gag aaa atc gat ttt gag gct gat 451  
 Ser Thr Leu Gly Ile Thr Thr Ile Glu Lys Ile Asp Phe Glu Ala Asp 115  
 105 110

gat gtg atc gcc acg ttg tct gtg gcg gcg aaa cct tta ggc ttt aag 499  
 Asp Val Ile Ala Thr Leu Ser Val Ala Ala Lys Pro Leu Gly Phe Lys 130  
 120 125

acg ctg att gtt acg ggt gac cgt gat tcc ttc cag ttg gtc aat gac 547  
 Thr Leu Ile Val Thr Gly Asp Arg Asp Ser Phe Gln Leu Val Asn Asp 145  
 135 140

acc acc acg gtg ttg tat ccg atg aag ggc gtg tct gtg ctg cac cgt 595  
 Thr Thr Thr Val Leu Tyr Pro Met Lys Gly Val Ser Val Leu His Arg 165  
 150 155 160

ttc acg ccg gaa gca gtg gag gag aag tat gga ctg aca ccg agg cag 643  
 Phe Thr Pro Glu Ala Val Glu Glu Lys Tyr Gly Leu Thr Pro Arg Gln 180  
 170 175

tat ccg gag ttt gca gcg ctg cgt ggt gat cct tcc gat aac ttg cct 691  
 Tyr Pro Glu Phe Ala Ala Leu Arg Gly Asp Pro Ser Asp Asn Leu Pro

185	190	195	
aat att cct ggc gtg ggc gag aag act gct acc aag tgg att gcc cag Asn Ile Pro Gly Val Gly Glu Lys Thr Ala Thr Lys Trp Ile Ala Gln 200 205 210			739
tat gaa act ttg gat aat ttg ctt gat cac gct gat gag atc aag ggc Tyr Glu Thr Leu Asp Asn Leu Leu Asp His Ala Asp Glu Ile Lys Gly 215 220 225			787
aag gtt ggc gcc agc ctg cgt gag cgc att gag cag gtc cgg atg aac Lys Val Gly Ala Ser Leu Arg Glu Arg Ile Glu Gln Val Arg Met Asn 230 235 240 245			835
cgc aag ctc acg gag atg gtg aag gat ctg gag ctg cgc ctt ggt cgc Arg Lys Leu Thr Glu Met Val Lys Asp Leu Glu Leu Pro Leu Gly Pro 250 255 260			883
gac gat ttt gag atg aag cct gtg cag gtt gcg gag gtt gcg gcg aag Asp Asp Phe Glu Met Lys Pro Val Gln Val Ala Glu Val Ala Ala Lys 265 270 275			931
ttt gac gat ctg gag ttt ggt acc aat ttg cgt gag cgg gtg ctg gcg Phe Asp Asp Leu Glu Phe Gly Thr Asn Leu Arg Glu Arg Val Leu Ala 280 285 290			979
gtg gtg aag gcc gag ggt tcc gct gcc ccc gtg gag gaa gtg gaa gcg Val Val Lys Ala Glu Gly Ser Ala Ala Pro Val Glu Glu Val Glu Ala 295 300 305			1027
gaa cag gtt gtc gtc gat acg caa tct ttg gcg caa tgg ctg cct gct Glu Gln Val Val Val Asp Thr Gln Ser Leu Ala Gln Trp Leu Pro Ala 310 315 320 325			1075
agg gct ggc cag gcg ctt gct tta gcg ctg gct gga gtg gct aaa cct Arg Ala Gly Gln Ala Leu Ala Leu Ala Leu Ala Gly Val Ala Lys Pro 330 335 340			1123
gct gct ggc gac acg tat gcg cta gcg att gcg gat acc aag gcg cat Ala Ala Gly Asp Thr Tyr Ala Leu Ala Ile Ala Asp Thr Lys Arg His 345 350 355			1171
gcg gtg ttg gtt gat gtg gct gat att tca gcg gag gat gaa aag gcg Ala Val Leu Val Asp Val Ala Asp Ile Ser Ala Glu Asp Glu Lys Ala 360 365 370			1219
ctg gcc acg tgg ttg gcg tgc gaa gat cca aag atg ctg cac gcc gct Leu Ala Thr Trp Leu Ala Ser Glu Asp Pro Lys Met Leu His Gly Ala 375 380 385			1267
aag gcc gcc tat cat atg ctc gct ggg gcg ggt ttt gag ctg cac gcc Lys Ala Ala Tyr His Met Leu Ala Gly Arg Gly Phe Glu Leu His Gly 390 395 400 405			1315
gtg gtg cat gac acg gcg atc gcg gca tac ttg ctg cgt ccg gcc caa Val Val His Asp Thr Ala Ile Ala Ala Tyr Leu Leu Arg Pro Gly Gln 410 415 420			1363
gcg acc tat gag ctt gcc gac gtc tac cag cgg cat ctt caa cga cag Arg Thr Tyr Glu Leu Ala Asp Val Tyr Gln Arg His Leu Gln Arg Gln 425 430 435			1411



tgt tct aca aac gac aat ggc ggc cag ctc acg ctg ctc gac gca gct Leu Ser Thr Asn Asp Asn Gly Gly Gln Leu Thr Leu Leu Asp Ala Ala	1459
gat gac caa tcg ctt gtt gat gat gtc att gca atc ctt gag ctg tct Asp Asp Gln Ser Leu Val Asp Asp Val Ile Ala Ile Leu Leu Glu Leu Ser	1507
gaa gaa ttg acc aat cag ctt cag gag att caa gct ttt gag ctt tac Glu Glu Leu Thr Lys Gln Leu Gln Glu Ile Gln Ala Phe Glu Leu Tyr	1555
cat gac ctg gaa att ccg ctg tcg gga att ctg gcg cgc atg gag gcc His Asp Leu Glu Ile Pro Leu Ser Gly Ile Leu Ala Arg Met Glu Ala	1603
atc ggt atc gct gtt gat gtt gcc act ttg gaa gag cag ctg aag act Ile Gly Ile Ala Val Asp Val Ala Thr Leu Glu Glu Gln Leu Lys Thr	1651
ttc att ggt cag gtt gct cag gaa gag gaa gca gct cgc gag ctc gct Phe Ile Gly Gln Val Ala Gln Glu Glu Glu Ala Ala Arg Glu Leu Ala	1699
gag gat cca acc ctg aat ctc tcg agc ccg aag cag ctg caa gtg gtg Glu Asp Pro Thr Leu Asn Leu Ser Ser Pro Lys Gln Leu Gln Val Val	1747
ctt ttt gag acg ttc gga atg ccg aaa acc aag aaa acc aag acc gcc Leu Phe Glu Thr Phe Gly Met Pro Lys Thr Lys Lys Thr Lys Thr Gly	1795
tac tct acg gct gcc gcg gaa att gaa gcc cta gcg atc aag aat ccg Tyr Ser Thr Ala Ala Ala Glu Ile Glu Ala Leu Ala Ile Lys Asn Pro	1843
cas cca ttc cta gat cac ctg ttg gca cac cgt cag tac caa aag atg His Pro Phe Leu Asp His Leu Leu Ala His Arg Gln Tyr Gln Lys Met	1891
aag acc act ctg gaa ggt ctc atc cgt gag gtg gct cct gat ggc cgt Lys Thr Thr Leu Glu Gly Leu Ile Arg Glu Val Ala Pro Asp Gly Arg	1939
att cac acc acc ttc aac cag acg gtg gcg tct acg gga cgt ttg tca Ile His Thr Thr Phe Asn Gln Thr Val Ala Ser Thr Gly Arg Leu Ser	1987
tcc act gat ccc aac ctg caa aac att cct gtg cgc act gag gct gcc Ser Thr Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Glu Ala Gly	2035
cga aag att cgt tcg gga ttc gtc gta gcc gag ggg tat gaa acc ttg Arg Lys Ile Arg Ser Gly Phe Val Val Gly Glu Gly Tyr Glu Thr Leu	2083
ctg act gcc gac tat tcg cag att gaa atg cgc gtg atg gct cac ctt Leu Thr Ala Asp Tyr Ser Gln Ile Glu Met Arg Val Met Ala His Leu	2131

tcc cag gac cca ggc ttg att gag gcg tac cgc gaa ggc gaa gac ctg 2179  
 Ser Gln Asp Pro Gly Leu Ile Glu Ala Tyr Arg Glu Gly Glu Asp Leu  
 680 685 690

cac aat tac gtg ggt tcc aag gtg ttt aat gtg ccc atc gat ggc gtg 2227  
 His Asn Tyr Val Gly Ser Lys Val Phe Asn Val Pro Ile Asp Gly Val  
 695 700 705

acc cct gag ctg cgt cgc cag gtc aag gcc atg tct tac ggt ctg gtg 2275  
 Thr Pro Glu Leu Arg Arg Gln Val Lys Ala Met Ser Tyr Gly Leu Val  
 710 715 720 725

tac ggc ttg tcc gcg ttt ggt ttg tct cag cag ctg agc att cct gct 2323  
 Tyr Gly Leu Ser Ala Phe Gly Leu Ser Gln Gln Leu Ser Ile Pro Ala  
 730 735 740

ggc gaa gcg aag cag atc atg gag tcc tac ttc gag cgc ttc ggc gga 2371  
 Gly Glu Ala Lys Gln Ile Met Glu Ser Tyr Phe Glu Arg Phe Gly Gly  
 745 750 755

gta cag cgc tac ctc cgg gag atc gtg gag gag gct cga aaa gct ggc 2419  
 Val Gln Arg Tyr Leu Arg Glu Ile Val Glu Glu Ala Arg Lys Ala Gly  
 760 765 770

tac acg gaa acg ctc ttt ggg cgt cgt cgc tac ctg ccg gaa ctg acc 2467  
 Tyr Thr Glu Thr Leu Phe Gly Arg Arg Tyr Phe Pro Glu Leu Thr  
 775 780 785

tcg gat aac cgt gtc gct cgt gaa aac gct gaa cgt gcc gca ctg aac 2515  
 Ser Asp Asn Arg Val Ala Arg Glu Asn Ala Glu Arg Ala Ala Leu Asn  
 790 795 800 805

gcc ccg att agg gaa ctg ccg cag aca tca tca agg tgg cca 2557  
 Ala Pro Ile Arg Glu Leu Pro Gln Thr Ser Ser Arg Trp Pro  
 810 815

tgatccgggt ggacgcttca ctc 2580

&lt;210&gt; 164

&lt;211&gt; 819

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 164

Val Thr Glu Lys Thr Asp Gln Thr Leu Met Leu Ile Asp Gly His Ser  
1 5 10 15

Met Ala Phe Arg Ala Phe Phe Ala Leu Pro Ala Glu Asn Phe Ser Thr  
20 25 30

Ser Gly Gly Gln Ala Thr Asn Ala Val Tyr Gly Phe Leu Ser Met Leu  
35 40 45

Ser Thr Leu Leu Lys Asp Glu Gln Pro Thr His Val Ala Val Ala Phe  
50 55 60

Asp Val Gly Arg Lys Thr Phe Arg Thr Asp Met Phe Pro Ala Tyr Lys  
65 70 75 80

Ala Gln Arg Glu Ala Thr Pro Pro Glu Phe Lys Gly Gln Val Glu Ile



Leu Arg Pro Gly Gln Arg Thr Tyr Glu Leu Ala Asp Val Tyr Gln Arg  
 420 425 430  
 His Leu Gln Arg Gln Leu Ser Thr Asn Asp Asn Gly Gly Gln Leu Thr  
 435 440 445  
 Leu Leu Asp Ala Ala Asp Asp Gln Ser Leu Val Asp Asp Val Ile Ala  
 450 455 460  
 Ile Leu Glu Leu Ser Glu Glu Leu Thr Lys Gln Leu Gln Glu Ile Gln  
 465 470 475 480  
 Ala Phe Glu Leu Tyr His Asp Leu Glu Ile Pro Leu Ser Gly Ile Leu  
 485 490 495  
 Ala Arg Met Glu Ala Ile Gly Ile Ala Val Asp Val Ala Thr Leu Glu  
 500 505 510  
 Glu Gln Leu Lys Thr Phe Ile Gly Gln Val Ala Gln Glu Glu Glu Ala  
 515 520 525  
 Ala Arg Glu Leu Ala Glu Asp Pro Thr Leu Asn Leu Ser Ser Pro Lys  
 530 535 540  
 Gln Leu Gln Val Val Leu Phe Glu Thr Phe Gly Met Pro Lys Thr Lys  
 545 550 555 560  
 Lys Thr Lys Thr Gly Tyr Ser Thr Ala Ala Ala Glu Ile Glu Ala Leu  
 565 570 575  
 Ala Ile Lys Asn Pro His Pro Phe Leu Asp His Leu Leu Ala His Arg  
 580 585 590  
 Gln Tyr Gln Lys Met Lys Thr Thr Leu Glu Gly Leu Ile Arg Glu Val  
 595 600 605  
 Ala Pro Asp Gly Arg Ile His Thr Thr Phe Asn Gln Thr Val Ala Ser  
 610 615 620  
 Thr Gly Arg Leu Ser Ser Thr Asp Pro Asn Leu Gln Asn Ile Pro Val  
 625 630 635 640  
 Arg Thr Glu Ala Gly Arg Lys Ile Arg Ser Gly Phe Val Val Gly Glu  
 645 650 655  
 Gly Tyr Glu Thr Leu Leu Thr Ala Asp Tyr Ser Gln Ile Glu Met Arg  
 660 665 670  
 Val Met Ala His Leu Ser Gln Asp Pro Gly Leu Ile Glu Ala Tyr Arg  
 675 680 685  
 Glu Gly Glu Asp Leu His Asn Tyr Val Gly Ser Lys Val Phe Asn Val  
 690 695 700  
 Pro Ile Asp Gly Val Thr Pro Glu Leu Arg Arg Gln Val Lys Ala Met  
 705 710 715 720  
 Ser Tyr Gly Leu Val Tyr Gly Leu Ser Ala Phe Gly Leu Ser Gln Gln  
 725 730 735

Leu Ser Ile Pro Ala Gly Glu Ala Lys Gln Ile Met Glu Ser Tyr Phe  
 740 745 750  
 Glu Arg Phe Gly Gly Val Gln Arg Tyr Leu Arg Glu Ile Val Glu Glu  
 755 760 765  
 Ala Arg Lys Ala Gly Tyr Thr Glu Thr Leu Phe Gly Arg Arg Arg Tyr  
 770 775 780  
 Leu Pro Glu Leu Thr Ser Asp Asn Arg Val Ala Arg Glu Asn Ala Glu  
 785 790 795 800  
 Arg Ala Ala Leu Asn Ala Pro Ile Arg Glu Leu Pro Gln Thr Ser Ser  
 805 810 815  
 Arg Trp Pro

<210> 165  
 <211> 333  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(310)  
 <223> FRXA00061

<400> 165  
 cggaactgac ctccgataaac cgtgtcgtc gtgaaaacgc tgaacgtgcc gcaactgaacg 60  
 ccccgattag ggaactgccg cagacatcat caaggtggcc atg atc cgg gtg gac 115  
 Met Ile Arg Val Asp  
 1 5  
 cgt tca ctc aag gaa gct gcc gtg aaa tct cgc gtg ctg ctt cag gtg 163  
 Arg Ser Leu Lys Glu Ala Ala Val Lys Ser Arg Val Leu Leu Gln Val  
 10 15 20  
 cat gat gaa ttg gtc gtg gaa gta gcg gcc ggt gag ttg gaa caa gtc 211  
 His Asp Glu Leu Val Val Glu Val Ala Ala Gly Glu Leu Glu Gln Val  
 25 30 35  
 cgt gag att ctg gaa cgc gaa atg gat aac gcc atc aag ctg tcc gtt 259  
 Arg Glu Ile Leu Glu Arg Glu Met Asp Asn Ala Ile Lys Leu Ser Val  
 40 45 50  
 cct ttg gaa gtt tca gct ggt gat ggc gtt aac tgg gat gct gca gcg 307  
 Pro Leu Glu Val Ser Ala Gly Asp Gly Val Asn Trp Asp Ala Ala Ala  
 55 60 65  
 cac taagaggtaa ctgccttttc gtc 333  
 His  
 70

<210> 166  
 <211> 70  
 <212> PRT  
 <213> Corynebacterium glutamicum

&lt;400&gt; 166

Met Ile Arg Val Asp Arg Ser Leu Lys Glu Ala Ala Val Lys Ser Arg  
 1 5 10 15

Val Leu Leu Gln Val His Asp Glu Leu Val Val Glu Val Ala Ala Gly  
 20 25 30

Glu Leu Glu Gln Val Arg Glu Ile Leu Glu Arg Glu Met Asp Asn Ala  
 35 40 45

Ile Lys Leu Ser Val Pro Leu Glu Val Ser Ala Gly Asp Gly Val Asn  
 50 55 60

Trp Asp Ala Ala Ala His  
 65 70

&lt;210&gt; 167

&lt;211&gt; 3705

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(3682)

&lt;223&gt; RXA02657

&lt;400&gt; 167

tatgcgagta gcgcgaaaat catagctgtt acctatatacc taggttagaa aagccgagat 60

caatgcggtta atgaaatagg agtttcacgg gtgtaaggag atg gct aga ctg tcc 115  
 Met Ala Arg Leu Ser  
 1 5

cac atg gcc aag caa tcc tca ttt gta cat ctt cac aac cac acc gag 163  
 His Met Ala Lys Gln Ser Ser Phe Val His Leu His Asn His Thr Glu  
 10 15 20

ttt tcc atg ctt gat gga atg gcc aag atc gat atg ttg gcc gat gag 211  
 Phe Ser Met Leu Asp Gly Met Ala Lys Ile Asp Met Leu Ala Asp Glu  
 25 30 35

gtt aaa gcc cag gga atg cct gcg gtc gga atc acc gac cac gcc aat 259  
 Val Lys Ala Gln Gly Met Pro Ala Val Gly Ile Thr Asp His Gly Asn  
 40 45 50

atg tat ggc tcc aac ccc ttt tat cgc aag atg aca gag atg ggc att 307  
 Met Tyr Gly Ser Asn Pro Phe Tyr Arg Lys Met Thr Glu Met Gly Ile  
 55 60 65

aag ccc atc att ggc att gaa acg tat atg gca cct gag tct cgt ttt 355  
 Lys Pro Ile Ile Gly Ile Glu Thr Tyr Met Ala Pro Glu Ser Arg Phe  
 70 75 80 85

aag aaa gag cgt gtg cgt tgg ggc gaa cca cac caa aaa tca gat gat 403  
 Lys Lys Glu Arg Val Arg Trp Gly Glu Pro His Gln Lys Ser Asp Asp  
 90 95 100

gtt tct ggt tcc ggt gcg tat ttg cac cag acg atg ctt gca gaa aac 451  
 Val Ser Gly Ser Gly Ala Tyr Leu His Gln Thr Met Leu Ala Glu Asn

105	110	115	
acc aca ggt tta aga aac ctc ttt tat cta tct tgc atg gca tgc tac Thr Thr Gly Leu Arg Asn Leu Phe Tyr Leu Ser Ser Met Ala Ser Tyr 120 125 130			499
gaa ggc cag cta ggc aag tgg ccc cgc atg gac gcc gat atc atc gct Glu Gly Gln Leu Gly Lys Trp Pro Arg Met Asp Ala Asp Ile Ile Ala 135 140 145			547
gag cac gcc gaa ggc atc atc gcc acc acg ggt tgc cct tcc ggc gat Glu His Ala Glu Gly Ile Ile Ala Thr Thr Gly Cys Pro Ser Gly Asp 150 155 160 165			595
gtg caa aca cgc ctg cgc ttg ggc cag ttc gac gaa gcc ctt gaa gca Val Gln Thr Arg Leu Arg Leu Gly Gln Phe Asp Glu Ala Leu Glu Ala 170 175 180			643
gcc gcc atg tgg cag gac atc tat ggt cgc gac aac tac ttc ctc gag Ala Ala Met Trp Gln Asp Ile Tyr Gly Arg Asp Asn Tyr Phe Leu Glu 185 190 195			691
ttg atg gac cac ggg ctc gac att gaa acc cgt gtg cgc agt gag ctg Leu Met Asp His Gly Leu Asp Ile Glu Thr Arg Val Arg Ser Glu Leu 200 205 210			739
ctc gaa atc gga cgc aag ctc aat ttg cca ccc ctg gtc acc aac gac Leu Glu Ile Gly Arg Lys Leu Asn Leu Pro Pro Leu Val Thr Asn Asp 215 220 225			787
tgc cac tat gtg ctg gaa tct cag gcg caa gcc cac gag gca atg ctc Cys His Tyr Val Leu Glu Ser Gln Ala Gln Ala His Glu Ala Met Leu 230 235 240 245			835
tgc gtg caa aca ggc aag acg ctt cat gat gaa gac cga ttc aaa ttc Cys Val Gln Thr Gly Lys Thr Leu His Asp Glu Asp Arg Phe Lys Phe 250 255 260			883
ggc gga acc ggc tat tac gtt aaa tct gca gaa caa atg cgt gca ctc Gly Gly Thr Gly Tyr Tyr Val Lys Ser Ala Glu Gln Met Arg Ala Leu 265 270 275			931
tgg gac gac atg gtt cca gat ggc tgc gac aac acc ctg tgg atc gct Trp Asp Asp Met Val Pro Asp Gly Cys Asp Asn Thr Leu Trp Ile Ala 280 285 290			979
gaa cgt gtg cag tcc tat gac gaa atc tgg gaa gaa cac tca cac gac Glu Arg Val Gln Ser Tyr Asp Glu Ile Trp Glu Glu His Ser His Asp 295 300 305			1027
cgc atg cct atc gct gat gtt cca gaa ggc tac acc cca acc act tgg Arg Met Pro Ile Ala Asp Val Pro Glu Gly Tyr Thr Pro Thr Thr 310 315 320 325			1075
ttg cac cat gaa gtg atg gct ggc ttg gag gat cgt ttc tct gga cag Leu His His Glu Val Met Ala Gly Leu Glu Asp Arg Phe Ser Gly Gln 330 335 340			1123
caa gtt cct gag gat tat att gag cgc gcg gag tat gag atc tcc gtt Gln Val Pro Glu Asp Tyr Ile Glu Arg Ala Glu Tyr Glu Ile Ser Val 345 350 355			1171

att gat atg aag ggc tac cct tcc tac ttc ctc atc gtt gct gaa att 1219  
 Ile Asp Met Lys Gly Tyr Pro Ser Tyr Phe Leu Ile Val Ala Glu Ile  
 360 365 370

atc aag cac gct cgt tcc att ggc atc cgt gta gga cct ggc cgt ggt 1267  
 Ile Lys His Ala Arg Ser Ile Gly Ile Arg Val Gly Pro Gly Arg Gly  
 375 380 385

tcg gct gca ggt gca ttg gtt gcc tac gcg ttg acc atc acc aac att 1315  
 Ser Ala Ala Gly Ala Leu Val Ala Tyr Ala Leu Thr Ile Thr Asn Ile  
 390 395 400 405

gac ccc atg gaa cac gga ttg ctg ttc gag aga ttc ctc aac cca gaa 1363  
 Asp Pro Met Glu His Gly Leu Leu Phe Glu Arg Phe Leu Asn Pro Glu  
 410 415 420

cga cca tcc gca ccc gat atc gat att gac ttc gat gat cgc cgc cgc 1411  
 Arg Pro Ser Ala Pro Asp Ile Asp Ile Asp Phe Asp Asp Arg Arg Arg  
 425 430 435

ggc gaa atg atc cgt tac gca gct gac cgt tgg ggc gag gac aag att 1459  
 Gly Glu Met Ile Arg Tyr Ala Ala Asp Arg Trp Gly Glu Asp Lys Ile  
 440 445 450

gct cag gtg atc acc ttc ggt acg gtg aaa aca aag cag gca ctg aaa 1507  
 Ala Gln Val Ile Thr Phe Gly Thr Val Lys Thr Lys Gln Ala Leu Lys  
 455 460 465

gac tcc gcc cgt gtg caa atg ggg cag cca ggc tat caa atc gct gac 1555  
 Asp Ser Ala Arg Val Gln Met Gly Gln Pro Gly Tyr Gln Ile Ala Asp  
 470 475 480 485

cgc gtg atc aag gag ctt cca cct gcc att atg gcg aag gat att ccg 1603  
 Arg Val Ile Lys Glu Leu Pro Pro Ala Ile Met Ala Lys Asp Ile Pro  
 490 495 500

ttg tcc ggt atc acc gat ccg gat cac cct cgt ttt aat gaa gca ggt 1651  
 Leu Ser Gly Ile Thr Asp Pro Asp His Pro Arg Phe Asn Glu Ala Gly  
 505 510 515

gcg gtg cgc cag ctg atc gaa acc gac cct gat gtg aag cgc att tac 1699  
 Ala Val Arg Gln Leu Ile Glu Thr Asp Pro Asp Val Lys Arg Ile Tyr  
 520 525 530

gac acc gct cgt ggt ttg gaa ggc gtg gtg cgc caa tct ggc gtg cac 1747  
 Asp Thr Ala Arg Gly Leu Glu Gly Val Val Arg Gln Ser Gly Val His  
 535 540 545

gcg tgt gcc gtg att atg tct tct gta ccg ctg ctg gac tgc att ccg 1795  
 Ala Cys Ala Val Ile Met Ser Ser Val Pro Leu Leu Asp Cys Ile Pro  
 550 555 560 565

atg tgg aag cgg cca gcc gac ggc gca ctg att aca ggc tgg gat tac 1843  
 Met Trp Lys Arg Pro Ala Asp Gly Ala Leu Ile Thr Gly Trp Asp Tyr  
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cca gca tgt gag gcc att ggc ctg ttg aag atg gac ttc ctg gga ctt 1891  
 Pro Ala Cys Glu Ala Ile Gly Leu Leu Lys Met Asp Phe Leu Gly Leu  
 585 590 595



cga aac ctt acc gtt att ggc gat gcg att gaa aac att aag gcc aac 1939  
 Arg Asn Leu Thr Val Ile Gly Asp Ala Ile Glu Asn Ile Lys Ala Asn  
 600 605 610

cgc gat ggg gaa gtg ctt gat cta gaa aac cta gcg atc gag gat gaa 1987  
 Arg Asp Gly Glu Val Leu Asp Leu Glu Asn Leu Ala Ile Glu Asp Glu  
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gaa acc tac aag ctg cta ggc cgt gga gaa acc ctt ggt gtg ttc cag 2035  
 Glu Thr Tyr Lys Leu Leu Gly Arg Gly Glu Thr Leu Gly Val Phe Gln  
 630 635 640 645

ctt gat ggt ggt ggc atg cag gag ctg ctg aag cgt atg cag cca acc 2083  
 Leu Asp Gly Gly Gly Met Gln Glu Leu Leu Lys Arg Met Gln Pro Thr  
 650 655

ggc ttc aat gac atc gtc gca gcg ctt gcg ctg tat cgc cca gcc ccc 2131  
 Gly Phe Asn Asp Ile Val Ala Ala Leu Ala Leu Tyr Arg Pro Gly Pro  
 665 670 675

atg ggt gtg aac gcg cac tgg gat tac gcc gac cgt aaa aac gga cgc 2179  
 Met Gly Val Asn Ala His Trp Asp Tyr Ala Asp Arg Lys Asn Gly Arg  
 680 685 690

aag ccc att act cca att cac cca gag ttg gag gaa gct ctg gaa gaa 2227  
 Lys Pro Ile Thr Pro Ile His Pro Glu Leu Glu Glu Ala Leu Glu Glu  
 695 700 705

atc ctt ggt gaa acc tat ggt ctg att gtg tac cag gag cag atc atg 2275  
 Ile Leu Gly Glu Thr Tyr Gly Leu Ile Val Tyr Gln Glu Gln Ile Met  
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agg atc tcc cag aag gtc gca aac tac acc gct ggt caa gca gat ggt 2323  
 Arg Ile Ser Gln Lys Val Ala Asn Tyr Thr Ala Gly Gln Ala Asp Gly  
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 Phe Arg Lys Ala Met Gly Lys Lys Lys Pro Glu Val Leu Glu Lys Glu  
 745 750 755

ttc gca aac ttc gaa ggt gga atg aag gcg aac gcc tat tca gat gcc 2419  
 Phe Ala Asn Phe Glu Gly Gly Met Lys Ala Asn Gly Tyr Ser Asp Ala  
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gcg att aag act ttg tgg gat acc att ctg ccg ttc gcc gcc tac gcg 2467  
 Ala Ile Lys Thr Leu Trp Asp Thr Ile Leu Pro Phe Ala Gly Tyr Ala  
 775 780 785

ttc aac aag tct cac gcc gca ggt tat gga ctt gta tcc ttc tgg act 2515  
 Phe Asn Lys Ser His Ala Ala Gly Tyr Gly Leu Val Ser Phe Trp Thr  
 790 795 800 805

gcc tat ttg aag gcg cac tac gcg ccg gaa tac atg gca gca ctg ctg 2563  
 Ala Tyr Leu Lys Ala His Tyr Ala Pro Glu Tyr Met Ala Ala Leu Leu  
 810 815 820

act tct gtg ggt gat aac aag gac aaa tcg gcg atc tac ctt tct gat 2611  
 Thr Ser Val Gly Asp Asn Lys Asp Lys Ser Ala Ile Tyr Leu Ser Asp  
 825 830 835

tgc cga cac ctt gga att cga gtg ctt tcg ccg gat att aac gag tcc 2659

002250-002250  
 002250-002250

Cys Arg His Leu Gly Ile Arg Val Leu Ser Pro Asp Ile Asn Glu Ser	
840	845 850
tcg ttg aac ttc ctt cct gtt ggc acc gat att cgc tat ggc ctg gga	2707
Ser Leu Asn Phe Leu Pro Val Gly Thr Asp Ile Arg Tyr Gly Leu Gly	
855	860 865
gcc att aga aac gtg ggt gct gaa gtt gtg gat tcc att ttg gat acc	2755
Ala Ile Arg Asn Val Gly Ala Glu Val Val Asp Ser Ile Leu Asp Thr	
870	875 880 885
cgc aag gaa aag ggc cta ttt aag gac ttc tca gac tac ttg gac aag	2803
Arg Lys Glu Lys Gly Leu Phe Lys Asp Phe Ser Asp Tyr Leu Asp Lys	
	890 895 900
atc gat acc ctg ccg tgt aac aag cgc atc acc gag tct ttg atc aag	2851
Ile Asp Thr Leu Pro Cys Asn Lys Arg Ile Thr Glu Ser Leu Ile Lys	
	905 910 915
ggg ggc gct ttt gac tcc ctt gga cac gca cga aaa ggc ctc atg ctg	2899
Gly Gly Ala Phe Asp Ser Leu Gly His Ala Arg Lys Gly Leu Met Leu	
	920 925 930
gtc ttc gaa gat gcc gtt gat tcc gtc atc gct acc aaa aaa gct gct	2947
Val Phe Glu Asp Ala Val Asp Ser Val Ile Ala Thr Lys Lys Ala Ala	
	935 940 945
gac aag gga caa ttt gat ctc ttt gca gct ttc gac tcg gat aac aac	2995
Asp Lys Gly Gln Phe Asp Leu Phe Ala Ala Phe Asp Ser Asp Asn Asn	
	950 955 960 965
gac gat gtg gca agt ttc ttc cag atc acc gtt cct gat gac gaa tgg	3043
Asp Asp Val Ala Ser Phe Phe Gln Ile Thr Val Pro Asp Asp Gly Trp	
	970 975 980
gac cgt aag cat gag ctc gca ctc gag cga gaa atg ctg ggt ctg tat	3091
Asp Arg Lys His Glu Leu Ala Leu Glu Arg Glu Met Leu Gly Leu Tyr	
	985 990 995
gtt tct gga cac cca ctc gat ggc tat gaa gat gcc att gct gcc cag	3139
Val Ser Gly His Pro Leu Asp Gly Tyr Glu Asp Ala Ile Ala Ala Gln	
	1000 1005 1010
gtt gat aca gca ctg acc att gtt gcc ggt gaa ctc aag cac gcc	3187
Val Asp Thr Ala Leu Thr Thr Ile Val Ala Gly Glu Leu Lys His Gly	
	1015 1020 1025
gca gaa gtg acc gtg ggt ggc att atc tct ggt gtg gat cga cgg ttc	3235
Ala Glu Val Thr Val Gly Gly Ile Ile Ser Gly Val Asp Arg Arg Phe	
	1030 1035 1040 1045
tcc aag aag gac ggt tcc cct tgg gcg att gtc acc att gaa gat cac	3283
Ser Lys Lys Asp Gly Ser Pro Trp Ala Ile Val Thr Ile Glu Asp His	
	1050 1055 1060
aac ggc gcg tcc gtt gaa ttg ttg gtc ttc aac aag gtg tat tcc atc	3331
Asn Gly Ala Ser Val Glu Leu Leu Val Phe Asn Lys Val Tyr Ser Ile	
	1065 1070 1075
gtt gga tcc atg att gtg gaa gac aac atc atc ttg gcc aag gca cac	3379
Val Gly Ser Met Ile Val Glu Asp Asn Ile Ile Leu Ala Lys Ala His	

1080	1085	1090	
atc tcc att cga gat gat cgt atg agc ctt ttc tgt gat gat ctc cgc			3427
Ile Ser Ile Arg Asp Asp Arg Met Ser Leu Phe Cys Asp Asp Leu Arg			
1095	1100	1105	
ggt cca gag ctt ggg cca gga aac ggg caa gga ctt ccg ctt cgt ttg			3475
Val Pro Glu Leu Gly Pro Gly Asn Gly Gln Gly Leu Pro Leu Arg Leu			
1110	1115	1120	1125
tcc atg cgt act gat cag tgc acc atg tcc aac att gcc aag ctc aag			3523
Ser Met Arg Thr Asp Gln Cys Thr Met Ser Asn Ile Ala Lys Leu Lys			
1130	1135	1140	
cag gtg ctg gtg gac aac aag ggt gaa tct gat gtg tac ctc aat ttg			3571
Gln Val Leu Val Asp Asn Lys Gly Glu Ser Asp Val Tyr Leu Asn Leu			
1145	1150	1155	
atc gat ggg gat aac tcc acg gtc atg att ttg ggt gat cac tta aga			3619
Ile Asp Gly Asp Asn Ser Thr Val Met Ile Leu Gly Asp His Leu Arg			
1160	1165	1170	
gtc aac cga tcc gca agt ttg atg ggc gac ctc aag gca acg atg ggg			3667
Val Asn Arg Ser Ala Ser Leu Met Gly Asp Leu Lys Ala Thr Met Gly			
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Pro Gly Ile Leu Gly			
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Met Leu Ala Asp Glu Val Lys Ala Gln Gly Met Pro Ala Val Gly Ile			
35	40	45	
Thr Asp His Gly Asn Met Tyr Gly Ser Asn Pro Phe Tyr Arg Lys Met			
50	55	60	
Thr Glu Met Gly Ile Lys Pro Ile Ile Gly Ile Glu Thr Tyr Met Ala			
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Pro Glu Ser Arg Phe Lys Lys Glu Arg Val Arg Trp Gly Glu Pro His			
85	90	95	
Gln Lys Ser Asp Asp Val Ser Gly Ser Gly Ala Tyr Leu His Gln Thr			
100	105	110	
Met Leu Ala Glu Asn Thr Thr Gly Leu Arg Asn Leu Phe Tyr Leu Ser			
115	120	125	

Ser Met Ala Ser Tyr Glu Gly Gln Leu Gly Lys Trp Pro Arg Met Asp  
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 Ala Asp Ile Ile Ala Glu His Ala Glu Gly Ile Ile Ala Thr Thr Gly  
 145 150 155 160  
 Cys Pro Ser Gly Asp Val Gln Thr Arg Leu Arg Leu Gly Gln Phe Asp  
 165 170 175  
 Glu Ala Leu Glu Ala Ala Ala Met Trp Gln Asp Ile Tyr Gly Arg Asp  
 180 185 190  
 Asn Tyr Phe Leu Glu Leu Met Asp His Gly Leu Asp Ile Glu Thr Arg  
 195 200 205  
 Val Arg Ser Glu Leu Leu Glu Ile Gly Arg Lys Leu Asn Leu Pro Pro  
 210 215 220  
 Leu Val Thr Asn Asp Cys His Tyr Val Leu Glu Ser Gln Ala Gln Ala  
 225 230 235 240  
 His Glu Ala Met Leu Cys Val Gln Thr Gly Lys Thr Leu His Asp Glu  
 245 250 255  
 Asp Arg Phe Lys Phe Gly Gly Thr Gly Tyr Tyr Val Lys Ser Ala Glu  
 260 265 270  
 Gln Met Arg Ala Leu Trp Asp Asp Met Val Pro Asp Gly Cys Asp Asn  
 275 280 285  
 Thr Leu Trp Ile Ala Glu Arg Val Gln Ser Tyr Asp Glu Ile Trp Glu  
 290 295 300  
 Glu His Ser His Asp Arg Met Pro Ile Ala Asp Val Pro Glu Gly Tyr  
 305 310 315 320  
 Thr Pro Thr Thr Trp Leu His His Glu Val Met Ala Gly Leu Glu Asp  
 325 330 335  
 Arg Phe Ser Gly Gln Gln Val Pro Glu Asp Tyr Ile Glu Arg Ala Glu  
 340 345 350  
 Tyr Glu Ile Ser Val Ile Asp Met Lys Gly Tyr Pro Ser Tyr Phe Leu  
 355 360 365  
 Ile Val Ala Glu Ile Ile Lys His Ala Arg Ser Ile Gly Ile Arg Val  
 370 375 380  
 Gly Pro Gly Arg Gly Ser Ala Ala Gly Ala Leu Val Ala Tyr Ala Leu  
 385 390 395 400  
 Thr Ile Thr Asn Ile Asp Pro Met Glu His Gly Leu Leu Phe Glu Arg  
 405 410 415  
 Phe Leu Asn Pro Glu Arg Pro Ser Ala Pro Asp Ile Asp Ile Asp Phe  
 420 425 430  
 Asp Asp Arg Arg Arg Gly Glu Met Ile Arg Tyr Ala Ala Asp Arg Trp  
 435 440 445  
 Gly Glu Asp Lys Ile Ala Gln Val Ile Thr Phe Gly Thr Val Lys Thr

450	455	460
Lys Gln Ala Leu Lys Asp Ser Ala Arg Val Gln Met Gly Gln Pro Gly		
465	470	475 480
Tyr Gln Ile Ala Asp Arg Val Ile Lys Glu Leu Pro Pro Ala Ile Met		
	485	490 495
Ala Lys Asp Ile Pro Leu Ser Gly Ile Thr Asp Pro Asp His Pro Arg		
	500	505 510
Phe Asn Glu Ala Gly Ala Val Arg Gln Leu Ile Glu Thr Asp Pro Asp		
	515	520 525
Val Lys Arg Ile Tyr Asp Thr Ala Arg Gly Leu Glu Gly Val Val Arg		
	530	535 540
Gln Ser Gly Val His Ala Cys Ala Val Ile Met Ser Ser Val Pro Leu		
	545	550 555 560
Leu Asp Cys Ile Pro Met Trp Lys Arg Pro Ala Asp Gly Ala Leu Ile		
	565	570 575
Thr Gly Trp Asp Tyr Pro Ala Cys Glu Ala Ile Gly Leu Leu Lys Met		
	580	585 590
Asp Phe Leu Gly Leu Arg Asn Leu Thr Val Ile Gly Asp Ala Ile Glu		
	595	600 605
Asn Ile Lys Ala Asn Arg Asp Gly Glu Val Leu Asp Leu Glu Asn Leu		
	610	615 620
Ala Ile Glu Asp Glu Glu Thr Tyr Lys Leu Leu Gly Arg Gly Glu Thr		
	625	630 635 640
Leu Gly Val Phe Gln Leu Asp Gly Gly Gly Met Gln Glu Leu Leu Lys		
	645	650 655
Arg Met Gln Pro Thr Gly Phe Asn Asp Ile Val Ala Ala Leu Ala Leu		
	660	665 670
Tyr Arg Pro Gly Pro Met Gly Val Asn Ala His Trp Asp Tyr Ala Asp		
	675	680 685
Arg Lys Asn Gly Arg Lys Pro Ile Thr Pro Ile His Pro Glu Leu Glu		
	690	695 700
Glu Ala Leu Glu Glu Ile Leu Gly Glu Thr Tyr Gly Leu Ile Val Tyr		
	705	710 715 720
Gln Glu Gln Ile Met Arg Ile Ser Gln Lys Val Ala Asn Tyr Thr Ala		
	725	730 735
Gly Gln Ala Asp Gly Phe Arg Lys Ala Met Gly Lys Lys Lys Pro Glu		
	740	745 750
Val Leu Glu Lys Glu Phe Ala Asn Phe Glu Gly Gly Met Lys Ala Asn		
	755	760 765
Gly Tyr Ser Asp Ala Ala Ile Lys Thr Leu Trp Asp Thr Ile Leu Pro		
	770	775 780

Phe Ala Gly Tyr Ala Phe Asn Lys Ser His Ala Ala Gly Tyr Gly Leu  
 785 790 795 800  
 Val Ser Phe Trp Thr Ala Tyr Leu Lys Ala His Tyr Ala Pro Glu Tyr  
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 Met Ala Ala Leu Leu Thr Ser Val Gly Asp Asn Lys Asp Lys Ser Ala  
 820 825 830  
 Ile Tyr Leu Ser Asp Cys Arg His Leu Gly Ile Arg Val Leu Ser Pro  
 835 840 845  
 Asp Ile Asn Glu Ser Ser Leu Asn Phe Leu Pro Val Gly Thr Asp Ile  
 850 855 860  
 Arg Tyr Gly Leu Gly Ala Ile Arg Asn Val Gly Ala Glu Val Val Asp  
 865 870 875 880  
 Ser Ile Leu Asp Thr Arg Lys Glu Lys Gly Leu Phe Lys Asp Phe Ser  
 885 890 895  
 Asp Tyr Leu Asp Lys Ile Asp Thr Leu Pro Cys Asn Lys Arg Ile Thr  
 900 905 910  
 Glu Ser Leu Ile Lys Gly Gly Ala Phe Asp Ser Leu Gly His Ala Arg  
 915 920 925  
 Lys Gly Leu Met Leu Val Phe Glu Asp Ala Val Asp Ser Val Ile Ala  
 930 935 940  
 Thr Lys Lys Ala Ala Asp Lys Gly Gln Phe Asp Leu Phe Ala Ala Phe  
 945 950 955 960  
 Asp Ser Asp Asn Asn Asp Asp Val Ala Ser Phe Phe Gln Ile Thr Val  
 965 970 975  
 Pro Asp Asp Glu Trp Asp Arg Lys His Glu Leu Ala Leu Glu Arg Glu  
 980 985 990  
 Met Leu Gly Leu Tyr Val Ser Gly His Pro Leu Asp Gly Tyr Glu Asp  
 995 1000 1005  
 Ala Ile Ala Ala Gln Val Asp Thr Ala Leu Thr Thr Ile Val Ala Gly  
 1010 1015 1020  
 Glu Leu Lys His Gly Ala Glu Val Thr Val Gly Gly Ile Ile Ser Gly  
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 Val Asp Arg Arg Phe Ser Lys Lys Asp Gly Ser Pro Trp Ala Ile Val  
 1045 1050 1055  
 Thr Ile Glu Asp His Asn Gly Ala Ser Val Glu Leu Leu Val Phe Asn  
 1060 1065 1070  
 Lys Val Tyr Ser Ile Val Gly Ser Met Ile Val Glu Asp Asn Ile Ile  
 1075 1080 1085  
 Leu Ala Lys Ala His Ile Ser Ile Arg Asp Asp Arg Met Ser Leu Phe  
 1090 1095 1100

Cys Asp Asp Leu Arg Val Pro Glu Leu Gly Pro Gly Asn Gly Gln Gly  
 1105 1110 1115 1120

Leu Pro Leu Arg Leu Ser Met Arg Thr Asp Gln Cys Thr Met Ser Asn  
 1125 1130 1135

Ile Ala Lys Leu Lys Gln Val Leu Val Asp Asn Lys Gly Glu Ser Asp  
 1140 1145 1150

Val Tyr Leu Asn Leu Ile Asp Gly Asp Asn Ser Thr Val Met Ile Leu  
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Gly Asp His Leu Arg Val Asn Arg Ser Ala Ser Leu Met Gly Asp Leu  
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Lys Ala Thr Met Gly Pro Gly Ile Leu Gly  
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<223> RXA01238

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 Val Ile Ala Ala Tyr  
 1 5

ggc gca tcc atc tct ttg gat gat tcc acc ctc acc atc tct tat tcc 163  
 Gly Ala Ser Ile Ser Leu Asp Asp Ser Thr Leu Thr Ile Ser Tyr Ser  
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cct ctt ctt gct gct ctt tct aag tcc agc gca caa tcg gaa tcg gtt 211  
 Pro Leu Leu Ala Ala Leu Ser Lys Ser Ser Ala Gln Ser Glu Ser Val  
 25 30 35

gat ctg aca cag gtc tct gga gta tct gtg cag gat ccc act gct ttt 259  
 Asp Leu Thr Gln Val Ser Gly Val Ser Val Gln Asp Pro Thr Ala Phe  
 40 45 50

act cac ggc ttt tta aac ctg gag ggc gtg gat aaa tcc atc gcc ttt 307  
 Thr His Gly Phe Leu Asn Leu Glu Gly Val Asp Lys Ser Ile Ala Phe  
 55 60 65

gcc cca aat agt tcg gca gat tta gct gcg ctg gca gct gat att gat 355  
 Ala Pro Asn Ser Ser Ala Asp Leu Ala Ala Leu Ala Ala Asp Ile Asp  
 70 75 80 85

gct gtg ttg aag ggt gaa aag cca cag cac ctg ggt ggc gga gcc cca 403  
 Ala Val Leu Lys Gly Glu Lys Pro Gln His Leu Gly Gly Gly Ala Pro  
 90 95 100

gta gtg cct tca gct cca tct act gtt gct ggt ctg aat ttc gtg ggc 451

Val Val Pro Ser Ala Pro Ser Thr Val Ala Gly Leu Asn Phe Val Gly  
 105 110 115

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 Phe Asp Val Glu Thr Ala Asn Asp Asp Trp Gly Ser Ile Cys Gln Ile  
 120 125 130

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 Gly Leu Val Lys Tyr Val Asp Gly Val Glu Glu Ser Ser Glu Ser Trp  
 135 140 145

ttg tgt act cct cct gag agc ctg aat ttc ttc aat gag atc aac att 595  
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 150 155 160 165

ggg att cac gcc atc acc cca gag atg gtt gct gat cag cct cgt ttt 643  
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 170 175 180

gca gac ctt gtg ccc aag atg gtg gag ttc gtt ggg gat ttg ccg ttg 691  
 Ala Asp Leu Val Pro Lys Met Val Glu Phe Val Gly Asp Leu Pro Leu  
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gtt gct cac aat gcg cag ttt gat ttc acc gca ttg tgc cgc gcg tgt 739  
 Val Ala His Asn Ala Gln Phe Asp Phe Thr Ala Leu Ser Arg Ala Cys  
 200 205 210

gct gcc tca ggg atc gat gtc cca gag atg att tat ggc tgc tgc ttg 787  
 Ala Ala Ser Gly Ile Asp Val Pro Glu Met Ile Tyr Gly Cys Ser Leu  
 215 220 225

acg ttg gca cgc aat gag aag ctg cag gtg gaa aac cat aag ctt cca 835  
 Thr Leu Ala Arg Asn Glu Lys Leu Gln Val Glu Asn His Lys Leu Pro  
 230 235 240 245

acg gtg gct agt cat tta ggg ttt gag ctg aaa aac cac cac gat gct 883  
 Thr Val Ala Ser His Leu Gly Phe Glu Leu Lys Asn His His Asp Ala  
 250 255 260

gct gaa gat gct cgc gcg tgt gct gcg att acc att gcg ttg gca aag 931  
 Ala Glu Asp Ala Arg Ala Cys Ala Ala Ile Thr Ile Ala Leu Ala Lys  
 265 270 275

cgc cac agc ttt gag gcc agc ttt gtg gat ttc gtt cac agc cgt ggt 979  
 Arg His Ser Phe Glu Gly Ser Phe Val Asp Phe Val His Ser Arg Gly  
 280 285 290

ttc acc atg gga acc gtg gat aac gcc cgg gtg tat ccg gtg ctg aag 1027  
 Phe Thr Met Gly Thr Val Asp Asn Ala Arg Val Tyr Pro Val Leu Lys  
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gat cgt tct gga gct aac gtt gcg ttg cag cgt cga aac ttt ggt ttg 1075  
 Asp Arg Ser Gly Ala Asn Val Ala Leu Gln Arg Arg Asn Phe Gly Leu  
 310 315 320 325

gat gca gcc aag acc gaa gtc ccc gtg cag cca gct gtt gat cca gcg 1123  
 Asp Ala Gly Lys Thr Glu Val Pro Val Gln Pro Ala Val Asp Pro Ala  
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tgg gaa acc ccg aag gcg gag cca aaa aag caa tct ggc cgc cgt gca 1171  
 Trp Glu Thr Pro Lys Ala Glu Pro Lys Lys Gln Ser Gly Arg Arg Ala



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ggg gat ttc gag cca tat gaa aag ggt gcg ctg tgg cag cgg atc gct Gly Asp Phe Glu Pro Tyr Glu Lys Gly Ala Leu Trp Gln Arg Ile Ala 390 395 400 405			1315
gat caa ggt gcg ctg atc ggt aag aac gtg act aag aag acc acc att Asp Gln Gly Ala Leu Ile Gly Lys Asn Val Thr Lys Lys Thr Thr Ile 410 415 420			1363
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Gln Ser Glu Ser Val Asp Leu Thr Gln Val Ser Gly Val Ser Val Gln 35 40 45			
Asp Pro Thr Ala Phe Thr His Gly Phe Leu Asn Leu Glu Gly Val Asp 50 55 60			
Lys Ser Ile Ala Phe Ala Pro Asn Ser Ser Ala Asp Leu Ala Ala Leu 65 70 75 80			
Ala Ala Asp Ile Asp Ala Val Leu Lys Gly Glu Lys Pro Gln His Leu 85 90 95			
Gly Gly Gly Ala Pro Val Val Pro Ser Ala Pro Ser Thr Val Ala Gly 100 105 110			
Leu Asn Phe Val Gly Phe Asp Val Glu Thr Ala Asn Asp Asp Trp Gly			

115	120	125
Ser Ile Cys Gln Ile Gly 130	Leu Val Lys Tyr Val 135	Asp Gly Val Glu Glu 140
Ser Ser Glu Ser Trp 145	Leu Cys Thr Pro 150	Pro Glu Ser Leu Asn Phe Phe 155 160
Asn Glu Ile Asn 165	Ile Gly Ile His Gly 170	Thr Pro Glu Met Val Ala 175
Asp Gln Pro Arg 180	Phe Ala Asp Leu Val 185	Pro Lys Met Val Glu Phe Val 190
Gly Asp Leu Pro 195	Leu Val Ala His Asn 200	Ala Gln Phe Asp Phe Thr Ala 205
Leu Ser Arg Ala Cys 210	Ala Ser Gly Ile 215	Asp Val Pro Glu Met Ile 220
Tyr Gly Cys Ser 225	Leu Thr Leu Ala Arg 230	Asn Glu Lys Leu Gln Val Glu 235 240
Asn His Lys Leu 245	Pro Thr Val Ala Ser 250	His Leu Gly Phe Glu Leu Lys 255
Asn His His Asp 260	Ala Ala Glu Asp 265	Ala Arg Ala Cys Ala Ala Ile Thr 270
Ile Ala Leu Ala 275	Lys Arg His Ser 280	Phe Glu Gly Ser Phe Val Asp Phe 285
Val His Ser Arg 290	Gly Phe Thr Met 295	Gly Thr Val Asp Asn Ala Arg Val 300
Tyr Pro Val Leu 305	Lys Asp Arg Ser 310	Gly Ala Asn Val Ala Leu Gln Arg 315 320
Arg Asn Phe Gly 325	Leu Asp Ala Gly 330	Lys Thr Glu Val Pro Val Gln Pro 335
Ala Val Asp 340	Pro Ala Trp Glu Thr 345	Pro Lys Ala Glu Pro Lys Lys Gln 350
Ser Gly Arg Arg 355	Ala Pro Trp Asp 360	Lys Val Ala Thr Pro Glu Val Ile 365
Pro Asp Pro Asn 370	Pro Asp Ala Asp 375	Pro Ser Ser Ile Leu Tyr Gly Gln 380
Asn Val Thr Leu 385	Thr Gly Asp Phe 390	Glu Pro Tyr Glu Lys Gly Ala Leu 395 400
Trp Gln Arg Ile 405	Ala Asp Gln Gly 410	Ala Leu Ile Gly Lys Asn Val Thr 415
Lys Lys Thr Thr 420	Thr Ile Leu Val Ala 425	Gly Pro Trp Ala Thr Ile Thr Ser 430
Lys Gln Lys Arg 435	Ala Glu Glu Leu 440	Lys Glu Lys Gly Gln Asp Ile Gln 445

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Pro Pro Phe  
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 Met Val Ala Glu His  
 1 5  
 gct gca ggg gat tgg gtg gtc ctt gca ggt ttt cag tgg ttg gac aaa 163  
 Ala Ala Gly Asp Trp Val Val Leu Ala Gly Phe Gln Trp Leu Asp Lys  
 10 15 20  
 atc gac tat gtg atc gat tgc ttt aaa ccg gaa aat att gtg ctg gaa 211  
 Ile Asp Tyr Val Ile Asp Cys Phe Lys Pro Glu Asn Ile Val Leu Glu  
 25 30 35  
 ttc ggt tca acc atg aca ccg gaa gac gcc gac cgc aat gaa tac ctc 259  
 Phe Gly Ser Thr Met Thr Pro Glu Asp Ala Asp Arg Asn Glu Tyr Leu  
 40 45 50  
 aga aga acg caa gcc aaa ttc cag ctt cga gcc atc cta agc acc aac 307  
 Arg Arg Thr Gln Ala Lys Phe Gln Leu Arg Gly Ile Leu Ser Thr Asn  
 55 60 65  
 cca gaa tcc gct gcc cgg ggg agc gtg cgg ctt gcc gcc gcc aag cag 355  
 Pro Glu Ser Ala Ala Arg Gly Ser Val Arg Leu Ala Gly Ala Lys Gln  
 70 75 80 85  
 gca cta gcc cgc aag atg ccg ctt gcc gac gcc gaa agc gag cta cat 403  
 Ala Leu Ala Arg Lys Met Pro Leu Ala Asp Ala Glu Ser Glu Leu His  
 90 95 100  
 ccc atg gcc act acc tgg atg cgc agc ggg gat aca ttg tta aaa gca 451  
 Pro Met Gly Thr Thr Trp Met Arg Ser Gly Asp Thr Leu Leu Lys Ala  
 105 110 115  
 cac cct gat tac gcg gat ctc att gca acc acg gtg gaa tta gct gct 499  
 His Pro Asp Tyr Ala Asp Leu Ile Ala Thr Thr Val Glu Leu Ala Ala  
 120 125 130  
 gaa tgt gct ttc acc cta gat ttg gtg gcc ccg aat ctg ccc aag tgg 547  
 Glu Cys Ala Phe Thr Leu Asp Leu Val Ala Pro Asn Leu Pro Lys Trp  
 135 140 145

gat acc cct ggt gaa cac acg gaa atg tcc tgg ctt gcg cac ctg gtt 595  
 Asp Thr Pro Gly Glu His Thr Glu Met Ser Trp Leu Ala His Leu Val  
 150 155 160 165

tcc act cgg att gat acc cgc tat gtg ggg cgc tcc gca gac atc aaa 643  
 Ser Thr Arg Ile Asp Thr Arg Tyr Val Gly Arg Ser Ala Asp Ile Lys  
 170 175 180

gca cga gct gcc aca caa att gac tat gaa tta ggc gtt att gaa aag 691  
 Ala Arg Ala Ala Thr Gln Ile Asp Tyr Glu Leu Gly Val Ile Glu Lys  
 185 190 195

ctg ggt ttt cca ggc tat ttc ctc gtc gtt aat gat ctg gtg gag ttt 739  
 Leu Gly Phe Pro Gly Tyr Phe Leu Val Val Asn Asp Leu Val Gly Phe  
 200 205 210

tgt cgc gat tcc aat att ttg tgc caa ggc aga ggt tcc gcg gcg aac 787  
 Cys Arg Asp Ser Asn Ile Leu Cys Gln Gly Arg Gly Ser Ala Ala Asn  
 215 220 225

tgc gcg gtg tgc ttt gtc cta ggc atc acc aac gcg gag ccg atc tct 835  
 Ser Ala Val Cys Phe Val Leu Gly Ile Thr Asn Ala Glu Pro Ile Ser  
 230 235 240 245

gct gga ttg ttg ttt gaa cgg ttt tta tct cct gac cgg gat ggt cca 883  
 Ala Gly Leu Leu Phe Glu Arg Phe Leu Ser Pro Asp Arg Asp Gly Pro  
 250 255 260

cca gat att gac att gat att gaa tcc ggc agg cgc gaa gaa gta atc 931  
 Pro Asp Ile Asp Ile Asp Ile Glu Ser Gly Arg Arg Glu Glu Val Ile  
 265 270 275

caa tac gtg tat gaa aaa tac gga agg gat aac gca gct caa gta gcc 979  
 Gln Tyr Val Tyr Glu Lys Tyr Gly Arg Asp Asn Ala Ala Gln Val Ala  
 280 285 290

aat gtc att acc tac cga aca aaa ggc gcg atg cgt gat gct gcc cgt 1027  
 Asn Val Ile Thr Tyr Arg Thr Lys Gly Ala Met Arg Asp Ala Ala Arg  
 295 300 305

gca ctg ggt tac ccg caa ggt gct gcc gat gcc tgg gct aaa gga acc 1075  
 Ala Leu Gly Tyr Pro Gln Gly Ala Ala Asp Ala Trp Ala Lys Gly Thr  
 310 315 320 325

tgc gaa cca ccc gat gat gtg ctg gaa tta gct gcg caa ttt aaa ggg 1123  
 Ser Glu Pro Pro Asp Asp Val Leu Glu Leu Ala Ala Gln Phe Lys Gly  
 330 335 340

caa cca cgg cat ttg ggt att cac tcc ggt ggc atg gtc att tgc gat 1171  
 Gln Pro Arg His Leu Gly Ile His Ser Gly Gly Met Val Ile Cys Asp  
 345 350 355

cgc ccc atc gcc gat gtg gtc cca gtg gaa tgg gct cgg atg gat aac 1219  
 Arg Pro Ile Ala Asp Val Val Pro Val Glu Trp Ala Arg Met Asp Asn  
 360 365 370

cgc tgc gtt gtg caa tgg gat aaa gat gac tgt gcc acg gca ggc ttg 1267  
 Arg Ser Val Val Gln Trp Asp Lys Asp Asp Cys Ala Thr Ala Gly Leu  
 375 380 385

gtc aaa ttc gac ctt ttg gga ttg ggc atg ttg gaa gcc atc cat cac 1315

Val Lys Phe Asp Leu Leu Gly Leu Gly Met Leu Glu Ala Ile His His  
390 395 400 405

atg ctg gat ctg gtg gca gaa cac cga ggt aaa aag atc aat ttg tgg 1363  
Met Leu Asp Leu Val Ala Glu His Arg Gly Lys Lys Ile Asn Leu Trp  
410 415 420

gaa cta gat ctg gcg gaa ccg gag gtc tat gac atg ttg tgc aag gca 1411  
Glu Leu Asp Leu Ala Glu Pro Glu Val Tyr Asp Met Leu Cys Lys Ala  
425 430 435

gat gcc gtg ggt gtg ttc cag gtg gaa tca cgt gcg cag tta tcc acg 1459  
Asp Ala Val Gly Val Phe Gln Val Glu Ser Arg Ala Gln Leu Ser Thr  
440 445 450

ctg cct cga ctc aag ccc cgc acc ttc ttt gac ctg gtc gtg gag gta 1507  
Leu Pro Arg Leu Lys Pro Arg Thr Phe Phe Asp Leu Val Val Glu Val  
455 460 465

gct ctg att cgt cca ggt ccc atc caa ggc gga tgc gtg cac ccg tat 1555  
Ala Leu Ile Arg Pro Gly Pro Ile Gln Gly Gly Ser Val His Pro Tyr  
470 475 480 485

ttg cgg cgc cgt gct ggt gaa gag gcc atc act tat gac cac ccc gtg 1603  
Leu Arg Arg Arg Ala Gly Glu Glu Ala Ile Thr Tyr Asp His Pro Val  
490 495 500

ttg gaa aag tct ttg ggt aaa acc tta gga atc cca ctg ttt cag gaa 1651  
Leu Glu Lys Ser Leu Gly Lys Thr Leu Gly Ile Pro Leu Phe Gln Glu  
505 510 515

cag ctc atg cag gta gct gtt gat gct gca ggt ttt agt ggt ggg gaa 1699  
Gln Leu Met Gln Val Ala Val Asp Ala Ala Gly Phe Ser Gly Gly Glu  
520 525 530

gcg gat tcc ttg cgc aga gcg atg ggg tgc aaa cgc tca cct gaa cgc 1747  
Ala Asp Ser Leu Arg Arg Ala Met Gly Ser Lys Arg Ser Pro Glu Arg  
535 540 545

atg gct gcg ttg cgc tgc cgg ttt ttc caa ggg ctg aaa gat acc aat 1795  
Met Ala Ala Leu Arg Ser Arg Phe Phe Gln Gly Leu Lys Asp Thr Asn  
550 555 560 565

ggg att gtg ggg gag acc gcc gag aaa ctg tgg aac aaa att gtg gcc 1843  
Gly Ile Val Gly Glu Thr Ala Glu Lys Leu Trp Asn Lys Ile Val Ala  
570 575 580

ttt gct gcc tac ggt ttt ccg gaa tgc cat tgc cag tgc ttt geg tcc 1891  
Phe Ala Ala Tyr Gly Phe Pro Glu Ser His Ser Gln Ser Phe Ala Ser  
585 590 595

ttg gtg tat ttc tcc gcg tgg ttt aaa tac cac tac ccg gct gaa ttc 1939  
Leu Val Tyr Phe Ser Ala Trp Phe Lys Tyr His Tyr Pro Ala Glu Phe  
600 605 610

tgc gtg gga tta ttg cgg gca caa ccc atg ggt ttc tat tca cca cag 1987  
Cys Val Gly Leu Leu Arg Ala Gln Pro Met Gly Phe Tyr Ser Pro Gln  
615 620 625

tct ttg atc agt gat gcc aga cgc cac gcc gtg agt atc ctg ccg atc 2035  
Ser Leu Ile Ser Asp Ala Arg Arg His Gly Val Ser Ile Leu Pro Ile

630	635	640	645
acg gtc aat gat tcc ggt gtg gag gcc gat gct ccg aat ggt gcg att Thr Val Asn Asp Ser Gly Val Glu Ala Asp Ala Pro Asn Gly Ala Ile 650 655 660			2083
cga ttg ggg ctc aac ctg gtg aaa ggc ctt ggc cac gat gcc gcg caa Arg Leu Gly Leu Asn Leu Val Lys Gly Leu Gly His Asp Ala Ala Gln 665 670 675			2131
aga ata gag gac aac gcc ccg ttt gat tcc att ccg gat tta tcg cgc Arg Ile Glu Asp Asn Ala Pro Phe Asp Ser Ile Pro Asp Leu Ser Arg 680 685 690			2179
cgg gct gat ctt aat gtt gct caa gtt gag gca ttg gcg cga gcg gga Arg Ala Asp Leu Asn Val Ala Gln Val Glu Ala Leu Ala Arg Ala Gly 695 700 705			2227
gcg gtg gac tgc ttg ggg gtc gga cgt cga caa gca tta tgg caa gcg Ala Val Asp Cys Leu Gly Val Gly Arg Arg Gln Ala Leu Trp Gln Ala 710 715 720 725			2275
ggc gtc gca gcg acc gaa aaa cct gga atg ctg cct ggc ctt tcg gtg Gly Val Ala Ala Thr Glu Lys Pro Gly Met Leu Pro Gly Leu Ser Val 730 735 740			2323
att gaa gct ccg gcg ttg ccg ggg atg agc gcc ttt gag ctg atg gcg Ile Glu Ala Pro Ala Leu Pro Gly Met Ser Ala Phe Glu Leu Met Ala 745 750 755			2371
acc aat att tcc gcc acg gga gtc acc gcg gat tat cag ccg atg gcg Thr Asn Ile Ser Ala Thr Gly Val Thr Ala Asp Tyr Gln Pro Met Ala 760 765 770			2419
ttg att ccg gag ccg atg gag gag ctg ggg atc gtg ccg gcg gat ccg Leu Ile Arg Glu Arg Met Glu Glu Leu Gly Ile Val Pro Ala Asp Arg 775 780 785			2467
cta ttg gag gtg gaa gat ggc acg ccg ctg ccg atc gct ggc att gtc Leu Leu Glu Val Glu Asp Gly Thr Arg Leu Arg Ile Ala Gly Ile Val 790 795 800 805			2515
acg cac ccg cag cgc ccg caa act gcg tcg ggg ctg aca ttt tta ggg Thr His Arg Gln Arg Pro Gln Thr Ala Ser Gly Leu Thr Phe Leu Gly 810 815 820			2563
atg gag gat gag acc ggg ctg atg aat gtg atg gtg tcc gtt ggg ttg Met Glu Asp Glu Thr Gly Leu Met Asn Val Met Val Ser Val Gly Leu 825 830 835			2611
tgg cag ccg cag cgc gtg ctg gcc aga aat gcc aag gcg ttg att att Trp Gln Arg Gln Arg Val Leu Ala Arg Asn Ala Lys Ala Leu Ile Ile 840 845 850			2659
cga ggg att gtg cag aat gcg caa ggg gtg gcg aca gtt gtc gct gac Arg Gly Ile Val Gln Asn Ala Gln Gly Val Ala Thr Val Val Ala Asp 855 860 865			2707
cgg ttg gaa ccg ttg gac atg ggg gag ttt ctg agc cgt ggc tca cga Arg Leu Glu Pro Leu Asp Met Gly Glu Phe Leu Ser Arg Gly Ser Arg 870 875 880 885			2755

gat ttt cga taatttggca aagtggacat tat  
Asp Phe Arg

2787

<210> 172  
<211> 888  
<212> PRT  
<213> Corynebacterium glutamicum

<400> 172  
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Gln Trp Leu Asp Lys Ile Asp Tyr Val Ile Asp Cys Phe Lys Pro Glu  
20 25 30  
Asn Ile Val Leu Glu Phe Gly Ser Thr Met Thr Pro Glu Asp Ala Asp  
35 40 45  
Arg Asn Glu Tyr Leu Arg Arg Thr Gln Ala Lys Phe Gln Leu Arg Gly  
50 55 60  
Ile Leu Ser Thr Asn Pro Glu Ser Ala Ala Arg Gly Ser Val Arg Leu  
65 70 75 80  
Ala Gly Ala Lys Gln Ala Leu Ala Arg Lys Met Pro Leu Ala Asp Ala  
85 90 95  
Glu Ser Glu Leu His Pro Met Gly Thr Thr Trp Met Arg Ser Gly Asp  
100 105 110  
Thr Leu Leu Lys Ala His Pro Asp Tyr Ala Asp Leu Ile Ala Thr Thr  
115 120 125  
Val Glu Leu Ala Ala Glu Cys Ala Phe Thr Leu Asp Leu Val Ala Pro  
130 135 140  
Asn Leu Pro Lys Trp Asp Thr Pro Gly Glu His Thr Glu Met Ser Trp  
145 150 155 160  
Leu Ala His Leu Val Ser Thr Arg Ile Asp Thr Arg Tyr Val Gly Arg  
165 170 175  
Ser Ala Asp Ile Lys Ala Arg Ala Ala Thr Gln Ile Asp Tyr Glu Leu  
180 185 190  
Gly Val Ile Glu Lys Leu Gly Phe Pro Gly Tyr Phe Leu Val Val Asn  
195 200 205  
Asp Leu Val Glu Phe Cys Arg Asp Ser Asn Ile Leu Cys Gln Gly Arg  
210 215 220  
Gly Ser Ala Ala Asn Ser Ala Val Cys Phe Val Leu Gly Ile Thr Asn  
225 230 235 240  
Ala Glu Pro Ile Ser Ala Gly Leu Leu Phe Glu Arg Phe Leu Ser Pro  
245 250 255  
Asp Arg Asp Gly Pro Pro Asp Ile Asp Ile Asp Ile Glu Ser Gly Arg

260	265	270
Arg Glu Glu Val Ile Gln Tyr Val Tyr Glu Lys Tyr Gly Arg Asp Asn 275 280 285		
Ala Ala Gln Val Ala Asn Val Ile Thr Tyr Arg Thr Lys Gly Ala Met 290 295 300		
Arg Asp Ala Ala Arg Ala Leu Gly Tyr Pro Gln Gly Ala Ala Asp Ala 305 310 315 320		
Trp Ala Lys Gly Thr Ser Glu Pro Pro Asp Asp Val Leu Glu Leu Ala 325 330 335		
Ala Gln Phe Lys Gly Gln Pro Arg His Leu Gly Ile His Ser Gly Gly 340 345 350		
Met Val Ile Cys Asp Arg Pro Ile Ala Asp Val Val Pro Val Glu Trp 355 360 365		
Ala Arg Met Asp Asn Arg Ser Val Val Gln Trp Asp Lys Asp Asp Cys 370 375 380		
Ala Thr Ala Gly Leu Val Lys Phe Asp Leu Leu Gly Leu Gly Met Leu 385 390 395 400		
Glu Ala Ile His His Met Leu Asp Leu Val Ala Glu His Arg Gly Lys 405 410 415		
Lys Ile Asn Leu Trp Glu Leu Asp Leu Ala Glu Pro Glu Val Tyr Asp 420 425 430		
Met Leu Cys Lys Ala Asp Ala Val Gly Val Phe Gln Val Glu Ser Arg 435 440 445		
Ala Gln Leu Ser Thr Leu Pro Arg Leu Lys Pro Arg Thr Phe Phe Asp 450 455 460		
Leu Val Val Glu Val Ala Leu Ile Arg Pro Gly Pro Ile Gln Gly Gly 465 470 475 480		
Ser Val His Pro Tyr Leu Arg Arg Arg Ala Gly Glu Glu Ala Ile Thr 485 490 495		
Tyr Asp His Pro Val Leu Glu Lys Ser Leu Gly Lys Thr Leu Gly Ile 500 505 510		
Pro Leu Phe Gln Glu Gln Leu Met Gln Val Ala Val Asp Ala Ala Gly 515 520 525		
Phe Ser Gly Gly Glu Ala Asp Ser Leu Arg Arg Ala Met Gly Ser Lys 530 535 540		
Arg Ser Pro Glu Arg Met Ala Ala Leu Arg Ser Arg Phe Phe Gln Gly 545 550 555 560		
Leu Lys Asp Thr Asn Gly Ile Val Gly Glu Thr Ala Glu Lys Leu Trp 565 570 575		
Asn Lys Ile Val Ala Phe Ala Ala Tyr Gly Phe Pro Glu Ser His Ser 580 585 590		



Gln Ser Phe Ala Ser Leu Val Tyr Phe Ser Ala Trp Phe Lys Tyr His  
 595 600 605  
 Tyr Pro Ala Glu Phe Cys Val Gly Leu Leu Arg Ala Gln Pro Met Gly  
 610 615 620  
 Phe Tyr Ser Pro Gln Ser Leu Ile Ser Asp Ala Arg Arg His Gly Val  
 625 630 635 640  
 Ser Ile Leu Pro Ile Thr Val Asn Asp Ser Gly Val Glu Ala Asp Ala  
 645 650 655  
 Pro Asn Gly Ala Ile Arg Leu Gly Leu Asn Leu Val Lys Gly Leu Gly  
 660 665 670  
 His Asp Ala Ala Gln Arg Ile Glu Asp Asn Ala Pro Phe Asp Ser Ile  
 675 680 685  
 Pro Asp Leu Ser Arg Arg Ala Asp Leu Asn Val Ala Gln Val Glu Ala  
 690 695 700  
 Leu Ala Arg Ala Gly Ala Val Asp Cys Leu Gly Val Gly Arg Arg Gln  
 705 710 715 720  
 Ala Leu Trp Gln Ala Gly Val Ala Ala Thr Glu Lys Pro Gly Met Leu  
 725 730 735  
 Pro Gly Leu Ser Val Ile Glu Ala Pro Ala Leu Pro Gly Met Ser Ala  
 740 745 750  
 Phe Glu Leu Met Ala Thr Asn Ile Ser Ala Thr Gly Val Thr Ala Asp  
 755 760 765  
 Tyr Gln Pro Met Ala Leu Ile Arg Glu Arg Met Glu Glu Leu Gly Ile  
 770 775 780  
 Val Pro Ala Asp Arg Leu Leu Glu Val Glu Asp Gly Thr Arg Leu Arg  
 785 790 795 800  
 Ile Ala Gly Ile Val Thr His Arg Gln Arg Pro Gln Thr Ala Ser Gly  
 805 810 815  
 Leu Thr Phe Leu Gly Met Glu Asp Glu Thr Gly Leu Met Asn Val Met  
 820 825 830  
 Val Ser Val Gly Leu Trp Gln Arg Gln Arg Val Leu Ala Arg Asn Ala  
 835 840 845  
 Lys Ala Leu Ile Ile Arg Gly Ile Val Gln Asn Ala Gln Gly Val Ala  
 850 855 860  
 Thr Val Val Ala Asp Arg Leu Glu Pro Leu Asp Met Gly Glu Phe Leu  
 865 870 875 880  
 Ser Arg Gly Ser Arg Asp Phe Arg  
 885

&lt;210&gt; 173

&lt;211&gt; 599

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(576)

&lt;223&gt; FRXA00407

&lt;400&gt; 173

ctt aat gtt gct caa gtt gag gca ttg gcg cga gcg gga gcg gtg gac 48  
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 1 5 10 15

tgc ttg ggg gtc gga cgt cga caa gca tta tgg caa gcg ggc gtc gca 96  
 Cys Leu Gly Val Gly Arg Arg Gln Ala Leu Trp Gln Ala Gly Val Ala  
 20 25 30

gcg acc gaa aaa cct gga atg ctg cct ggc ctt tgg gtg att gaa gct 144  
 Ala Thr Glu Lys Pro Gly Met Leu Pro Gly Leu Ser Val Ile Glu Ala  
 35 40 45

ccg gcg ttg ccg ggg atg agc gcc ttt gag ctg atg gcg acc aat att 192  
 Pro Ala Leu Pro Gly Met Ser Ala Phe Glu Leu Met Ala Thr Asn Ile  
 50 55 60

tcc gcc acg gga gtc acc gcg gat tat cag ccg atg gcg ttg att cgg 240  
 Ser Ala Thr Gly Val Thr Ala Asp Tyr Gln Pro Met Ala Leu Ile Arg  
 65 70 75 80

gag cgg atg gag gag ctg ggg atc gtg ccg gcg gat cgg cta ttg gag 288  
 Glu Arg Met Glu Glu Leu Gly Ile Val Pro Ala Asp Arg Leu Leu Glu  
 85 90 95

gtg gaa gat ggc acg cgg ctg cgg atc gct ggc att gtc acg cac cgg 336  
 Val Glu Asp Gly Thr Arg Leu Arg Ile Ala Gly Ile Val Thr His Arg  
 100 105 110

cag cgc ccg caa act gcg tgg ggg ctg aca ttt tta ggg atg gag gat 384  
 Gln Arg Pro Gln Thr Ala Ser Gly Leu Thr Phe Leu Gly Met Glu Asp  
 115 120 125

gag acc ggg ctg atg aat gtg atg gtg tcc gtt ggg ttg tgg cag cgg 432  
 Glu Thr Gly Leu Met Asn Val Met Val Ser Val Gly Leu Trp Gln Arg  
 130 135 140

cag cgc gtg ctg gcc aga aat gcc aag gcg ttg att att cga ggg att 480  
 Gln Arg Val Leu Ala Arg Asn Ala Lys Ala Leu Ile Ile Arg Gly Ile  
 145 150 155 160

gtg cag aat gcg caa ggg gtg gcg aca gtt gtc gct gac cgg ttg gaa 528  
 Val Gln Asn Ala Gln Gly Val Ala Thr Val Val Ala Asp Arg Leu Glu  
 165 170 175

ccg ttg gac atg ggg gag ttt etc agc cgt ggc tca cga gat ttt cga 576  
 Pro Leu Asp Met Gly Glu Phe Leu Ser Arg Gly Ser Arg Asp Phe Arg  
 180 185 190

taatttgcca aagtgacat tat 599

&lt;210&gt; 174

&lt;211&gt; 192

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

<400> 174

<400> 174  
Leu Asn Val Ala Gln Val Glu Ala Leu Ala Arg Ala Gly Ala Val Asp  
1 5 10 15

Cys Leu Gly Val Gly Arg Arg Gln Ala Leu Trp Gln Ala Gly Val Ala  
20 25 30

Ala Thr Glu Lys Pro Gly Met Leu Pro Gly Leu Ser Val Ile Glu Ala  
35 40 45

Pro Ala Leu Pro Gly Met Ser Ala Phe Glu Leu Met Ala Thr Asn Ile  
50 55 60

Ser Ala Thr Gly Val Thr Ala Asp Tyr Gln Pro Met Ala Leu Ile Arg  
65 70 75 80

Glu Arg Met Glu Glu Leu Gly Ile Val Pro Ala Asp Arg Leu Leu Glu  
85 90 95

Val Glu Asp Gly Thr Arg Leu Arg Ile Ala Gly Ile Val Thr His Arg  
100 105 110

Gln Arg Pro Gln Thr Ala Ser Gly Leu Thr Phe Leu Gly Met Glu Asp  
115 120 125

Glu Thr Gly Leu Met Asn Val Met Val Ser Val Gly Leu Trp Gln Arg  
130 135 140

Gln Arg Val Leu Ala Arg Asn Ala Lys Ala Leu Ile Ile Arg Gly Ile  
145 150 155 160

Val Gln Asn Ala Gln Gly Val Ala Thr Val Val Ala Asp Arg Leu Glu  
165 170 175

Pro Leu Asp Met Gly Glu Phe Leu Ser Arg Gly Ser Arg Asp Phe Arg  
180 185 190

<210> 175

<211> 2062

<212> DNA

<213> *Corynebacterium glutamicum*

 $\langle 220 \rangle$ 

&lt;221&gt; CDS

<222> (101) . . (2062)

<223> FRXA00415

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<400> 175  
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cacggggaga aaaggggaag ttcgctatcc gccgctgcc a t g g t t g c t g a a c a t 115  
Met Val Ala Glu His  
1 5

gct gca ggg gat tgg gtg gtc ctt gca ggt ttt cag tgg ttg gac aaa 163  
 Ala Ala Gly Asp Trp Val Val Leu Ala Gly Phe Gln Trp Leu Asp Lys  
 10 15 20

atc gac tat gtg atc gat tgc ttt aaa ccg gaa aat att gtg ctg gaa 211  
 Ile Asp Tyr Val Ile Asp Cys Phe Lys Pro Glu Asn Ile Val Leu Glu  
 25 30 35

ttc ggt tca acc atg aca ccg gaa gac gcc gac cgc aat gaa tac ctc 259  
 Phe Gly Ser Thr Met Thr Pro Glu Asp Ala Asp Arg Asn Glu Tyr Leu  
 40 45 50

aga aga acg caa gcc aaa ttc cag ctt cga ggc atc cta agc acc aac 307  
 Arg Arg Thr Gln Ala Lys Phe Gln Leu Arg Gly Ile Leu Ser Thr Asn  
 55 60 65

cca gaa tcc gct gcc cgg ggg agc gtg cgg ctt gcc ggc gcc aag cag 355  
 Pro Glu Ser Ala Ala Arg Gly Ser Val Arg Leu Ala Gly Ala Lys Gln  
 70 75 80 85

gca cta gcc cgc aag atg ccg ctt gcc gac gcc gaa agc gag cta cat 403  
 Ala Leu Ala Arg Lys Met Pro Leu Ala Asp Ala Glu Ser Glu Leu His  
 90 95 100

ccc atg ggc act acc tgg atg cgc agc ggg gat aca ttg tta aaa gca 451  
 Pro Met Gly Thr Thr Trp Met Arg Ser Gly Asp Thr Leu Leu Lys Ala  
 105 110 115

cac cct gat tac gcg gat ctc att gca acc acg gtg gaa tta gct gct 499  
 His Pro Asp Tyr Ala Asp Leu Ile Ala Thr Thr Val Glu Leu Ala Ala  
 120 125 130

gaa tgt gct ttc acc cta gat ttg gtg gcc ccg aat ctg ccc aag tgg 547  
 Glu Cys Ala Phe Thr Leu Asp Leu Val Ala Pro Asn Leu Pro Lys Trp  
 135 140 145

gat acc cct ggt gaa cac acg gaa atg tcc tgg ctt gcg cac ctg gtt 595  
 Asp Thr Pro Gly Glu His Thr Glu Met Ser Trp Leu Ala His Leu Val  
 150 155 160 165

tcc act cgg att gat acc cgc tat gtg ggg cgc tcc gca gac atc aaa 643  
 Ser Thr Arg Ile Asp Thr Arg Tyr Val Gly Arg Ser Ala Asp Ile Lys  
 170 175 180

gca cga gct gcc aca caa att gac tat gaa tta ggc gtt att gaa aag 691  
 Ala Arg Ala Ala Thr Gln Ile Asp Tyr Glu Leu Gly Val Ile Glu Lys  
 185 190 195

ctg ggt ttt cca ggc tat ttc ctc gtc gtt aat gat ctg gtg gag ttt 739  
 Leu Gly Phe Pro Gly Tyr Phe Leu Val Val Asn Asp Leu Val Glu Phe  
 200 205 210

tgt cgc gat tcc aat att ttg tgc caa ggc aga ggt tcc gcg gcg aac 787  
 Cys Arg Asp Ser Asn Ile Leu Cys Gln Gly Arg Gly Ser Ala Ala Asn  
 215 220 225

tgc gcg gtg tgc ttt gtc cta ggc atc acc aac gcg gag ccg atc tct 835  
 Ser Ala Val Cys Phe Val Leu Gly Ile Thr Asn Ala Glu Pro Ile Ser  
 230 235 240 245

gct gga ttg ttg ttt gaa cgg ttt tta tct cct gac cgg gat ggt cca 883  
Ala Gly Leu Leu Phe Glu Arg Phe Leu Ser Pro Asp Arg Asp Gly Pro  
250 255 260

cca gat att gac att gat att gaa tcc ggc agg cgc gaa gaa gta atc 931  
Pro Asp Ile Asp Ile Asp Ile Glu Ser Gly Arg Arg Glu Glu Val Ile  
265 270 275

caa tac gtg tat gaa aaa tac gga agg gat aac gca gct caa gta gcc 979  
Gln Tyr Val Tyr Glu Lys Tyr Gly Arg Asp Asn Ala Ala Gln Val Ala  
280 285 290

aat gtc att acc tac cga aca aaa ggc gcg atg cgt gat gct gcc cgt 1027  
Asn Val Ile Thr Tyr Arg Thr Lys Gly Ala Met Arg Asp Ala Ala Arg  
295 300 305

gca ctg ggt tac ccg caa ggt gct gcc gat gcc tgg gct aaa gga acc 1075  
Ala Leu Gly Tyr Pro Gln Gly Ala Ala Asp Ala Trp Ala Lys Gly Thr  
310 315 320 325

tcg gaa cca ccc gat gat gtg ctg gaa tta gct gcg caa ttt aaa ggg 1123  
Ser Glu Pro Pro Asp Asp Val Leu Glu Leu Ala Ala Gln Phe Lys Gly  
330 335 340

caa cca cgg cat ttg ggt att cac tcc ggt ggc atg gtc att tgc gat 1171  
Gln Pro Arg His Leu Gly Ile His Ser Gly Gly Met Val Ile Cys Asp  
345 350 355

cgc ccc atc gcc gat gtg gtg cca gtg gaa tgg gct cgg atg gat aac 1219  
Arg Pro Ile Ala Asp Val Val Pro Val Glu Trp Ala Arg Met Asp Asn  
360 365 370

cgc tcg gtt gtg caa tgg gat aaa gat gac tgt gcc acg gca ggc ttg 1267  
Arg Ser Val Val Gln Trp Asp Lys Asp Asp Cys Ala Thr Ala Gly Leu  
375 380 385

gtc aaa ttc gac ctt ttg gga ttg ggc atg ttg gaa gcc atc cat cac 1315  
Val Lys Phe Asp Leu Leu Gly Leu Gly Met Leu Glu Ala Ile His His  
390 395 400 405

atg ctg gat ctg gtg gca gaa cac cga ggt aaa aag atc aat ttg tgg 1363  
Met Leu Asp Leu Val Ala Glu His Arg Gly Lys Lys Ile Asn Leu Trp  
410 415 420

gaa cta gat ctg gcg gaa ccg gag gtc tat gac atg ttg tgc aag gca 1411  
Glu Leu Asp Leu Ala Glu Pro Glu Val Tyr Asp Met Leu Cys Lys Ala  
425 430 435

gat gcc gtg ggt gtg ttc cag gtg gaa tca cgt gcg cag tta tcc acg 1459  
Asp Ala Val Gly Val Phe Gln Val Glu Ser Arg Ala Gln Leu Ser Thr  
440 445 450

ctg cct cga ctc aag ccc cgc acc ttc ttt gac ctg gtc gtg gag gta 1507  
Leu Pro Arg Leu Lys Pro Arg Thr Phe Phe Asp Leu Val Val Glu Val  
455 460 465

gct ctg att cgt cca ggt ccc atc caa ggc gga tcg gtg cac ccg tat 1555  
Ala Leu Ile Arg Pro Gly Pro Ile Gln Gly Gly Ser Val His Pro Tyr  
470 475 480 485

ttg cgg cgc cgt gct ggt gaa gag gcc atc act tat gac cac ccc gtg 1603

Leu Arg Arg Arg Ala Gly Glu Glu Ala Ile Thr Tyr Asp His Pro Val  
490 495 500

ttg gaa aag tct ttg ggt aaa acc tta gga atc cca ctg ttt cag gaa 1651  
Leu Glu Lys Ser Leu Gly Lys Thr Leu Gly Ile Pro Leu Phe Gln Glu  
505 510 515

cag ctc atg cag gta gct gtt gat gct gca ggt ttt agt ggt ggg gaa 1699  
Gln Leu Met Gln Val Ala Val Asp Ala Ala Gly Phe Ser Gly Gly Glu  
520 525 530

gcg gat tcc ttg cgc aga gcg atg ggg tcg aaa cgc tca cct gaa cgc 1747  
Ala Asp Ser Leu Arg Arg Ala Met Gly Ser Lys Arg Ser Pro Glu Arg  
535 540 545

atg gct gcg ttg cgc tcg cgg ttt ttc caa ggg ctg aaa gat acc aat 1795  
Met Ala Ala Leu Arg Ser Arg Phe Phe Gln Gly Leu Lys Asp Thr Asn  
550 555 560 565

ggg att gtg ggg gag acc gcc gag aaa ctg tgg aac aaa att gtg gcc 1843  
Gly Ile Val Gly Glu Thr Ala Glu Lys Leu Trp Asn Lys Ile Val Ala  
570 575 580

ttt gct gcc tac ggt ttt ccg gaa tcg cat tcg cag tcg ttt gcg tcc 1891  
Phe Ala Ala Tyr Gly Phe Pro Glu Ser His Ser Gln Ser Phe Ala Ser  
585 590 595

ttg gtg tat ttc tcc gcg tgg ttt aaa tac cac tac ccg gct gaa ttc 1939  
Leu Val Tyr Phe Ser Ala Trp Phe Lys Tyr His Tyr Pro Ala Glu Phe  
600 605 610

tgc gtg gga tta ttg cgg gca caa ccc atg ggt ttc tat tca cca cag 1987  
Cys Val Gly Leu Leu Arg Ala Gln Pro Met Gly Phe Tyr Ser Pro Gln  
615 620 625

tct ttg atc agt gat gcc aga cgc cac gcc gtg agt atc ctg ccg atc 2035  
Ser Leu Ile Ser Asp Ala Arg Arg His Gly Val Ser Ile Leu Pro Ile  
630 635 640 645

acg gtc aat gat tcc ggt gtg gag gcc 2062  
Thr Val Asn Asp Ser Gly Val Glu Ala  
650

<210> 176

<211> 654

<212> PRT

<213> Corynebacterium glutamicum

<400> 176

Met Val Ala Glu His Ala Ala Gly Asp Trp Val Val Leu Ala Gly Phe  
1 5 10 15

Gln Trp Leu Asp Lys Ile Asp Tyr Val Ile Asp Cys Phe Lys Pro Glu  
20 25 30

Asn Ile Val Leu Glu Phe Gly Ser Thr Met Thr Pro Glu Asp Ala Asp  
35 40 45

Arg Asn Glu Tyr Leu Arg Arg Thr Gln Ala Lys Phe Gln Leu Arg Gly  
50 55 60

Ile Leu Ser Thr Asn Pro Glu Ser Ala Ala Arg Gly Ser Val Arg Leu  
 65 70 75 80  
 Ala Gly Ala Lys Gln Ala Leu Ala Arg Lys Met Pro Leu Ala Asp Ala  
 85 90 95  
 Glu Ser Glu Leu His Pro Met Gly Thr Trp Met Arg Ser Gly Asp  
 100 105 110  
 Thr Leu Leu Lys Ala His Pro Asp Tyr Ala Asp Leu Ile Ala Thr Thr  
 115 120 125  
 Val Glu Leu Ala Ala Glu Cys Ala Phe Thr Leu Asp Leu Val Ala Pro  
 130 135 140  
 Asn Leu Pro Lys Trp Asp Thr Pro Gly Glu His Thr Glu Met Ser Trp  
 145 150 155 160  
 Leu Ala His Leu Val Ser Thr Arg Ile Asp Thr Arg Tyr Val Gly Arg  
 165 170 175  
 Ser Ala Asp Ile Lys Ala Arg Ala Ala Thr Gln Ile Asp Tyr Glu Leu  
 180 185 190  
 Gly Val Ile Glu Lys Leu Gly Phe Pro Gly Tyr Phe Leu Val Val Asn  
 195 200 205  
 Asp Leu Val Glu Phe Cys Arg Asp Ser Asn Ile Leu Cys Gln Gly Arg  
 210 215 220  
 Gly Ser Ala Ala Asn Ser Ala Val Cys Phe Val Leu Gly Ile Thr Asn  
 225 230 235 240  
 Ala Glu Pro Ile Ser Ala Gly Leu Leu Phe Glu Arg Phe Leu Ser Pro  
 245 250 255  
 Asp Arg Asp Gly Pro Pro Asp Ile Asp Ile Asp Ile Glu Ser Gly Arg  
 260 265 270  
 Arg Glu Glu Val Ile Gln Tyr Val Tyr Glu Lys Tyr Gly Arg Asp Asn  
 275 280 285  
 Ala Ala Gln Val Ala Asn Val Ile Thr Tyr Arg Thr Lys Gly Ala Met  
 290 295 300  
 Arg Asp Ala Ala Arg Ala Leu Gly Tyr Pro Gln Gly Ala Ala Asp Ala  
 305 310 315 320  
 Trp Ala Lys Gly Thr Ser Glu Pro Pro Asp Asp Val Leu Glu Leu Ala  
 325 330 335  
 Ala Gln Phe Lys Gly Gln Pro Arg His Leu Gly Ile His Ser Gly Gly  
 340 345 350  
 Met Val Ile Cys Asp Arg Pro Ile Ala Asp Val Val Pro Val Glu Trp  
 355 360 365  
 Ala Arg Met Asp Asn Arg Ser Val Val Gln Trp Asp Lys Asp Asp Cys  
 370 375 380

Ala Thr Ala Gly Leu Val Lys Phe Asp Leu Leu Gly Leu Gly Met Leu  
 385 390 395 400

Glu Ala Ile His Met Leu Asp Leu Val Ala Glu His Arg Gly Lys  
 405 410 415

Lys Ile Asn Leu Trp Glu Leu Asp Leu Ala Glu Pro Glu Val Tyr Asp  
 420 425 430

Met Leu Cys Lys Ala Asp Ala Val Gly Val Phe Gln Val Glu Ser Arg  
 435 440 445

Ala Gln Leu Ser Thr Leu Pro Arg Leu Lys Pro Arg Thr Phe Phe Asp  
 450 455 460

Leu Val Val Glu Val Ala Leu Ile Arg Pro Gly Pro Ile Gln Gly Gly  
 465 470 475 480

Ser Val His Pro Tyr Leu Arg Arg Arg Ala Gly Glu Glu Ala Ile Thr  
 485 490 495

Tyr Asp His Pro Val Leu Glu Lys Ser Leu Gly Lys Thr Leu Gly Ile  
 500 505 510

Pro Leu Phe Gln Glu Gln Leu Met Gln Val Ala Val Asp Ala Ala Gly  
 515 520 525

Phe Ser Gly Gly Glu Ala Asp Ser Leu Arg Arg Ala Met Gly Ser Lys  
 530 535 540

Arg Ser Pro Glu Arg Met Ala Ala Leu Arg Ser Arg Phe Phe Gln Gly  
 545 550 555 560

Leu Lys Asp Thr Asn Gly Ile Val Gly Glu Thr Ala Glu Lys Leu Trp  
 565 570 575

Asn Lys Ile Val Ala Phe Ala Ala Tyr Gly Phe Pro Glu Ser His Ser  
 580 585 590

Gln Ser Phe Ala Ser Leu Val Tyr Phe Ser Ala Trp Phe Lys Tyr His  
 595 600 605

Tyr Pro Ala Glu Phe Cys Val Gly Leu Leu Arg Ala Gln Pro Met Gly  
 610 615 620

Phe Tyr Ser Pro Gln Ser Leu Ile Ser Asp Ala Arg Arg His Gly Val  
 625 630 635 640

Ser Ile Leu Pro Ile Thr Val Asn Asp Ser Gly Val Glu Ala  
 645 650

&lt;210&gt; 177

&lt;211&gt; 477

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(454)

&lt;223&gt; RXN00414



&lt;400&gt; 177

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ggtagctgcat gagccggatg cgcaggcgccc ttcattctgcc atg cag ggg gaa gcg 115  
 Met Gln Gly Glu Ala  
 1 5

tcg gtt cct ttt gcc gag ctg cat gcc acc agc agt tat aac ttt ctc 163  
 Ser Val Pro Phe Ala Glu Leu His Ala Thr Ser Ser Tyr Asn Phe Leu  
 10 15 20

act ggc gca tcg gat ccg tct gat gtg gtt gtg cag gcc aaa aag tta 211  
 Thr Gly Ala Ser Asp Pro Ser Asp Val Val Val Gln Ala Lys Lys Leu  
 25 30 35

gga ctt gct gct cta tca gtc atg gat agg gat ggt ttt tat ggt gca 259  
 Gly Leu Ala Ala Leu Ser Val Met Asp Arg Asp Gly Phe Tyr Gly Ala  
 40 45 50

gtg aga ttt gcg gaa gct gcc gcg gaa gct gga atg cat acc gtt tat 307  
 Val Arg Phe Ala Glu Ala Ala Glu Ala Gly Met His Thr Val Tyr  
 55 60 65

ggt gcg gag ctg agt ctg caa gaa ggc gtg ttg aca gtc ttg tgt aaa 355  
 Gly Ala Glu Leu Ser Leu Gln Glu Gly Val Leu Thr Val Leu Cys Lys  
 70 75 80 85

aat ccg gaa ggc tac aaa aag ctc agt cac ctg atc agt gac gcg aaa 403  
 Asn Pro Glu Gly Tyr Lys Lys Leu Ser His Leu Ile Ser Asp Ala Lys  
 90 95 100

atg gca cgg gag aaa agg gga agt tcg cta tcc gcc gct gcc aat ggt 451  
 Met Ala Arg Glu Lys Arg Gly Ser Ser Leu Ser Ala Ala Ala Asn Gly  
 105 110 115

tgc tgaacatgct gcaggggatt ggg 477  
 Cys

&lt;210&gt; 178

&lt;211&gt; 118

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 178

Met Gln Gly Glu Ala Ser Val Pro Phe Ala Glu Leu His Ala Thr Ser  
 1 5 10 15

Ser Tyr Asn Phe Leu Thr Gly Ala Ser Asp Pro Ser Asp Val Val Val  
 20 25 30

Gln Ala Lys Lys Leu Gly Leu Ala Ala Leu Ser Val Met Asp Arg Asp  
 35 40 45

Gly Phe Tyr Gly Ala Val Arg Phe Ala Glu Ala Ala Ala Glu Ala Gly  
 50 55 60

Met His Thr Val Tyr Gly Ala Glu Leu Ser Leu Gln Glu Gly Val Leu  
 65 70 75 80

Thr Val Leu Cys Lys Asn Pro Glu Gly Tyr Lys Lys Leu Ser His Leu  
85 95

Ile Ser Asp Ala Lys Met Ala Arg Glu Lys Arg Gly Ser Ser Leu Ser  
100 105 110

Ala Ala Ala Asn Gly Cys  
115

<210> 179

<211> 543

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(520)

<223> FRXA00414

<400> 179  
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gggtcgtcat gagccggatg cgcagggcgc ttcattctgcc atg cag ggg gaa gcg 115  
Met Gln Gly Glu Ala  
1 5  
tcg gtt cct ttt gcc gag ctg cat gcc acc agc agt tat aac ttt ctc 163  
Ser Val Pro Phe Ala Glu Leu His Ala Thr Ser Ser Tyr Asn Phe Leu  
10 15 20  
act ggc gca tcg gat ccg tct gat gtg gtt gtg cag gcc aaa aag tta 211  
Thr Gly Ala Ser Asp Pro Ser Asp Val Val Val Gln Ala Lys Lys Leu  
25 30 35  
gga ctt gct gct cta tca gtc atg gat agg gat ggt ttt tat ggt gca 259  
Gly Leu Ala Ala Leu Ser Val Met Asp Arg Asp Gly Phe Tyr Gly Ala  
40 45 50  
gtg aga ttt gcg gaa gct gcc gcg gaa gct gga atg cat acc gtt tat 307  
Val Arg Phe Ala Glu Ala Ala Glu Ala Gly Met His Thr Val Tyr  
55 60 65  
ggg gcg gag ctg agt ctg caa gaa ggc gtg ttg aca gtc ttg tgt aaa 355  
Gly Ala Glu Leu Ser Leu Gln Glu Gly Val Leu Thr Val Leu Cys Lys  
70 75 80 85  
aat ccg gaa ggc tac aaa aag ctc agt cac ctg atc agt gac gcg aaa 403  
Asn Pro Glu Gly Tyr Lys Lys Leu Ser His Leu Ile Ser Asp Ala Lys  
90 95 100  
atg gca cgg gga gaa aag ggg aag ttc gct atc cgc cgc tgc caa tgg 451  
Met Ala Arg Gly Glu Lys Gly Lys Phe Ala Ile Arg Arg Cys Gln Trp  
105 110 115  
ttg ctg aac atg ctg cag ggg att ggg tgg tcc ttg cag gtt ttc agt 499  
Leu Leu Asn Met Leu Gln Gly Ile Gly Trp Ser Leu Gln Val Phe Ser  
120 125 130  
ggg tgg aca aaa tcg act atg tgatcgattg ctttaaaccg gaa 543

Gly Trp Thr Lys Ser Thr Met  
135 140

<210> 180  
<211> 140  
<212> PRT  
<213> Corynebacterium glutamicum

<400> 180  
Met Gln Gly Glu Ala Ser Val Pro Phe Ala Glu Leu His Ala Thr Ser  
1 5 10 15

Ser Tyr Asn Phe Leu Thr Gly Ala Ser Asp Pro Ser Asp Val Val Val  
20 25 30

Gln Ala Lys Lys Leu Gly Leu Ala Ala Leu Ser Val Met Asp Arg Asp  
35 40 45

Gly Phe Tyr Gly Ala Val Arg Phe Ala Glu Ala Ala Glu Ala Gly  
50 55 60

Met His Thr Val Tyr Gly Ala Glu Leu Ser Leu Gln Glu Gly Val Leu  
65 70 75 80

Thr Val Leu Cys Lys Asn Pro Glu Gly Tyr Lys Lys Leu Ser His Leu  
85 90 95

Ile Ser Asp Ala Lys Met Ala Arg Gly Glu Lys Gly Lys Phe Ala Ile  
100 105 110

Arg Arg Cys Gln Trp Leu Leu Asn Met Leu Gln Gly Ile Gly Trp Ser  
115 120 125

Leu Gln Val Phe Ser Gly Trp Thr Lys Ser Thr Met  
130 135 140

<210> 181  
<211> 1365  
<212> DNA  
<213> Corynebacterium glutamicum

<220>  
<221> CDS  
<222> (101)..(1342)  
<223> RXN00807

<400> 181  
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gtagtgagga agtagtgtag agatcgtgac taattcgagt gtg ttt gac agt ctc 115  
Val Phe Asp Ser Leu 5  
1

gcc gcc tcc aaa aca gtg tcc aag acg ctt ttc gac gcg gcc tcc agc 163  
Ala Gly Ser Lys Thr Val Ser Lys Thr Leu Phe Asp Ala Ala Ser Ser  
10 15 20

gcg cgt gcc ctt gtc cgc gcc cga acc aca gaa cgt gcc cgc gcc cgg 211  
Ala Arg Ala Leu Val Arg Ala Arg Thr Thr Glu Arg Ala Arg Ala Arg

25	30	35	
gca gaa cac caa aac cct gca atg atc cac gac tcc ggc ttt gcc cag			259
Ala Glu His Gln Asn Pro Ala Met Ile His Asp Ser Gly Phe Ala Gln			
40	45	50	
tca tgg ctg ttt aca ggc cct ccc gga tgc gga cgt tct gtg gca gcc			307
Ser Trp Leu Phe Thr Gly Pro Pro Gly Ser Gly Arg Ser Val Ala Ala			
55	60	65	
aag gtt ttc gcc gct acg ctc gta tgt tgc aat ccg gat gtt gtg ggc			355
Lys Val Phe Ala Ala Thr Leu Val Cys Ser Asn Pro Asp Val Val Gly			
70	75	80	85
tgt gga caa tgc gag gat tgc cgc gcc gcc atg gga ggc agc cac ccc			403
Cys Gly Gln Cys Glu Asp Cys Arg Ala Ala Met Gly Gly Ser His Pro			
90	95	100	
gat att gaa cac atc gtc ccg cag caa ttg tct atc ggt gtt gat gca			451
Asp Ile Glu His Ile Val Pro Gln Gln Leu Ser Ile Gly Val Asp Ala			
105	110	115	
gct aga gag gtc atc aaa gcc gca gcg gtc agt cct gtt gca gga aac			499
Ala Arg Glu Val Ile Lys Ala Ala Val Ser Pro Val Ala Gly Asn			
120	125	130	
tgg cga gtc gtc atc ttc gaa aac gcc gac cga ctc acc atg caa gcc			547
Trp Arg Val Val Ile Phe Glu Asn Ala Asp Arg Leu Thr Met Gln Ala			
135	140	145	
gcc aac gcc ttg ctg aaa acc gtg gag gaa cca acc gaa agc acc gtg			595
Ala Asn Ala Leu Leu Lys Thr Val Glu Glu Pro Thr Glu Ser Thr Val			
150	155	160	165
atg att ctg tgc gca ccc acc aca gac ccc cgc gac att gcg atc acc			643
Met Ile Leu Cys Ala Pro Thr Thr Asp Pro Arg Asp Ile Ala Ile Thr			
170	175	180	
ctc cgc tcc cgc tgc agg cac ctc tac att ccc acc ccc tcc atc gcg			691
Leu Arg Ser Arg Cys Arg His Leu Tyr Ile Pro Thr Pro Ser Ile Ala			
185	190	195	
gaa gtc gca cga atc ctc gta gct gaa ggc aac gtc agc caa gcg gat			739
Glu Val Ala Arg Ile Leu Val Ala Glu Gly Asn Val Ser Gln Ala Asp			
200	205	210	
gca gaa tta gcg gcg gct gcc tca ggc gct cac atc ggc agg gct cga			787
Ala Glu Leu Ala Ala Ala Ala Ser Gly Ala His Ile Gly Arg Ala Arg			
215	220	225	
tac tta gcg cac aac aac gcc gcc caa cgc aga cgc gcc agc atc ctc			835
Tyr Leu Ala His Asn Asn Ala Ala Gln Arg Arg Arg Ala Ser Ile Leu			
230	235	240	245
aac ctg gcc gaa tta atc ttc cac ggt gat gtc gcc ttc cgc tcc gta			883
Asn Leu Ala Glu Leu Ile Phe His Gly Asp Val Ala Phe Arg Ser Val			
250	255	260	
aac acc ttg gtc aaa atg gtg gaa acc gaa gcc aaa gac agc aac aaa			931
Asn Thr Leu Val Lys Met Val Glu Thr Glu Ala Lys Asp Ser Asn Lys			
265	270	275	

gaa aaa gaa gaa ggc gat ctc gaa gcc gta aga atc tca ctc ggc atg 979  
 Glu Lys Glu Glu Gly Asp Leu Glu Ala Val Arg Ile Ser Leu Gly Met  
 280 285 290

ggg gcc aaa ggc aaa ggt gtc cac aaa gca gta cgt gga gga gcg gga 1027  
 Gly Ala Lys Gly Lys Gly Val His Lys Ala Val Arg Gly Gly Ala Gly  
 295 300 305

gat ttc aaa gca ctc gaa gac caa caa aaa ctc cga cgc acc cga ttc 1075  
 Asp Phe Lys Ala Leu Glu Asp Gln Gln Lys Leu Arg Arg Thr Arg Phe  
 310 315 320 325

ctc cgc gac agc ctc gac ctc gca ctc gtc gac cta gcc ggc atc tac 1123  
 Leu Arg Asp Ser Leu Asp Leu Ala Leu Val Asp Leu Ala Gly Ile Tyr  
 330 335 340

cgc gat gcc atc atc att tcc tcc caa gcc caa gtc gga ctc aca cac 1171  
 Arg Asp Ala Ile Ile Ile Ser Ser Gln Ala Gln Val Gly Leu Thr His  
 345 350 355

ccc gat atg gaa ggc ctc tcc caa gaa ctc gca aca aaa gta agc caa 1219  
 Pro Asp Met Glu Gly Leu Ser Gln Glu Leu Ala Thr Lys Val Ser Gln  
 360 365 370

gaa gga ctc ctg gca tgc ctc gac gcg atc tcc aaa tgc cgc gaa tcc 1267  
 Glu Gly Leu Leu Ala Cys Leu Asp Ala Ile Ser Lys Cys Arg Glu Ser  
 375 380 385

ttc ggc ttc aat gta cga ccc atc gtg gcc atg gac gcc ctg gta gga 1315  
 Phe Gly Phe Asn Val Arg Pro Ile Val Ala Met Asp Ala Leu Val Gly  
 390 395 400 405

cgc ctg cgc aaa gcc tac aaa gtg tcc taaacacccc aaattattga 1362  
 Arg Leu Arg Lys Ala Tyr Lys Val Ser  
 410

agt 1365

<210> 182  
 <211> 414  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 182  
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Asp Ala Ala Ser Ser Ala Arg Ala Leu Val Arg Ala Arg Thr Thr Glu  
 20 25 30

Arg Ala Arg Ala Arg Ala Glu His Gln Asn Pro Ala Met Ile His Asp  
 35 40 45

Ser Gly Phe Ala Gln Ser Trp Leu Phe Thr Gly Pro Pro Gly Ser Gly  
 50 55 60

Arg Ser Val Ala Ala Lys Val Phe Ala Ala Thr Leu Val Cys Ser Asn  
 65 70 75 80

Pro Asp Val Val Gly Cys Gly Gln Cys Glu Asp Cys Arg Ala Ala Met  
85 90 95

Gly Gly Ser His Pro Asp Ile Glu His Ile Val Pro Gln Gln Leu Ser  
100 105 110

Ile Gly Val Asp Ala Ala Arg Glu Val Ile Lys Ala Ala Val Ser  
115 120 125

Pro Val Ala Gly Asn Trp Arg Val Val Ile Phe Glu Asn Ala Asp Arg  
130 135 140

Leu Thr Met Gln Ala Ala Asn Ala Leu Leu Lys Thr Val Glu Glu Pro  
145 150 155 160

Thr Glu Ser Thr Val Met Ile Leu Cys Ala Pro Thr Thr Asp Pro Arg  
165 170 175

Asp Ile Ala Ile Thr Leu Arg Ser Arg Cys Arg His Leu Tyr Ile Pro  
180 185 190

Thr Pro Ser Ile Ala Glu Val Ala Arg Ile Leu Val Ala Glu Gly Asn  
195 200 205

Val Ser Gln Ala Asp Ala Glu Leu Ala Ala Ala Ala Ser Gly Ala His  
210 215 220

Ile Gly Arg Ala Arg Tyr Leu Ala His Asn Asn Ala Ala Gln Arg Arg  
225 230 235 240

Arg Ala Ser Ile Leu Asn Leu Ala Glu Leu Ile Phe His Gly Asp Val  
245 250 255

Ala Phe Arg Ser Val Asn Thr Leu Val Lys Met Val Glu Thr Glu Ala  
260 265 270

Lys Asp Ser Asn Lys Glu Lys Glu Glu Gly Asp Leu Glu Ala Val Arg  
275 280 285

Ile Ser Leu Gly Met Gly Ala Lys Gly Lys Gly Val His Lys Ala Val  
290 295 300

Arg Gly Gly Ala Gly Asp Phe Lys Ala Leu Glu Asp Gln Gln Lys Leu  
305 310 315 320

Arg Arg Thr Arg Phe Leu Arg Asp Ser Leu Asp Leu Ala Leu Val Asp  
325 330 335

Leu Ala Gly Ile Tyr Arg Asp Ala Ile Ile Ser Ser Gln Ala Gln  
340 345 350

Val Gly Leu Thr His Pro Asp Met Glu Gly Leu Ser Gln Glu Leu Ala  
355 360 365

Thr Lys Val Ser Gln Glu Gly Leu Leu Ala Cys Leu Asp Ala Ile Ser  
370 375 380

Lys Cys Arg Glu Ser Phe Gly Phe Asn Val Arg Pro Ile Val Ala Met  
385 390 395 400

Asp Ala Leu Val Gly Arg Leu Arg Lys Ala Tyr Lys Val Ser

405

410

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<210> 183
<211> 1242
<212> DNA
<213> Corynebacterium glutamicum
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<220>
<221> CDS
<222> (101)..(1219)
<223> FRXA00807
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 Leu Arg Ser Arg Cys Arg His Leu Tyr Ile Pro Thr Pro Ser Ile Ala  
 185 190 195

gaa gtc gca cga atc ctc gta gct gaa ggc aac gtc agc caa gcg gat 739  
 Glu Val Ala Arg Ile Leu Val Ala Glu Gly Asn Val Ser Gln Ala Asp  
 200 205 210

gca gaa tta gcg gcg gct gcc tca ggc gct cac atc ggc agg gct cga 787  
 Ala Glu Leu Ala Ala Ala Ser Gly Ala His Ile Gly Arg Ala Arg  
 215 220 225

tac tta gcg cac aac aac gcc gcc caa cgc aga cgc gcc agc atc ctc 835  
 Tyr Leu Ala His Asn Asn Ala Ala Gln Arg Arg Ala Ser Ile Leu  
 230 235 240 245

aac ctg gcc gaa tta atc ttc cac ggt gat gtc gcc ttc cgc tcc gta 883  
 Asn Leu Ala Glu Leu Ile Phe His Gly Asp Val Ala Phe Arg Ser Val  
 250 255 260

aac acc ttg gtc aaa atg gtg gaa acc gaa gcc aaa gac agc aac aaa 931  
 Asn Thr Leu Val Lys Met Val Glu Thr Glu Ala Lys Asp Ser Asn Lys  
 265 270 275

gaa aaa gaa gaa ggc gat ctc gaa gcc gta aga atc tca ctc ggc atg 979  
 Glu Lys Glu Glu Gly Asp Leu Glu Ala Val Arg Ile Ser Leu Gly Met  
 280 285 290

gcg gcc aaa ggc aaa ggt gtc cac aaa gca gta cgt gga gga gcg gga 1027  
 Ala Ala Lys Gly Lys Gly Val His Lys Ala Val Arg Gly Gly Ala Gly  
 295 300 305

gat ttc aaa gca ctc gaa gac caa caa aaa ctc cga cgc acc cga ttc 1075  
 Asp Phe Lys Ala Leu Glu Asp Gln Gln Lys Leu Arg Arg Thr Arg Phe  
 310 315 320 325

ctc cgc gac agc ctc gac ctc gca ctc gtc gac cta gcc ggc atc tac 1123  
 Leu Arg Asp Ser Leu Asp Leu Ala Leu Val Asp Leu Ala Gly Ile Tyr  
 330 335 340

cgc gat gcc atc atc att tcc tcc caa gcc caa gtc gga ctc aca cac 1171  
 Arg Asp Ala Ile Ile Ser Ser Gln Ala Gln Val Gly Leu Thr His  
 345 350 355

ccc gat atg gaa ggc ctc tcc caa gaa ctc gca aca aaa gta agc caa 1219  
 Pro Asp Met Glu Gly Leu Ser Gln Glu Leu Ala Thr Lys Val Ser Gln  
 360 365 370

taagcactcc tggcatgcct cca 1242

&lt;210&gt; 184

&lt;211&gt; 373

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 184

Val Phe Asp Ser Leu Ala Gly Ser Lys Thr Val Ser Lys Thr Leu Phe



1 5 10 15

Asp Ala Ala Ser Ser Ala Arg Ala Leu Val Arg Ala Arg Thr Thr Glu  
20 25 30

Arg Ala Arg Ala Arg Ala Glu His Gln Asn Pro Ala Met Ile His Asp  
35 40 45

Ser Gly Phe Ala Gln Ser Trp Leu Phe Thr Gly Pro Pro Gly Ser Gly  
50 55 60

Arg Ser Val Ala Ala Lys Val Phe Ala Ala Thr Leu Val Cys Ser Asn  
65 70 75 80

Pro Asp Val Val Gly Cys Gly Gln Cys Glu Asp Cys Arg Ala Ala Met  
85 90 95

Gly Gly Ser His Pro Asp Ile Glu His Ile Val Pro Gln Gln Leu Ser  
100 105 110

Ile Gly Val Asp Ala Ala Arg Glu Val Ile Lys Ala Ala Ala Val Ser  
115 120 125

Pro Val Ala Gly Asn Trp Arg Val Val Ile Phe Glu Asn Ala Asp Arg  
130 135 140

Leu Thr Met Gln Ala Ala Asn Ala Leu Leu Lys Thr Val Glu Glu Pro  
145 150 155 160

Thr Glu Ser Thr Val Met Ile Leu Cys Ala Pro Thr Thr Asp Pro Arg  
165 170 175

Asp Ile Ala Ile Thr Leu Arg Ser Arg Cys Arg His Leu Tyr Ile Pro  
180 185 190

Thr Pro Ser Ile Ala Glu Val Ala Arg Ile Leu Val Ala Glu Gly Asn  
195 200 205

Val Ser Gln Ala Asp Ala Glu Leu Ala Ala Ala Ala Ser Gly Ala His  
210 215 220

Ile Gly Arg Ala Arg Tyr Leu Ala His Asn Asn Ala Ala Gln Arg Arg  
225 230 235 240

Arg Ala Ser Ile Leu Asn Leu Ala Glu Leu Ile Phe His Gly Asp Val  
245 250 255

Ala Phe Arg Ser Val Asn Thr Leu Val Lys Met Val Glu Thr Glu Ala  
260 265 270

Lys Asp Ser Asn Lys Glu Lys Glu Glu Gly Asp Leu Glu Ala Val Arg  
275 280 285

Ile Ser Leu Gly Met Ala Ala Lys Gly Lys Gly Val His Lys Ala Val  
290 295 300

Arg Gly Gly Ala Gly Asp Phe Lys Ala Leu Glu Asp Gln Gln Lys Leu  
305 310 315 320

Arg Arg Thr Arg Phe Leu Arg Asp Ser Leu Asp Leu Ala Leu Val Asp  
325 330 335

Leu Ala Gly Ile Tyr Arg Asp Ala Ile Ile Ile Ser Ser Gln Ala Gln  
340 345 350

Val Gly Leu Thr His Pro Asp Met Glu Gly Leu Ser Gln Glu Leu Ala  
355 360 365

Thr Lys Val Ser Gln  
370

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<223> RXA00214

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gggcaccocgg tgtcccatgc gactattagc gtttaggaacc atg aac tca cca agc 115  
Met Asn Ser Pro Ser  
1 5  
aat cca tct ccc acc gtc cca agc ttg gac acc acc aag atg ctc tcc 163  
Asn Pro Ser Pro Thr Val Pro Ser Leu Asp Thr Thr Lys Met Leu Ser  
10 15 20  
ttc gac ctg gaa aca acg ggc gtc aat ccc ttt gac acc cgc atc gtc 211  
Phe Asp Leu Glu Thr Thr Gly Val Asn Pro Phe Asp Thr Arg Ile Val  
25 30 35  
acc tcc gca atg gtt acg atc acc agc aaa ggc gct gag cct att gag 259  
Thr Ser Ala Met Val Thr Ile Thr Ser Lys Gly Ala Glu Pro Ile Glu  
40 45 50  
cta ttg gct gac ccc ggc atc gaa atc ccc gag gcc gcc act gca gtc 307  
Leu Leu Ala Asp Pro Gly Ile Glu Ile Pro Glu Ala Ala Thr Ala Val  
55 60 65  
cac ggc atc acc acc gaa cat gcc cgc gcc aac ggc cgt cgc cac gat 355  
His Gly Ile Thr Thr Glu His Ala Arg Ala Asn Gly Arg Pro His Asp  
70 75 80 85  
gag gtg tta gcc gaa acc atc tcc agg ctg cgc gcc ggc tgg cag gca 403  
Glu Val Leu Ala Glu Thr Ile Ser Arg Leu Arg Ala Gly Trp Gln Ala  
90 95 100  
gga ctg tgc gtc att gtc ttc aac gca tcc tat gac ctg acc gta tta 451  
Gly Leu Ser Val Ile Val Phe Asn Ala Ser Tyr Asp Leu Thr Val Leu  
105 110 115  
aga aac cat gat cca agc ttc acc atc gac gcc cta gtt tat gac ccc 499  
Arg Asn His Asp Pro Ser Phe Thr Ile Asp Gly Leu Val Tyr Asp Pro  
120 125 130  
ttc gtt atc gac aaa gtc aaa gac cgt tac cgc aaa ggc aag cgc aca 547

Phe Val Ile Asp Lys Val Lys Asp Arg Tyr Arg Lys Gly Lys Arg Thr  
 135 140 145  
 ctc act gat atg tgt gct cac tac gac gtt caa tta ggc aac gcc cac 595  
 Leu Thr Asp Met Cys Ala His Tyr Asp Val Gln Leu Gly Asn Ala His  
 150 155 160 165  
 gaa gcc acc tca gat gcg ctc gca gcc gca cgc atc gcc tgg aag cag 643  
 Glu Ala Thr Ser Asp Ala Leu Ala Ala Ala Arg Ile Ala Trp Lys Gln  
 170 175 180  
 gtc cgc ctg tgg cca gaa ctc acc aag atg aca ggc gaa gaa ctc atg 691  
 Val Arg Leu Trp Pro Glu Leu Thr Lys Met Thr Gly Glu Glu Leu Met  
 185 190 195  
 gag ttc caa gca gtc aac tat tac gag caa caa aag agc ttc cgt agc 739  
 Glu Phe Gln Ala Val Asn Tyr Tyr Glu Gln Gln Lys Ser Phe Arg Ser  
 200 205 210  
 tat ctc atc ggg caa ggc cgc gat gcc agc gat gtg aac act tca tgg 787  
 Tyr Leu Ile Gly Gln Gly Arg Asp Ala Ser Asp Val Asn Thr Ser Trp  
 215 220 225  
 cca gtg caa act gac ccc gca tcc taaaccgcgc cagatttcta cct 834  
 Pro Val Gln Thr Asp Pro Ala Ser  
 230 235  
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 <211> 237  
 <212> PRT  
 <213> Corynebacterium glutamicum  
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 Asp Thr Arg Ile Val Thr Ser Ala Met Val Thr Ile Thr Ser Lys Gly  
 35 40 45  
 Ala Glu Pro Ile Glu Leu Leu Ala Asp Pro Gly Ile Glu Ile Pro Glu  
 50 55 60  
 Ala Ala Thr Ala Val His Gly Ile Thr Thr Glu His Ala Arg Ala Asn  
 65 70 75 80  
 Gly Arg Pro His Asp Glu Val Leu Ala Glu Thr Ile Ser Arg Leu Arg  
 85 90 95  
 Ala Gly Trp Gln Ala Gly Leu Ser Val Ile Val Phe Asn Ala Ser Tyr  
 100 105 110  
 Asp Leu Thr Val Leu Arg Asn His Asp Pro Ser Phe Thr Ile Asp Gly  
 115 120 125  
 Leu Val Tyr Asp Pro Phe Val Ile Asp Lys Val Lys Asp Arg Tyr Arg  
 130 135 140

Lys Gly Lys Arg Thr Leu Thr Asp Met Cys Ala His Tyr Asp Val Gln  
 145 150 155 160  
 Leu Gly Asn Ala His Glu Ala Thr Ser Asp Ala Leu Ala Ala Arg  
 165 170 175  
 Ile Ala Trp Lys Gln Val Arg Leu Trp Pro Glu Leu Thr Lys Met Thr  
 180 185 190  
 Gly Glu Glu Leu Met Glu Phe Gln Ala Val Asn Tyr Tyr Glu Gln Gln  
 195 200 205  
 Lys Ser Phe Arg Ser Tyr Leu Ile Gly Gln Gly Arg Asp Ala Ser Asp  
 210 215 220  
 Val Asn Thr Ser Trp Pro Val Gln Thr Asp Pro Ala Ser  
 225 230 235

&lt;210&gt; 187

&lt;211&gt; 1203

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1180)

&lt;223&gt; RXA01255

&lt;400&gt; 187

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 aaatgctgtg aaacctctct aagcaactag agttgtaaaa atg agc acc act tcg 115  
 Met Ser Thr Thr Ser 5  
 1

gaa tca caa gat cac gcc gca aga atc gaa gct gag cgc caa gaa gct 163  
 Glu Ser Gln Asp His Ala Ala Arg Ile Glu Ala Glu Arg Gln Glu Ala  
 10 15 20

att gag gcg gct cct ttt gtt tcc gtc agc att caa tca agt gga atc 211  
 Ile Glu Ala Ala Pro Phe Val Ser Val Ser Ile Gln Ser Ser Gly Ile  
 25 30 35

cac cca tcg act tca cgc atg gtc acc att gat ttg gta acg etg tcc 259  
 His Pro Ser Thr Ser Arg Met Val Thr Ile Asp Leu Val Thr Leu Ser  
 40 45 50

cct aat ttg gag ccg gtg gaa act ttt cat gcc gtg ttg gat tcc aaa 307  
 Pro Asn Leu Glu Pro Val Glu Thr Phe His Ala Val Leu Asp Ser Lys  
 55 60 65

act gat cct ggc ccc ttc cac ctt cat ggc gtg aca gag gaa gaa ttt 355  
 Thr Asp Pro Gly Pro Phe His Leu His Gly Val Thr Glu Glu Glu Phe  
 70 75 80 85

gcc agc gct aag cgt ttc ggc cag att ttg aaa agc ttg gac cgc ctc 403  
 Ala Ser Ala Lys Arg Phe Gly Gln Ile Leu Lys Ser Leu Asp Arg Leu  
 90 95 100

atc gat ggt cgt acc ctg ttg atc cac aat gct gcg cga agt tgg gcc 451

Ile Asp Gly Arg Thr Leu Leu Ile His Asn Ala Ala Arg Ser Trp Gly  
 105 110 115 499

ttt att gtt tcc gaa gcc aag cgc gct atg aat gat gct gcg cgc gcc  
 Phe Ile Val Ser Glu Ala Lys Arg Ala Met Asn Asp Ala Ala Arg Ala  
 120 125 130

aat cgc aac agc aat cgt gga aat cgc cgt ggt ggt cgc gga cgc cgc  
 Asn Arg Asn Ser Asn Arg Gly Asn Arg Arg Gly Gly Arg Gly Arg Arg  
 135 140 145 547

agg cag cgc gtg ggg cac atc cca aag ccg ctg gtg atc gtc gat acg  
 Arg Gln Arg Val Gly His Ile Pro Lys Pro Leu Val Ile Val Asp Thr  
 150 155 160 165 595

ctt gca tcg gcg cgt cga caa gca atc gct tta gac gac gtg cgc atc  
 Leu Ala Ser Ala Arg Arg Gln Ala Ile Ala Leu Asp Asp Val Arg Ile  
 170 175 180 643

egg ggt gtc gca cac acc ctc ggc ctt gac gcg cct gca gcg gag gcg  
 Arg Gly Val Ala His Thr Leu Gly Leu Asp Ala Pro Ala Ala Glu Ala  
 185 190 195 691

tcg gtg gaa cgc gcg cag gtg tcg cac cgc cag ttg tgc cgc gaa gaa  
 Ser Val Glu Arg Ala Gln Val Ser His Arg Gln Leu Cys Arg Glu Glu  
 200 205 210 739

act ttg ctt gtg gca cgg ctt tat ggt gcg ttg aag cag tca gga ccg  
 Thr Leu Leu Val Ala Arg Leu Tyr Gly Ala Leu Lys Gln Ser Gly Pro  
 215 220 225 787

ctg gcg gaa atc gat ccc cag tcc ttg cgc gcc gat aag ttt ggt ttg  
 Leu Ala Glu Ile Asp Pro Gln Ser Leu Arg Ala Asp Lys Phe Gly Leu  
 230 235 240 245 835

caa cgc tcg atc atc cgg gtg cag gcg cag gaa gct tcg cca acg ctg  
 Gln Arg Ser Ile Ile Arg Val Gln Ala Gln Glu Ala Ser Pro Thr Leu  
 250 255 260 883

gtc aac cct ggt acg tat gag ccg gga aag acg ctg atc gct ggg atg  
 Val Asn Pro Gly Thr Tyr Glu Pro Gly Lys Thr Leu Ile Ala Gly Met  
 265 270 275 931

gaa gtt gtg gtc gcg ccg gaa att gag atg gat ccg gac atc att atc  
 Glu Val Val Val Ala Pro Glu Ile Glu Met Asp Pro Asp Ile Ile Ile  
 280 285 290 979

caa gcg tgc gtc gat gca gat ttg tcc tat tct gag aag ctc acc cgg  
 Gln Ala Cys Val Asp Ala Asp Leu Ser Tyr Ser Glu Lys Leu Thr Arg  
 295 300 305 1027

caa acc tca gtg gtg gtg tgc aat caa acc cgc gac att gac ggc aaa  
 Gln Thr Ser Val Val Val Cys Asn Gln Thr Arg Asp Ile Asp Gly Lys  
 310 315 320 325 1075

gcg atg cat gcc cag cgt aaa gga att ccg ctg ctg tcc gat gtt gcc  
 Ala Met His Ala Gln Arg Lys Gly Ile Pro Leu Leu Ser Asp Val Ala  
 330 335 340 1123

ttc tta gca gct gtt aaa agg gta aaa gaa ggg aag aaa gtg gac gtc  
 Phe Leu Ala Ala Val Lys Arg Val Lys Glu Gly Lys Lys Val Asp Val  
 1171

345

350

355

gaa aag cgc tagtgccact tgcttaacta gac  
 Glu Lys Arg  
 360

1203

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 <213> Corynebacterium glutamicum

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 20 25 30  
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 35 40 45  
 Leu Val Thr Leu Ser Pro Asn Leu Glu Pro Val Glu Thr Phe His Ala  
 50 55 60  
 Val Leu Asp Ser Lys Thr Asp Pro Gly Pro Phe His Leu His Gly Val  
 65 70 75 80  
 Thr Glu Glu Glu Phe Ala Ser Ala Lys Arg Phe Gly Gln Ile Leu Lys  
 85 90 95  
 Ser Leu Asp Arg Leu Ile Asp Gly Arg Thr Leu Leu Ile His Asn Ala  
 100 105 110  
 Ala Arg Ser Trp Gly Phe Ile Val Ser Glu Ala Lys Arg Ala Met Asn  
 115 120 125  
 Asp Ala Ala Arg Ala Asn Arg Asn Ser Asn Arg Gly Asn Arg Arg Gly  
 130 135 140  
 Gly Arg Gly Arg Arg Arg Gln Arg Val Gly His Ile Pro Lys Pro Leu  
 145 150 155 160  
 Val Ile Val Asp Thr Leu Ala Ser Ala Arg Arg Gln Ala Ile Ala Leu  
 165 170 175  
 Asp Asp Val Arg Ile Arg Gly Val Ala His Thr Leu Gly Leu Asp Ala  
 180 185 190  
 Pro Ala Ala Glu Ala Ser Val Glu Arg Ala Gln Val Ser His Arg Gln  
 195 200 205  
 Leu Cys Arg Glu Glu Thr Leu Leu Val Ala Arg Leu Tyr Gly Ala Leu  
 210 215 220  
 Lys Gln Ser Gly Pro Leu Ala Glu Ile Asp Pro Gln Ser Leu Arg Ala  
 225 230 235 240  
 Asp Lys Phe Gly Leu Gln Arg Ser Ile Ile Arg Val Gln Ala Gln Glu  
 245 250 255

Ala Ser Pro Thr Leu Val Asn Pro Gly Thr Tyr Glu Pro Gly Lys Thr  
260 265 270

Leu Ile Ala Gly Met Glu Val Val Val Ala Pro Glu Ile Glu Met Asp  
275 280 285

Pro Asp Ile Ile Ile Gln Ala Cys Val Asp Ala Asp Leu Ser Tyr Ser  
290 295 300

Glu Lys Leu Thr Arg Gln Thr Ser Val Val Val Cys Asn Gln Thr Arg  
305 310 315 320

Asp Ile Asp Gly Lys Ala Met His Ala Gln Arg Lys Gly Ile Pro Leu  
325 330 335

Leu Ser Asp Val Ala Phe Leu Ala Ala Val Lys Arg Val Lys Glu Gly  
340 345 350

Lys Lys Val Asp Val Glu Lys Arg  
355 360

<210> 189

<211> 913

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(913)

<223> RXN00066

<400> 189

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tcgaccggca agttttggtg aactagtgtg gcagtcgcaa gtg act gac cct ctg 115  
Val Thr Asp Pro Leu  
1 5

tcc gca gct ttg gat agc ggg cgc atc aac cat gcg tac ctt ttt tcg 163  
Ser Ala Ala Leu Asp Ser Gly Arg Ile Asn His Ala Tyr Leu Phe Ser  
10 15 20

ggt ccg cgt ggt tgt ggc aag acg tcg tcg gca cgc atc ctt gcc cgg 211  
Gly Pro Arg Gly Cys Gly Lys Thr Ser Ser Ala Arg Ile Leu Ala Arg  
25 30 35

tcc etc aac tgc gtg gaa ggc cca act tcc acg ccg tgt ggg gtg tgt 259  
Ser Leu Asn Cys Val Glu Gly Pro Thr Ser Thr Pro Cys Gly Val Cys  
40 45 50

aat tct tgc gta gcg ctg gcc ccg ggt ggc cct gga acc ctt gat gta 307  
Asn Ser Cys Val Ala Leu Ala Pro Gly Gly Pro Gly Thr Leu Asp Val  
55 60 65

aca gag etc gac gcc gcg agt aac aat ggt gtc gat gac atg cgt gaa 355  
Thr Glu Leu Asp Ala Ala Ser Asn Asn Gly Val Asp Asp Met Arg Glu  
70 75 80 85

ctg cgc gaa cgc gcg aac tac gcc ccg gcg gaa tct cgc tac cgc gtg 403  
Leu Arg Glu Arg Ala Asn Tyr Ala Pro Ala Glu Ser Arg Tyr Arg Val

	90	95	100	
ttc atc att gac gaa gcc cac atg atc agt acc caa ggc ttc aac gcc				451
Phe Ile Ile Asp Glu Ala His Met Ile Ser Thr Gln Gly Phe Asn Ala				
	105	110	115	
ttg ctg aaa atc gtt gaa gag cca cca gcg cac ctg att ttc atc ttc				499
Leu Leu Lys Ile Val Glu Glu Pro Pro Ala His Leu Ile Phe Ile Phe				
	120	125	130	
gcc acc acc gag cgg gac aaa atg atc ggt acg atc cgt tcc cgc acg				547
Ala Thr Thr Glu Pro Asp Lys Met Ile Gly Thr Ile Arg Ser Arg Thr				
	135	140	145	
cac aat tac cca ttc cgc ctg ctc acc cca ggg gat atg cgc aaa gtg				595
His Asn Tyr Pro Phe Arg Leu Leu Thr Pro Gly Asp Met Arg Lys Val				
	150	155	160	165
ctg aaa aat gcg gtc gat ggc gaa ggc gtc cac gtc gac gat tcc gtt				643
Leu Lys Asn Ala Val Asp Gly Glu Gly Val His Val Asp Asp Ser Val				
	170	175	180	
tac cca ctg gtc atc cgc gcc ggc ggc ggc agc ccc cgc gac agc ctc				691
Tyr Pro Leu Val Ile Arg Ala Gly Gly Ser Pro Arg Asp Ser Leu				
	185	190	195	
tcc atc ctc gac cag ctc atc gcc ggc tgg ggc cgg gag ggc ttg aca				739
Ser Ile Leu Asp Gln Leu Ile Ala Gly Ser Gly Pro Glu Gly Leu Thr				
	200	205	210	
tat gag cgc gcc ttg cgg ctg ctc ggt gtc aca agc ttc acg ctt atc				787
Tyr Glu Arg Ala Leu Pro Leu Leu Gly Val Thr Ser Phe Thr Leu Ile				
	215	220	225	
gac gat tgg atc cat gcc ctt gca tct aaa gac aac gca agc atg ttc				835
Asp Asp Ser Ile His Ala Leu Ala Ser Lys Asp Asn Ala Ser Met Phe				
	230	235	240	245
acc acg atc gat aac gtc atc gaa gaa ggc ctc gaa cgg cga cgc ttc				883
Thr Thr Ile Asp Asn Val Ile Glu Glu Gly Leu Glu Pro Arg Arg Phe				
	250	255	260	
acg atc gac ttt ctt tgg acc cgc tcc ggg				913
Thr Ile Asp Phe Leu Ser Thr Arg Ser Gly				
	265	270		
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Val Thr Asp Pro Leu Ser Ala Ala Leu Asp Ser Gly Arg Ile Asn His				
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Ala Tyr Leu Phe Ser Gly Pro Arg Gly Cys Gly Lys Thr Ser Ser Ala				
20	25	30		
Arg Ile Leu Ala Arg Ser Leu Asn Cys Val Glu Gly Pro Thr Ser Thr				
35	40	45		



Pro Cys Gly Val Cys Asn Ser Cys Val Ala Leu Ala Pro Gly Gly Pro  
50 55 60

Gly Thr Leu Asp Val Thr Glu Leu Asp Ala Ala Ser Asn Asn Gly Val  
65 70 75 80

Asp Asp Met Arg Glu Leu Arg Glu Arg Ala Asn Tyr Ala Pro Ala Glu  
85 90 95

Ser Arg Tyr Arg Val Phe Ile Ile Asp Glu Ala His Met Ile Ser Thr  
100 105 110

Gln Gly Phe Asn Ala Leu Leu Lys Ile Val Glu Glu Pro Pro Ala His  
115 120 125

Leu Ile Phe Ile Phe Ala Thr Thr Glu Pro Asp Lys Met Ile Gly Thr  
130 135 140

Ile Arg Ser Arg Thr His Asn Tyr Pro Phe Arg Leu Leu Thr Pro Gly  
145 150 155 160

Asp Met Arg Lys Val Leu Lys Asn Ala Val Asp Gly Glu Gly Val His  
165 170 175

Val Asp Asp Ser Val Tyr Pro Leu Val Ile Arg Ala Gly Gly Gly Ser  
180 185 190

Pro Arg Asp Ser Leu Ser Ile Leu Asp Gln Leu Ile Ala Gly Ser Gly  
195 200 205

Pro Glu Gly Leu Thr Tyr Glu Arg Ala Leu Pro Leu Leu Gly Val Thr  
210 215 220

Ser Phe Thr Leu Ile Asp Asp Ser Ile His Ala Leu Ala Ser Lys Asp  
225 230 235 240

Asn Ala Ser Met Phe Thr Thr Ile Asp Asn Val Ile Glu Glu Gly Leu  
245 250 255

Glu Pro Arg Arg Phe Thr Ile Asp Phe Leu Ser Thr Arg Ser Gly  
260 265 270

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<211> 913

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(913)

<223> PRXA00066

<400> 191

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tcgaccggca agttttgggtg aactagttgg gcagtcgcaa gtg act gac cct ctg 115  
Val Thr Asp Pro Leu

1

5

tcc gca gct ttg gat agc ggg cgc atc aac cat gcg tac ctt ttt tcg 163  
 Ser Ala Ala Leu Asp Ser Gly Arg Ile Asn His Ala Tyr Leu Phe Ser  
                     10                    15

ggt ccg cgt ggt tgt ggc aag acg tcg tcg gca cgc atc ctt gcc cgg 211  
 Gly Pro Arg Gly Cys Gly Lys Thr Ser Ser Ala Arg Ile Leu Ala Arg  
                     25                    30                    35

tcc ctc aac tgc gtg gaa ggc cca act tcc acg ccg tgt ggg gtg tgt 259  
 Ser Leu Asn Cys Val Glu Gly Pro Thr Ser Thr Pro Cys Gly Val Cys  
                     40                    45                    50

aat tct tgc gta gcg ctg gcc ccg ggt ggc cct gga acc ctt gat gta 307  
 Asn Ser Cys Val Ala Leu Ala Pro Gly Gly Pro Gly Thr Leu Asp Val  
                     55                    60                    65

aca gag ctc gac gcc gcg agt aac aat ggt gtc gat gac atg cgt gaa 355  
 Thr Glu Leu Asp Ala Ala Ser Asn Asn Gly Val Asp Asp Met Arg Glu  
                     70                    75                    80                    85

ctg cgc gaa cgc gcg aac tac gcc ccg gcg gaa tct cgc tac cgc gtg 403  
 Leu Arg Glu Arg Ala Asn Tyr Ala Pro Ala Glu Ser Arg Tyr Arg Val  
                     90                    95                    100

ttc atc att gac gaa gcc cac atg atc agt acc caa ggc ttc aac gcc 451  
 Phe Ile Ile Asp Glu Ala His Met Ile Ser Thr Gln Gly Phe Asn Ala  
                     105                    110                    115

ttg ctg aaa atc gtt gaa gag cca cca gcg cac ctg att ttc atc ttc 499  
 Leu Leu Lys Ile Val Glu Glu Pro Pro Ala His Leu Ile Phe Ile Phe  
                     120                    125                    130

gcc acc acc gag ccg gac aaa atg atc ggt acg atc cgt tcc cgc acg 547  
 Ala Thr Thr Glu Pro Asp Lys Met Ile Gly Thr Ile Arg Ser Arg Thr  
                     135                    140                    145

cac aat tac cca ttc cgc ctg ctc acc cca ggg gat atg cgc aaa gtg 595  
 His Asn Tyr Pro Phe Arg Leu Leu Thr Pro Gly Asp Met Arg Lys Val  
                     150                    155                    160                    165

ctg aaa aat gcg gtc gat ggc gaa ggc gtc cac gtc gac gat tcc gtt 643  
 Leu Lys Asn Ala Val Asp Gly Glu Gly Val His Val Asp Asp Ser Val  
                     170                    175                    180

tac cca ctg gtc atc cgc gcc ggc ggc ggc agc ccc cgc gac agc ctc 691  
 Tyr Pro Leu Val Ile Arg Ala Gly Gly Gly Ser Pro Arg Asp Ser Leu  
                     185                    190                    195

tcc atc ctc gac cag ctc atc gcc ggc tcg ggc ccg gag ggc ttg aca 739  
 Ser Ile Leu Asp Gln Leu Ile Ala Gly Ser Gly Pro Glu Gly Leu Thr  
                     200                    205                    210

tat gag cgc gcc ttg ccg ctg ctc ggt gtc aca agc ttc acg ctt atc 787  
 Tyr Glu Arg Ala Leu Pro Leu Leu Gly Val Thr Ser Phe Thr Leu Ile  
                     215                    220                    225

gac gat tcg atc cat gcc ctt gca tct aaa gac aac gca agc atg ttc 835  
 Asp Asp Ser Ile His Ala Leu Ala Ser Lys Asp Asn Ala Ser Met Phe  
                     230                    235                    240                    245

acc acg atc gat aac gtc atc gaa gaa ggc ctc gaa ccg cga cgc ttc 883

Thr Thr Ile Asp Asn Val Ile Glu Glu Gly Leu Glu Pro Arg Arg Phe  
250 255 260

acg atc gac ctt cct tcc gac ccg ctc cgg  
Thr Ile Asp Leu Pro Ser Asp Pro Leu Arg  
265 270

913

&lt;210&gt; 192

&lt;211&gt; 271

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 192

Val Thr Asp Pro Leu Ser Ala Ala Leu Asp Ser Gly Arg Ile Asn His  
1 5 10 15

Ala Tyr Leu Phe Ser Gly Pro Arg Gly Cys Gly Lys Thr Ser Ser Ala  
20 25 30

Arg Ile Leu Ala Arg Ser Leu Asn Cys Val Glu Gly Pro Thr Ser Thr  
35 40 45

Pro Cys Gly Val Cys Asn Ser Cys Val Ala Leu Ala Pro Gly Gly Pro  
50 55 60

Gly Thr Leu Asp Val Thr Glu Leu Asp Ala Ala Ser Asn Asn Gly Val  
65 70 75 80

Asp Asp Met Arg Glu Leu Arg Glu Arg Ala Asn Tyr Ala Pro Ala Glu  
85 90 95

Ser Arg Tyr Arg Val Phe Ile Ile Asp Glu Ala His Met Ile Ser Thr  
100 105 110

Gln Gly Phe Asn Ala Leu Leu Lys Ile Val Glu Glu Pro Pro Ala His  
115 120 125

Leu Ile Phe Ile Phe Ala Thr Thr Glu Pro Asp Lys Met Ile Gly Thr  
130 135 140

Ile Arg Ser Arg Thr His Asn Tyr Pro Phe Arg Leu Leu Thr Pro Gly  
145 150 155 160

Asp Met Arg Lys Val Leu Lys Asn Ala Val Asp Gly Glu Gly Val His  
165 170 175

Val Asp Asp Ser Val Tyr Pro Leu Val Ile Arg Ala Gly Gly Ser Gly  
180 185 190

Pro Arg Asp Ser Leu Ser Ile Leu Asp Gln Leu Ile Ala Gly Ser Gly  
195 200 205

Pro Glu Gly Leu Thr Tyr Glu Arg Ala Leu Pro Leu Leu Gly Val Thr  
210 215 220

Ser Phe Thr Leu Ile Asp Asp Ser Ile His Ala Leu Ala Ser Lys Asp  
225 230 235 240

Asn Ala Ser Met Phe Thr Thr Ile Asp Asn Val Ile Glu Glu Gly Leu  
245 250 255

cgc acc tca atc atg ctg acc gaa gcg cga gtt ttg gga ctg cga ggc 595  
 Arg Thr Ser Ile Met Leu Thr Glu Ala Arg Val Leu Gly Leu Arg Gly  
 155 160 165

Ile Leu Val Lys Val Leu Ala Glu Glu Thr Gly Leu Gln Leu Lys Val

195	200	205
Glu Cys Ile Val Gly Thr Asn Pro Ala Glu Ala Gly Phe		
210	215	220
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<211> 409		
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<213> <i>Corynebacterium glutamicum</i>		
 <220>		
<221> CDS		
<222> (101)..(409)		
<223> PRXA01637		
 <400> 195		
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cgccgggaac ccggaamccg scaggraamc agtggtggaa	gtg cgg gag gcg agc	115
	Val Arg Glu Ala Ser	
	1 5	
gtc gaa aag cag cct gca agc agt gat ccc ctc gaa acc att cga agc		163
Val Glu Lys Gln Pro Ala Ser Ser Asp Pro Leu Glu Thr Ile Arg Ser		
10 15 20		
cgc tgg tca gag ctg cgc aac atc gtg gaa aaa caa agt gtg cgc acc		211
Arg Trp Ser Glu Leu Arg Asn Ile Val Glu Lys Gln Ser Val Arg Thr		
25 30 35		
tca atc atg ctg acc gaa gcg cga gtt ttg gga ctg cga ggc gat acc		259
Ser Ile Met Leu Thr Glu Ala Arg Val Leu Gly Leu Arg Gly Asp Thr		
40 45 50		
ctc gtg ctc ggt cac agc acc ggg gcg ttg gct gcg cgt ttg aac gct		307
Leu Val Leu Gly His Ser Thr Gly Ala Leu Ala Arg Leu Asn Ala		
55 60 65		
gct gat cac aac gga att ttg gtc aag gtg ttg gct gag gaa act ggt		355
Ala Asp His Asn Gly Ile Leu Val Lys Val Leu Ala Glu Glu Thr Gly		
70 75 80 85		
ctg cag ctc aag gtc gaa tgc att gtg ggc acg aac cca gcc gaa gct		403
Leu Gln Leu Lys Val Glu Cys Ile Val Gly Thr Asn Pro Ala Glu Ala		
90 95 100		
gga ttt		409
Gly Phe		

&lt;210&gt; 196

&lt;211&gt; 103

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 196

Val Arg Glu Ala Ser	Val Glu Lys Gln	Pro Ala Ser Ser Asp	Pro Leu
1	5	10	15

Glu Thr Ile Arg Ser Arg Trp Ser Glu Leu Arg Asn Ile Val Glu Lys  
 20 25 30  
 Gln Ser Val Arg Thr Ser Ile Met Leu Thr Glu Ala Arg Val Leu Gly  
 35 40 45  
 Leu Arg Gly Asp Thr Leu Val Leu Gly His Ser Thr Gly Ala Leu Ala  
 50 55 60  
 Ala Arg Leu Asn Ala Ala Asp His Asn Gly Ile Leu Val Lys Val Leu  
 65 70 75 80  
 Ala Glu Glu Thr Gly Leu Gln Leu Lys Val Glu Cys Ile Val Gly Thr  
 85 90 95  
 Asn Pro Ala Glu Ala Gly Phe  
 100

&lt;210&gt; 197

&lt;211&gt; 1683

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1660)

&lt;223&gt; RXA00212

&lt;400&gt; 197

ttagagcgtg ccgctactcg tggatgatggt cgcgtgggagc aggcacatcac ggccaatgct 60  
 cgcgtgatcg aagatataccc gcaccagctt cagggcactg atg aat atc ctg tgc 115  
 Met Asn Ile Leu Cys  
 1 5  
 ctg ctg tgc tgg aaa ttc gcg gtg agg tgt tca tca ctg tgg agg att 163  
 Leu Leu Cys Trp Lys Phe Ala Val Arg Cys Ser Ser Leu Trp Arg Ile  
 10 15 20  
 tcc cag gag gtc aac gcg cag cgc att gct gat ggt ggc aag ccg ttt 211  
 Ser Gln Glu Val Asn Ala Gln Arg Ile Ala Asp Gly Gly Lys Pro Phe  
 25 30 35  
 gcc aac ccg cgt aat gct gcg gct ggt tct ctg cgt cag aaa aat att 259  
 Ala Asn Pro Arg Asn Ala Ala Ala Gly Ser Leu Arg Gln Lys Asn Ile  
 40 45 50  
 gag gac gtg aag aag cgc cgc ctg cgg atg atc agc cat ggc atc ggt 307  
 Glu Asp Val Lys Lys Arg Arg Leu Arg Met Ile Ser His Gly Ile Gly  
 55 60 65  
 ttc act gaa ggc ttt agc cct gcg tct cag cat gat gcg tat ctg gca 355  
 Phe Thr Glu Gly Phe Ser Pro Ala Ser Gln His Asp Ala Tyr Leu Ala  
 70 75 80 85  
 ttg gct gcc tgg ggt ttg ccc acc tcg ccg tac aca gag gct gtg act 403  
 Leu Ala Ala Trp Gly Leu Pro Thr Ser Pro Tyr Thr Glu Ala Val Thr  
 90 95 100  
 gat cca gaa gat gtg gtg aaa aag gtc agc tac tgg gct gat cac cgc 451

Asp	Pro	Glu	Asp	Val	Val	Lys	Lys	Val	Ser	Tyr	Trp	Ala	Asp	His	Arg	
			105					110					115			
cac	gac	gca	ctc	cat	gag	atg	gat	ggc	ctg	gtg	att	aag	gtc	gat	gac	499
His	Asp	Ala	Leu	His	Glu	Met	Asp	Gly	Leu	Val	Ile	Lys	Val	Asp	Asp	
		120					125					130				
atc	gca	tct	cag	cgt	gct	ttg	ggc	tcc	acc	agc	cgc	gcg	cct	cgc	tgg	547
Ile	Ala	Ser	Gln	Arg	Ala	Leu	Gly	Ser	Thr	Ser	Arg	Ala	Pro	Arg	Trp	
		135				140					145					
gcc	att	gcg	tac	aag	tac	cct	ccg	gag	gag	gtc	acc	acc	aag	ctg	ctt	595
Ala	Ile	Ala	Tyr	Lys	Tyr	Pro	Pro	Glu	Glu	Val	Thr	Thr	Lys	Leu	Leu	
		150			155					160					165	
gat	att	cag	gtt	ggc	gtt	ggc	cgc	acc	ggc	cgt	gtc	acc	cca	ttc	gcg	643
Asp	Ile	Gln	Val	Gly	Val	Gly	Arg	Thr	Gly	Arg	Val	Thr	Pro	Phe	Ala	
			170						175					180		
gtc	atg	gag	ccg	gtt	ctt	gtt	gca	gga	tca	acg	gtg	tct	atg	gcg	acg	691
Val	Met	Glu	Pro	Val	Leu	Val	Ala	Gly	Ser	Thr	Val	Ser	Met	Ala	Thr	
			185					190					195			
ctg	cat	aac	cag	agc	gaa	gtc	aag	cgt	aaa	ggc	gtg	ctc	atc	ggc	gac	739
Leu	His	Asn	Gln	Ser	Glu	Val	Lys	Arg	Lys	Gly	Val	Leu	Ile	Gly	Asp	
		200						205				210				
acc	gtg	gtt	atc	cgc	aag	gcg	ggc	gag	gtt	atc	cca	gag	gtg	ctt	ggc	787
Thr	Val	Val	Ile	Arg	Lys	Ala	Gly	Glu	Val	Ile	Pro	Glu	Val	Leu	Gly	
		215				220					225					
cct	gtc	gta	gag	ctt	cgt	gac	ggc	aca	gag	cgc	gag	tac	atc	ttc	cca	835
Pro	Val	Val	Glu	Leu	Arg	Asp	Gly	Thr	Glu	Arg	Glu	Tyr	Ile	Phe	Pro	
				235						240				245		
acg	ctg	tgc	cct	gaa	tgc	ggc	acc	cgt	ctg	gcg	ccc	gcg	aag	gcc	gat	883
Thr	Leu	Cys	Pro	Glu	Cys	Gly	Thr	Arg	Leu	Ala	Pro	Ala	Lys	Ala	Asp	
			250						255					260		
gac	gtg	gat	tgg	cgt	tgc	ccc	aac	atg	caa	agc	tgt	cca	ggc	cag	ctg	931
Asp	Val	Asp	Trp	Arg	Cys	Pro	Asn	Met	Gln	Ser	Cys	Pro	Gly	Gln	Leu	
		265						270					275			
tcc	acg	cgt	ttg	acc	tac	ctt	gct	ggc	cgt	ggc	gct	ttt	gat	att	gaa	979
Ser	Thr	Arg	Leu	Thr	Tyr	Leu	Ala	Gly	Arg	Gly	Ala	Phe	Asp	Ile	Glu	
		280					285					290				
gca	ttg	ggc	gaa	aag	ggc	gct	gaa	gac	ctc	att	cgc	acc	ggc	att	ttg	1027
Ala	Leu	Gly	Glu	Lys	Gly	Ala	Glu	Asp	Leu	Ile	Arg	Thr	Gly	Ile	Leu	
		295				300					305					
ctt	gac	gag	tct	ggc	ctg	ttc	gac	ctc	aca	gag	gac	gat	ctg	ctg	agc	1075
Leu	Asp	Glu	Ser	Gly	Leu	Phe	Asp	Leu	Thr	Glu	Asp	Asp	Leu	Leu	Ser	
		310			315					320				325		
tcc	aat	gtc	tac	acc	acc	aac	gcc	ggc	aaa	gta	aat	gcc	agc	ggc	aag	1123
Ser	Asn	Val	Tyr	Thr	Thr	Asn	Ala	Gly	Lys	Val	Asn	Ala	Ser	Gly	Lys	
				330					335					340		
aaa	ctg	ctg	gac	aac	ctg	caa	aaa	tcc	aag	cag	acc	gac	ctc	tgg	cga	1171
Lys	Leu	Leu	Asp	Asn	Leu	Gln	Lys	Ser	Lys	Gln	Thr	Asp	Leu	Trp	Arg	



345	350	355	
gtc ctc gtg gca tta tct atc agg cac gta ggc ccc acc gca gcg cgc Val Leu Val Ala Leu Ser Ile Arg His Val Gly Pro Thr Ala Ala Arg 360 365 370			1219
gcc ctt gca ggt cgc tac cac tcc atc cag gcg ctt atc gac gcc ccc Ala Leu Ala Gly Arg Tyr His Ser Ile Gln Ala Leu Ile Asp Ala Pro 375 380 385			1267
ctc gag gaa ctc tcc gaa acc gat gga gta ggt acc atc att gcc caa Leu Glu Glu Leu Ser Glu Thr Asp Gly Val Gly Thr Ile Ile Ala Gln 390 395 400 405			1315
tcc ttc aag gac tgg ttc gag gtt gat tgg cac aag gcc atc gtg gac Ser Phe Lys Asp Trp Phe Glu Val Asp Trp His Lys Ala Ile Val Asp 410 415 420			1363
aag tgg gca gcc gct ggt gtg act atg gag gaa gaa gta ggg gag gtc Lys Trp Ala Ala Gly Val Thr Met Glu Glu Glu Val Gly Glu Val 425 430 435			1411
gct gaa caa acc ctt gaa ggc cta acc atc gtg gtc acc gga ggg ttg Ala Glu Gln Thr Leu Glu Gly Leu Thr Ile Val Val Thr Gly Gly Leu 440 445 450			1459
gaa ggc ttc acc aga gat tgc gtg aag gaa gcc atc atc tcc cgt ggc Glu Gly Phe Thr Arg Asp Ser Val Lys Glu Ala Ile Ile Ser Arg Gly 455 460 465			1507
gga aaa gcc tct gga tct gtc tgc aag aaa act gac tac gtg gtg att Gly Lys Ala Ser Gly Ser Val Ser Lys Lys Thr Asp Tyr Val Val Ile 470 475 480 485			1555
ggt gaa aac gca ggt tcc aag gcc acc aag gca gaa gaa cta ggg ctg Gly Glu Asn Ala Gly Ser Lys Ala Thr Lys Ala Glu Glu Leu Gly Leu 490 495 500			1603
cgc att ctg gat gag gca gga ttc gtc cgt ttg ctc aat acc ggc tca Arg Ile Leu Asp Glu Ala Gly Phe Val Arg Leu Leu Asn Thr Gly Ser 505 510 515			1651
gct gac gaa tagtgcaca tgaaaatgcc cca Ala Asp Glu 520			1683
<210> 198			
<211> 520			
<212> PRT			
<213> Corynebacterium glutamicum			
<400> 198			
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Ser Leu Trp Arg Ile Ser Gln Glu Val Asn Ala Gln Arg Ile Ala Asp 20 25 30			
Gly Gly Lys Pro Phe Ala Asn Pro Arg Asn Ala Ala Ala Gly Ser Leu 35 40 45			

Arg Gln Lys Asn Ile Glu Asp Val Lys Lys Arg Arg Leu Arg Met Ile  
 50 55 60  
 Ser His Gly Ile Gly Phe Thr Glu Gly Phe Ser Pro Ala Ser Gln His  
 65 70 75 80  
 Asp Ala Tyr Leu Ala Leu Ala Ala Trp Gly Leu Pro Thr Ser Pro Tyr  
 85 90 95  
 Thr Glu Ala Val Thr Asp Pro Glu Asp Val Val Lys Lys Val Ser Tyr  
 100 105 110  
 Trp Ala Asp His Arg His Asp Ala Leu His Glu Met Asp Gly Leu Val  
 115 120 125  
 Ile Lys Val Asp Asp Ile Ala Ser Gln Arg Ala Leu Gly Ser Thr Ser  
 130 135 140  
 Arg Ala Pro Arg Trp Ala Ile Ala Tyr Lys Tyr Pro Pro Glu Glu Val  
 145 150 155 160  
 Thr Thr Lys Leu Leu Asp Ile Gln Val Gly Val Gly Arg Thr Gly Arg  
 165 170 175  
 Val Thr Pro Phe Ala Val Met Glu Pro Val Leu Val Ala Gly Ser Thr  
 180 185 190  
 Val Ser Met Ala Thr Leu His Asn Gln Ser Glu Val Lys Arg Lys Gly  
 195 200 205  
 Val Leu Ile Gly Asp Thr Val Val Ile Arg Lys Ala Gly Glu Val Ile  
 210 215 220  
 Pro Glu Val Leu Gly Pro Val Val Glu Leu Arg Asp Gly Thr Glu Arg  
 225 230 235 240  
 Glu Tyr Ile Phe Pro Thr Leu Cys Pro Glu Cys Gly Thr Arg Leu Ala  
 245 250 255  
 Pro Ala Lys Ala Asp Asp Val Asp Trp Arg Cys Pro Asn Met Gln Ser  
 260 265 270  
 Cys Pro Gly Gln Leu Ser Thr Arg Leu Thr Tyr Leu Ala Gly Arg Gly  
 275 280 285  
 Ala Phe Asp Ile Glu Ala Leu Gly Glu Lys Gly Ala Glu Asp Leu Ile  
 290 295 300  
 Arg Thr Gly Ile Leu Leu Asp Glu Ser Gly Leu Phe Asp Leu Thr Glu  
 305 310 315 320  
 Asp Asp Leu Leu Ser Ser Asn Val Tyr Thr Thr Asn Ala Gly Lys Val  
 325 330 335  
 Asn Ala Ser Gly Lys Lys Leu Leu Asp Asn Leu Gln Lys Ser Lys Gln  
 340 345 350  
 Thr Asp Leu Trp Arg Val Leu Val Ala Leu Ser Ile Arg His Val Gly  
 355 360 365

Pro Thr Ala Ala Arg Ala Leu Ala Gly Arg Tyr His Ser Ile Gln Ala  
370 375 380

Leu Ile Asp Ala Pro Leu Glu Glu Leu Ser Glu Thr Asp Gly Val Gly  
385 390 395 400

Thr Ile Ile Ala Gln Ser Phe Lys Asp Trp Phe Glu Val Asp Trp His  
405 410 415

Lys Ala Ile Val Asp Lys Trp Ala Ala Ala Gly Val Thr Met Glu Glu  
420 425 430

Glu Val Gly Glu Val Ala Glu Gln Thr Leu Glu Gly Leu Thr Ile Val  
435 440 445

Val Thr Gly Gly Leu Glu Gly Phe Thr Arg Asp Ser Val Lys Glu Ala  
450 455 460

Ile Ile Ser Arg Gly Gly Lys Ala Ser Gly Ser Val Ser Lys Lys Thr  
465 470 475 480

Asp Tyr Val Val Ile Gly Glu Asn Ala Gly Ser Lys Ala Thr Lys Ala  
485 490 495

Glu Glu Leu Gly Leu Arg Ile Leu Asp Glu Ala Gly Phe Val Arg Leu  
500 505 510

Leu Asn Thr Gly Ser Ala Asp Glu  
515 520

<210> 199

<211> 696

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(673)

<223> RXA00213

<400> 199

aggtctgcac ccattccatc gcgaattttg acgtgagttt tagctttccg agcacctgtg 60

cgaaatggccc tgtccaccct taggggttaga atcggaacc gtg act gaa gat aat 115  
Val Thr Glu Asp Asn  
1 5

gct caa ctg cgt aga acg tgg aac gac tta gcc gag aag gtt cgt tat 163  
Ala Gln Leu Arg Arg Thr Trp Asn Asp Leu Ala Glu Lys Val Arg Tyr  
10 15 20

cac cga gat cgt tat tac aac gaa cag cca gag atc cct gat gct gat 211  
His Arg Asp Arg Tyr Tyr Asn Glu Gln Pro Glu Ile Pro Asp Ala Asp  
25 30 35

ttt gat gcg ctt ttt aag cag ctt cag cag ttg gaa gaa gac cac ccg 259  
Phe Asp Ala Leu Phe Lys Gln Leu Gln Gln Leu Glu Glu Asp His Pro  
40 45 50

gag ctc gcc gtc cct gat agc ccc acc atg gtt gtg ggc gct ccg gtg 307

Glu Leu Ala Val Pro Asp Ser Pro Thr Met Val Val Gly Ala Pro Val  
 55 60 65  
 gca gag caa tca agc ttt gac aat gtt gag cac ttg gag cga atg ctc 355  
 Ala Glu Gln Ser Ser Phe Asp Asn Val Glu His Leu Glu Arg Met Leu  
 70 75 80 85  
 agc ttg gac aat gtt ttt gat gag cag gag ttg cgt gat tgg ttg ggc 403  
 Ser Leu Asp Asn Val Phe Asp Glu Gln Glu Leu Arg Asp Trp Leu Gly  
 90 95 100  
 agg acg cca gcc aag cag tat ttg acg gag ttg aaa att gat ggc ttg 451  
 Arg Thr Pro Ala Lys Gln Tyr Leu Thr Glu Leu Lys Ile Asp Gly Leu  
 105 110 115  
 tcc atc gac ttg gtg tat cgc aat ggc cag tta gag cgt gcc gct act 499  
 Ser Ile Asp Ala Leu Val Tyr Arg Asn Gly Gln Leu Glu Arg Ala Ala Thr  
 120 125 130  
 cgt ggt gat ggt cgc gtg ggc gag gac atc acg gcc aat gct cgc gtg 547  
 Arg Gly Asp Gly Arg Val Gly Glu Asp Ile Thr Ala Asn Ala Arg Val  
 135 140 145  
 atc gaa gat atc ccg cac cag ctt cag ggc act gat gaa tat cct gtg 595  
 Ile Glu Asp Ile Pro His Gln Leu Gln Gly Thr Asp Glu Tyr Pro Val  
 150 155 160 165  
 cct gct gtg ctg gaa att cgc ggt gag gtg ttc atc act gtg gag gat 643  
 Pro Ala Val Leu Glu Ile Arg Gly Glu Val Phe Ile Thr Val Glu Asp  
 170 175 180  
 ttc cca gga ggt caa cgc gca gcg cat tgc tgatggtggc aagccgtttg 693  
 Phe Pro Gly Gly Gln Arg Ala Ala His Cys  
 185 190  
 cca 696  
 <210> 200  
 <211> 191  
 <212> PRT  
 <213> Corynebacterium glutamicum  
 <400> 200  
 Val Thr Glu Asp Asn Ala Gln Leu Arg Arg Thr Trp Asn Asp Leu Ala  
 1 5 10 15  
 Glu Lys Val Arg Tyr His Arg Asp Arg Tyr Tyr Asn Glu Gln Pro Glu  
 20 25 30  
 Ile Pro Asp Ala Asp Phe Asp Ala Leu Phe Lys Gln Leu Gln Gln Leu  
 35 40 45  
 Glu Glu Asp His Pro Glu Leu Ala Val Pro Asp Ser Pro Thr Met Val  
 50 55 60  
 Val Gly Ala Pro Val Ala Glu Gln Ser Ser Phe Asp Asn Val Glu His  
 65 70 75 80  
 Leu Glu Arg Met Leu Ser Leu Asp Asn Val Phe Asp Glu Gln Glu Leu  
 85 90 95

Arg Asp Trp Leu Gly Arg Thr Pro Ala Lys Gln Tyr Leu Thr Glu Leu  
100 105 110

Lys Ile Asp Gly Leu Ser Ile Asp Leu Val Tyr Arg Asn Gly Gln Leu  
115 120 125

Glu Arg Ala Ala Thr Arg Gly Asp Gly Arg Val Gly Glu Asp Ile Thr  
130 135 140

Ala Asn Ala Arg Val Ile Glu Asp Ile Pro His Gln Leu Gln Gly Thr  
145 150 155 160

Asp Glu Tyr Pro Val Pro Ala Val Leu Glu Ile Arg Gly Glu Val Phe  
165 170 175

Ile Thr Val Glu Asp Phe Pro Gly Gly Gln Arg Ala Ala His Cys  
180 185 190

<210> 201

<211> 366

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(343)

<223> RXA00789

<400> 201

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gcaccagca agcaaaactaa aaacttagga gaatgaagaa atg acc aat cca gat 115  
Met Thr Asn Pro Asp  
1 5

atc gtc ggt tcc ggc caa ggc aac gat tcc ttc gag cca gtc gcc caa 163  
Ile Val Gly Ser Gly Gln Gly Asn Asp Ser Phe Glu Pro Val Ala Gln  
10 15 20

tta tcc tac gag cgt gca cgc gat gaa ctc gtt gaa att gta aaa att 211  
Leu Ser Tyr Glu Arg Ala Arg Asp Glu Leu Val Glu Ile Val Lys Ile  
25 30 35

ttg gag ctc ggc caa atg ggc ctc gac gaa tcc ctc aaa tac tgg gag 259  
Leu Glu Leu Gly Gln Met Gly Leu Asp Glu Ser Leu Lys Tyr Trp Glu  
40 45 50

cgc ggc gaa gcc cta gca aag cgc tgc gaa gag cac ctg gcc gcc gcc 307  
Arg Gly Glu Ala Leu Ala Lys Arg Cys Glu Glu His Leu Ala Gly Ala  
55 60 65

tca gcg cgc gtc gag caa gca tta aac cag gca gaa taatgctttt 353  
Ser Ala Arg Val Glu Gln Ala Leu Asn Gln Ala Glu  
70 75 80

cgacgcaccc ctc 366

<210> 202

<211> 81  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 202  
 Met Thr Asn Pro Asp Ile Val Gly Ser Gly Gln Gly Asn Asp Ser Phe  
 1 5 10 15  
 Glu Pro Val Ala Gln Leu Ser Tyr Glu Arg Ala Arg Asp Glu Leu Val  
 20 25 30  
 Glu Ile Val Lys Ile Leu Glu Leu Gly Gln Met Gly Leu Asp Glu Ser  
 35 40 45  
 Leu Lys Tyr Trp Glu Arg Gly Glu Ala Leu Ala Lys Arg Cys Glu Glu  
 50 55 60  
 His Leu Ala Gly Ala Ser Ala Arg Val Glu Gln Ala Leu Asn Gln Ala  
 65 70 75 80  
 Glu

<210> 203  
 <211> 1185  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1162)  
 <223> RXN00790

<400> 203  
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 aaagctgtcg aatttgacgc ttcgtgatgt ggagcaagaa atg tct gtg cag ctg 115  
 Met Ser Val Gln Leu  
 1 5  
 acc tgc ccg acg gac att atc cgc aat cgc ccc aca ccg ctc aag gat 163  
 Thr Cys Pro Thr Asp Ile Ile Arg Asn Arg Pro Thr Pro Leu Lys Asp  
 10 15 20  
 ggc gac cgc gtg att gtg tac ggc aag ccc gcg ttt tat gca ggc cgc 211  
 Gly Asp Arg Val Ile Val Tyr Gly Lys Pro Ala Phe Tyr Ala Gly Arg  
 25 30 35  
 ggc act ttt tgc ctg tgg gtg act gat atc cgt ccc gtg ggt att ggt 259  
 Gly Thr Phe Ser Leu Trp Val Thr Asp Ile Arg Pro Val Gly Ile Gly  
 40 45 50  
 gag ttg ctg gcg cgc att gag gag ctg cgt aaa agg ctt gcc gcg gag 307  
 Glu Leu Leu Ala Arg Ile Glu Glu Leu Arg Lys Arg Leu Ala Ala Glu  
 55 60 65  
 ggt ctt ttt gat cca gct cgg aag aag cga ctg cca ttt ctg ccc aac 355  
 Gly Leu Phe Asp Pro Ala Arg Lys Lys Arg Leu Pro Phe Leu Pro Asn  
 70 75 80 85

cgc gtt ggt ttg atc acg gga cgt ggt tca gcg gct gag cgc gat gtg 403  
 Arg Val Gly Leu Ile Thr Gly Arg Gly Ser Ala Ala Glu Arg Asp Val  
 90 95 100

ctg agc gtg gct aag gat cgc tgg ccg gaa gtg cag ttt gag gtg atc 451  
 Leu Ser Val Ala Lys Asp Arg Trp Pro Glu Val Gln Phe Glu Val Ile  
 105 110 115

aac acg gca gtt cag ggc gct tca gct gtt cct gaa atc atc gaa gcg 499  
 Asn Thr Ala Val Gln Gly Ala Ser Ala Val Pro Glu Ile Ile Glu Ala  
 120 125 130

ttg ccg gtt tta gat cag gac cct cgc gtg gat gtc atc atc att gcc 547  
 Leu Arg Val Leu Asp Gln Asp Pro Arg Val Asp Val Ile Ile Ile Ala  
 135 140 145

cgc ggc ggc ggt tct gtg gag gat ctg ctc ccc ttc tct gag gag gcc 595  
 Arg Gly Gly Gly Ser Val Glu Asp Leu Leu Pro Phe Ser Glu Glu Ala  
 150 155 160 165

ttg cag cgc gca gtc gcg gca gcg cag acg ccc gtg gtg tcc gcg att 643  
 Leu Gln Arg Ala Val Ala Ala Ala Gln Thr Pro Val Val Ser Ala Ile  
 170 175 180

ggc cac gaa cca gat acg ccg gtg ttg gac aat gtc gcc gac ctt cgc 691  
 Gly His Glu Thr Pro Asp Thr Pro Val Leu Asp Asn Val Ala Asp Leu Arg  
 185 190 195

gcg ccg acc ccg acc gat gca gca aag cgc gtg gtg cct gat gtg gca 739  
 Ala Ala Thr Pro Thr Asp Ala Ala Lys Arg Val Val Pro Asp Val Ala  
 200 205 210

gaa gaa cgc atg ttg atc aat cag ctt cgc agt cgt agt gcc gcg gcg 787  
 Glu Glu Arg Met Leu Ile Asn Gln Leu Arg Ser Arg Ser Ala Ala Ala  
 215 220 225

ttg cgc ggt tgg gtg cag cgc gag cag cag gcg ttg gca gcg att cgc 835  
 Leu Arg Gly Trp Val Gln Arg Glu Gln Gln Ala Leu Ala Ala Ile Arg  
 230 235 240 245

acc agg ccg gtg ctg gct gat ccg atg acc ccg att aac cgc cga cgt 883  
 Thr Arg Pro Val Leu Ala Asp Pro Met Thr Pro Ile Asn Arg Arg Arg  
 250 255 260

gat gag att gcc cag gct gtg ggc ttg att agg cgc gat gtc acc cat 931  
 Asp Glu Ile Ala Gln Ala Val Gly Leu Ile Arg Arg Asp Val Thr His  
 265 270 275

ctc gtc cgc acc gag caa gca ctg gtg gcg tcg ttg cgc gca cag gtt 979  
 Leu Val Arg Thr Glu Gln Ala Leu Val Ala Ser Leu Arg Ala Gln Val  
 280 285 290

tcc gcg ctc ggc ccg tcc gca acc ttg gcg cgc ggt tat tcc gtg gtg 1027  
 Ser Ala Leu Gly Pro Ser Ala Thr Leu Ala Arg Gly Tyr Ser Val Val  
 295 300 305

cag gtt att cct cgc gac ggc agc gcc ccg gaa gtg gtc acc acc atc 1075  
 Gln Val Ile Pro Arg Asp Gly Ser Ala Pro Glu Val Val Thr Thr Ile  
 310 315 320 325

gag caa tca ccg ccc ggc agc cag ctg cgc atc cgc gtt gcc gac ggc 1123

Glu Gln Ser Pro Gly Ser Gln Leu Arg Ile Arg Val Ala Asp Gly  
330 335 340

tcc atc act gcg gca tcc atg ggc acc cag caa gca aac taaaaactta 1172  
Ser Ile Thr Ala Ala Ser Met Gly Thr Gln Gln Ala Asn  
345 350

ggagaatgaa gaa 1185

<210> 204

<211> 354

<212> PRT

<213> Corynebacterium glutamicum

<400> 204

Met Ser Val Gln Leu Thr Cys Pro Thr Asp Ile Ile Arg Asn Arg Pro  
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Thr Pro Leu Lys Asp Gly Asp Arg Val Ile Val Tyr Gly Lys Pro Ala  
20 25 30

Phe Tyr Ala Gly Arg Gly Thr Phe Ser Leu Trp Val Thr Asp Ile Arg  
35 40 45

Pro Val Gly Ile Gly Glu Leu Leu Ala Arg Ile Glu Glu Leu Arg Lys  
50 55 60

Arg Leu Ala Ala Glu Gly Leu Phe Asp Pro Ala Arg Lys Lys Arg Leu  
65 70 75 80

Pro Phe Leu Pro Asn Arg Val Gly Leu Ile Thr Gly Arg Gly Ser Ala  
85 90 95

Ala Glu Arg Asp Val Leu Ser Val Ala Lys Asp Arg Trp Pro Glu Val  
100 105 110

Gln Phe Glu Val Ile Asn Thr Ala Val Gln Gly Ala Ser Ala Val Pro  
115 120 125

Glu Ile Ile Glu Ala Leu Arg Val Leu Asp Gln Asp Pro Arg Val Asp  
130 135 140

Val Ile Ile Ile Ala Arg Gly Gly Gly Ser Val Glu Asp Leu Leu Pro  
145 150 155 160

Phe Ser Glu Glu Ala Leu Gln Arg Ala Val Ala Ala Ala Gln Thr Pro  
165 170 175

Val Val Ser Ala Ile Gly His Glu Pro Asp Thr Pro Val Leu Asp Asn  
180 185 190

Val Ala Asp Leu Arg Ala Ala Thr Pro Thr Asp Ala Ala Lys Arg Val  
195 200 205

Val Pro Asp Val Ala Glu Glu Arg Met Leu Ile Asn Gln Leu Arg Ser  
210 215 220

Arg Ser Ala Ala Ala Leu Arg Gly Trp Val Gln Arg Glu Gln Gln Ala  
225 230 235 240



Leu Ala Ala Ile Arg Thr Arg Pro Val Leu Ala Asp Pro Met Thr Pro  
 245 250 255  
 Ile Asn Arg Arg Arg Asp Glu Ile Ala Gln Ala Val Gly Leu Ile Arg  
 260 265 270  
 Arg Asp Val Thr His Leu Val Arg Thr Glu Gln Ala Leu Val Ala Ser  
 275 280 285  
 Leu Arg Ala Gln Val Ser Ala Leu Gly Pro Ser Ala Thr Leu Ala Arg  
 290 295 300  
 Gly Tyr Ser Val Val Gln Val Ile Pro Arg Asp Gly Ser Ala Pro Glu  
 305 310 315 320  
 Val Val Thr Thr Ile Glu Gln Ser Pro Pro Gly Ser Gln Leu Arg Ile  
 325 330 335  
 Arg Val Ala Asp Gly Ser Ile Thr Ala Ala Ser Met Gly Thr Gln Gln  
 340 345 350  
 Ala Asn

<210> 205  
 <211> 1049  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (1) .. (1026)  
 <223> FRXA00790

<400> 205  
 cgc aat cgc ccc aca cgc ctc aag gat ggc gac cgc gtg att gtg tac 48  
 Arg Asn Arg Pro Thr Pro Leu Lys Asp Gly Asp Arg Val Ile Val Tyr  
 1 5 10 15  
 ggc aag ccc gcg ttt tat gca gcc cgc gcc act ttt tcg ctg tgg gtg 96  
 Gly Lys Pro Ala Phe Tyr Ala Gly Arg Gly Thr Phe Ser Leu Trp Val  
 20 25 30  
 act gat atc cgt ccc gtg ggt att ggt gag ttg ctg gcg cgc att gag 144  
 Thr Asp Ile Arg Pro Val Gly Ile Gly Glu Leu Leu Ala Arg Ile Glu  
 35 40 45  
 gag ctg cgt aaa agg ctt gcc gcg gag ggt ctt ttt gat cca gct cgg 192  
 Glu Leu Arg Lys Arg Leu Ala Ala Glu Gly Leu Phe Asp Pro Ala Arg  
 50 55 60  
 aag aag cga ctg cca ttt ctg ccc aac cgc gtt ggt ttg atc acg gga 240  
 Lys Lys Arg Leu Pro Phe Leu Pro Asn Arg Val Gly Leu Ile Thr Gly  
 65 70 75 80  
 cgt ggt tca gcg gct gag cgc gat gtg ctg agc gtg gct aag gat cgc 288  
 Arg Gly Ser Ala Ala Glu Arg Asp Val Leu Ser Val Ala Lys Asp Arg  
 85 90 95  
 tgg ccg gaa gtg cag ttt gag gtg atc aac acg gca gtt cag gcc gct 336

Trp	Pro	Glu	Val	Gln	Phe	Glu	Val	Ile	Asn	Thr	Ala	Val	Gln	Gly	Ala	
			100					105					110			
tca	gct	ggt	cct	gaa	atc	atc	gaa	gcg	ttg	cgg	ggt	tta	gat	cag	gac	384
Ser	Ala	Val	Pro	Glu	Ile	Ile	Glu	Ala	Leu	Arg	Val	Leu	Asp	Gln	Asp	
		115					120					125				
cct	cgc	gtg	gat	gtc	atc	atc	att	gcc	cgc	ggc	ggc	ggt	tct	gtg	gag	432
Pro	Arg	Val	Asp	Val	Ile	Ile	Ile	Ala	Arg	Gly	Gly	Gly	Ser	Val	Glu	
		130					135					140				
gat	ctg	ctc	ccc	ttc	tct	gag	gag	gcc	ttg	cag	cgc	gca	gtc	gcg	gca	480
Asp	Leu	Leu	Pro	Phe	Ser	Glu	Glu	Ala	Leu	Gln	Arg	Ala	Val	Ala	Ala	
		145				150				155					160	
gcg	cag	acg	ccc	gtg	gtg	tcc	gcg	att	ggc	cac	gaa	cca	gat	acg	ccg	528
Ala	Gln	Thr	Pro	Val	Val	Ser	Ala	Ile	Gly	His	Glu	Pro	Asp	Thr	Pro	
			165						170					175		
gtg	ttg	gac	aat	gtc	gcc	gac	ctt	cgc	gcg	gcg	acc	ccg	acc	gat	gca	576
Val	Leu	Asp	Asn	Val	Ala	Asp	Leu	Arg	Ala	Ala	Thr	Pro	Thr	Asp	Ala	
			180					185						190		
gca	aag	cgc	gtg	gtg	cct	gat	gtg	gca	gaa	gaa	cgc	atg	ttg	atc	aat	624
Ala	Lys	Arg	Val	Val	Pro	Asp	Val	Ala	Glu	Glu	Arg	Met	Leu	Ile	Asn	
		195					200					205				
cag	ctt	cgc	agt	cg	agt	gcc	gcg	gcg	ttg	cg	ggt	tgg	gtg	cag	cg	672
Gln	Leu	Arg	Ser	Arg	Ser	Ala	Ala	Ala	Leu	Arg	Gly	Trp	Val	Gln	Arg	
		210				215					220					
gag	cag	cag	gcg	ttg	gca	gcg	att	cg	acc	agg	ccg	gtg	ctg	gct	gat	720
Glu	Gln	Gln	Ala	Leu	Ala	Ala	Ile	Arg	Thr	Arg	Pro	Val	Leu	Ala	Asp	
		225			230					235					240	
ccg	atg	acc	ccg	att	aac	cg	cga	cgt	gat	gag	att	gcc	cag	gct	gtg	768
Pro	Met	Thr	Pro	Ile	Asn	Arg	Arg	Arg	Asp	Glu	Ile	Ala	Gln	Ala	Val	
			245						250					255		
ggc	ttg	att	agg	cg	gat	gtc	acc	cat	ctc	gtc	cg	acc	gag	caa	gca	816
Gly	Leu	Ile	Arg	Arg	Asp	Val	Thr	His	Leu	Val	Arg	Thr	Glu	Gln	Ala	
			260					265					270			
ctg	gtg	gcg	tgc	ttg	cg	gca	cag	ggt	tcc	gcg	ctc	ggc	ccg	tcc	gca	864
Leu	Val	Ala	Ser	Leu	Arg	Ala	Gln	Val	Ser	Ala	Leu	Gly	Pro	Ser	Ala	
		275					280					285				
acc	ttg	gcg	cg	ggt	tat	tcc	gtg	gtg	cag	ggt	att	cct	cg	gac	ggc	912
Thr	Leu	Ala	Arg	Gly	Tyr	Ser	Val	Val	Gln	Val	Ile	Pro	Arg	Asp	Gly	
		290				295						300				
agc	gcc	ccg	gaa	gtg	gtc	acc	acc	atc	gag	caa	tca	ccg	ccc	ggc	agc	960
Ser	Ala	Pro	Glu	Val	Val	Thr										

340

&lt;210&gt; 206

&lt;211&gt; 342

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 206

Arg Asn Arg Pro Thr Pro Leu Lys Asp Gly Asp Arg Val Ile Val Tyr  
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Gly Lys Pro Ala Phe Tyr Ala Gly Arg Gly Thr Phe Ser Leu Trp Val  
 20 25 30

Thr Asp Ile Arg Pro Val Gly Ile Gly Glu Leu Leu Ala Arg Ile Glu  
 35 40 45

Glu Leu Arg Lys Arg Leu Ala Ala Glu Gly Leu Phe Asp Pro Ala Arg  
 50 55 60

Lys Lys Arg Leu Pro Phe Leu Pro Asn Arg Val Gly Leu Ile Thr Gly  
 65 70 75 80

Arg Gly Ser Ala Ala Glu Arg Asp Val Leu Ser Val Ala Lys Asp Arg  
 85 90 95

Trp Pro Glu Val Gln Phe Glu Val Ile Asn Thr Ala Val Gln Gly Ala  
 100 105 110

Ser Ala Val Pro Glu Ile Ile Glu Ala Leu Arg Val Leu Asp Gln Asp  
 115 120 125

Pro Arg Val Asp Val Ile Ile Ile Ala Arg Gly Gly Ser Val Glu  
 130 135 140

Asp Leu Leu Pro Phe Ser Glu Glu Ala Leu Gln Arg Ala Val Ala Ala  
 145 150 155 160

Ala Gln Thr Pro Val Val Ser Ala Ile Gly His Glu Pro Asp Thr Pro  
 165 170 175

Val Leu Asp Asn Val Ala Asp Leu Arg Ala Ala Thr Pro Thr Asp Ala  
 180 185 190

Ala Lys Arg Val Val Pro Asp Val Ala Glu Glu Arg Met Leu Ile Asn  
 195 200 205

Gln Leu Arg Ser Arg Ser Ala Ala Ala Leu Arg Gly Trp Val Gln Arg  
 210 215 220

Glu Gln Gln Ala Leu Ala Ala Ile Arg Thr Arg Pro Val Leu Ala Asp  
 225 230 235 240

Pro Met Thr Pro Ile Asn Arg Arg Arg Asp Glu Ile Ala Gln Ala Val  
 245 250 255

Gly Leu Ile Arg Arg Asp Val Thr His Leu Val Arg Thr Glu Gln Ala  
 260 265 270

Leu Val Ala Ser Leu Arg Ala Gln Val Ser Ala Leu Gly Pro Ser Ala

	275							280										285	
Thr	Leu	Ala	Arg	Gly	Tyr	Ser	Val	Val	Gln	Val	Ile	Pro	Arg	Asp	Gly				
	290					295					300								
Ser	Ala	Pro	Glu	Val	Val	Thr	Thr	Ile	Glu	Gln	Ser	Pro	Pro	Gly	Ser				
305					310				315						320				
Gln	Leu	Arg	Ile	Arg	Val	Ala	Asp	Gly	Ser	Ile	Thr	Ala	Ala	Ser	Met				
			325					330						335					
Gly	Thr	Gln	Gln	Ala	Asn														
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<213>	Corynebacterium glutamicum																		
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<223>	RXA00898																		
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aacggaaatt	ctaaaatocca	aaacagctag	gggtataagtc	atg	cgc	atc	gtt	aat										115	
				Met	Arg	Ile	Val	Asn										5	
				1															
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tgg	aac	gtc	aac	tct	gct	cgc	act	cgt	gtg	gac	cgg	atg	gtc	gat	ttt			163	
Trp	Asn	Val	Asn	Ser	Ala	Arg	Thr	Arg	Val	Asp	Arg	Met	Val	Asp	Phe				
			10						15					20					
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ttg	ctt	cgc	cat	gat	gtt	gat	gta	tta	gcg	gtg	cag	gaa	acc	aag	tgt			211	
Leu	Leu	Arg	His	Asp	Val	Asp	Val	Leu	Ala	Val	Gln	Glu	Thr	Lys	Cys				
			25					30					35						
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aaa	gat	gag	caa	ttt	ccc	acc	gag	cgt	ttc	acc	gaa	atc	ggc	tat	gag			259	
Lys	Asp	Glu	Gln	Phe	Pro	Thr	Glu	Arg	Phe	Thr	Glu	Ile	Gly	Tyr	Glu				
		40					45					50							
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gta	gcc	cat	ttc	ggc	ctt	aac	cag	tgg	aat	ggg	gtc	gcc	att	att	tcc			307	
Val	Ala	His	Phe	Gly	Leu	Asn	Gln	Trp	Asn	Gly	Val	Ala	Ile	Ile	Ser				
		55				60					65								
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cgc	gtt	ggc	att	gaa	aat	gtg	gaa	acc	cac	ttc	cct	gcc	caa	ccg	gga			355	
Arg	Val	Gly	Ile	Glu	Asn	Val	Glu	Thr	His	Phe	Pro	Ala	Gln	Pro	Gly				
	70				75					80					85				
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ttc	aac	aaa	gac	atc	acc	aag	gaa	caa	tcc	atc	gaa	gcc	cgc	gcc	atc			403	
Phe	Asn	Lys	Asp	Ile	Thr	Lys	Glu	Gln	Ser	Ile	Glu	Ala	Arg	Ala	Ile				
			90						95					100					
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ggc	gcc	cgc	tgc	ggg	ggg	gtc	cag	gtg	tgg	agc	ctc	tat	gtt	ccc	aac			451	
Gly	Ala	Arg	Cys	Gly	Gly	Val	Gln	Val	Trp	Ser	Leu	Tyr	Val	Pro	Asn				
			105					110											

Gly Arg Glu Ile Ala Asp Pro His Tyr Asp Tyr Lys Leu Arg Trp Leu  
 120 125 130

ttc tcc ctg cgc aac tac gtg atc gac acc ttg gaa tac cgc ccc gag 547  
 Phe Ser Leu Arg Asn Tyr Val Ile Asp Thr Leu Glu Tyr Arg Pro Glu  
 135 140 145

gaa aaa ctg gtg ttg ctc ggc gac ttc aac atc gcg ccc aca gac atc 595  
 Glu Lys Leu Val Leu Leu Gly Asp Phe Asn Ile Ala Pro Thr Asp Ile  
 150 155 160 165

gac gtc tgg gac atc gca gcc ttc gaa gga aaa acc cac gtc acc gaa 643  
 Asp Val Trp Asp Ile Ala Ala Phe Glu Gly Lys Thr His Val Thr Glu  
 170 175 180

cca gaa cgt gca gct ttc gac ggc ctc atc gaa gcc gga ctc aaa gaa 691  
 Pro Glu Arg Ala Ala Phe Asp Gly Leu Ile Glu Ala Gly Leu Lys Glu  
 185 190 195

acc acc ccc gga cct ggt acc tac acc tac tgg gat tac aaa ggc gca 739  
 Thr Thr Pro Gly Pro Gly Thr Tyr Thr Tyr Trp Asp Tyr Lys Gly Ala  
 200 205 210

cgc ttc ctc aaa ggc gaa ggc atg cgc atc gat ttc cag ctc gca tcc 787  
 Arg Phe Leu Lys Gly Glu Gly Met Arg Ile Asp Phe Gln Leu Ala Ser  
 215 220 225

ccg gcc ctt gct gca acc gcg ggt gaa acc ttt gtg gac gtt gaa gaa 835  
 Pro Ala Leu Ala Ala Thr Ala Gly Glu Thr Phe Val Asp Val Glu Glu  
 230 235 240 245

cgc agc gga acc ggc gcc tct gac cac gca cca gtc atc gtt gat tac 883  
 Arg Ser Gly Thr Gly Ala Ser Asp His Ala Pro Val Ile Val Asp Tyr  
 250 255 260

aag gtg taactgcgta tgatctttca gat 912  
 Lys Val

<210> 208  
 <211> 263  
 <212> PRT  
 <213> *Corynebacterium glutamicum*

<400> 208  
 Met Arg Ile Val Asn Trp Asn Val Asn Ser Ala Arg Thr Arg Val Asp  
 1 5 10 15

Arg Met Val Asp Phe Leu Leu Arg His Asp Val Asp Val Leu Ala Val  
 20 25 30

Gln Glu Thr Lys Cys Lys Asp Glu Gln Phe Pro Thr Glu Arg Phe Thr  
 35 40 45

Glu Ile Gly Tyr Glu Val Ala His Phe Gly Leu Asn Gln Trp Asn Gly  
 50 55 60

Val Ala Ile Ile Ser Arg Val Gly Ile Glu Asn Val Glu Thr His Phe  
 65 70 75 80

Pro Ala Gln Pro Gly Phe Asn Lys Asp Ile Thr Lys Glu Gln Ser Ile  
85 90 95

Glu Ala Arg Ala Ile Gly Ala Arg Cys Gly Gly Val Gln Val Trp Ser  
100 105 110

Leu Tyr Val Pro Asn Gly Arg Glu Ile Ala Asp Pro His Tyr Asp Tyr  
115 120 125

Lys Leu Arg Trp Leu Phe Ser Leu Arg Asn Tyr Val Ile Asp Thr Leu  
130 135 140

Glu Tyr Arg Pro Glu Glu Lys Leu Val Leu Leu Gly Asp Phe Asn Ile  
145 150 155 160

Ala Pro Thr Asp Ile Asp Val Trp Asp Ile Ala Ala Phe Glu Gly Lys  
165 170 175

Thr His Val Thr Glu Pro Glu Arg Ala Ala Phe Asp Gly Leu Ile Glu  
180 185 190

Ala Gly Leu Lys Glu Thr Thr Pro Gly Pro Gly Thr Tyr Thr Tyr Trp  
195 200 205

Asp Tyr Lys Gly Ala Arg Phe Leu Lys Gly Glu Gly Met Arg Ile Asp  
210 215 220

Phe Gln Leu Ala Ser Pro Ala Leu Ala Ala Thr Ala Gly Glu Thr Phe  
225 230 235 240

Val Asp Val Glu Glu Arg Ser Gly Thr Gly Ala Ser Asp His Ala Pro  
245 250 255

Val Ile Val Asp Tyr Lys Val  
260

&lt;210&gt; 209

&lt;211&gt; 806

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(783)

&lt;223&gt; RXN03175

&lt;400&gt; 209

gtc cgc gca agc gaa aaa gac acc gcc acc gca ctg caa ccc gcc tta 48  
Val Arg Ala Ser Glu Lys Asp Thr Ala Thr Ala Leu Gln Pro Ala Leu  
1 5 10 15

gat aac gga tgg cac tac att ggt gcc cca gca gct gcc aag gga cgt 96  
Asp Asn Gly Trp His Tyr Ile Gly Ala Pro Ala Ala Ala Lys Gly Arg  
20 25 30

gcc ggt gtc ggc att ttg tct agg cat gaa ctt gaa gat gtg aac atc 144  
Ala Gly Val Gly Ile Leu Ser Arg His Glu Leu Glu Asp Val Asn Ile  
35 40 45

ggg ttt gga tct ttc ctt gac tcc ggc cgc tac att gaa gca acc atc 192

Gly Phe Gly Ser Phe Leu Asp Ser Gly Arg Tyr Ile Glu Ala Thr Ile  
 50 55 60  
 aaa gac acc acc ctg gat gtg cca gta acc gtg gca tct ctt tac ctc 240  
 Lys Asp Thr Thr Leu Asp Val Pro Val Thr Val Ala Ser Leu Tyr Leu  
 65 70 75 80  
 ccc tca ggt tca gcg ggc acc gac aag cag gat gaa aag tac cgc ttc 288  
 Pro Ser Gly Ser Ala Gly Thr Asp Lys Gln Asp Glu Lys Tyr Arg Phe  
 85 90 95  
 ctc gat gaa ttc gaa ggg ttc ctg gac cag cgc gct aaa gaa cgc tcc 336  
 Leu Asp Glu Phe Glu Gly Phe Leu Asp Gln Arg Ala Lys Glu Arg Ser  
 100 105 110  
 cac atg gtc atc ggt ggc gac tgg aac atc tgc cac cgc cgc gaa gac 384  
 His Met Val Ile Gly Gly Asp Trp Asn Ile Cys His Arg Glu Asp  
 115 120 125  
 ctg aaa aac tgg aaa acc aac caa aag aaa tcc ggt ttc ctt ccc gac 432  
 Leu Lys Asn Trp Lys Thr Asn Gln Lys Lys Ser Gly Phe Leu Pro Asp  
 130 135 140  
 gaa cgc gca ttc atg gat tca gtc ttt ggc acc ttc cca gat gag gca 480  
 Glu Arg Ala Phe Met Asp Ser Val Phe Gly Thr Phe Pro Asp Glu Ala  
 145 150 155 160  
 acc cag gtt gca ggg gcc ggc gac ttc ttc ggt gcc gtg gac tat gaa 528  
 Thr Gln Val Ala Gly Ala Gly Asp Phe Phe Gly Ala Val Asp Tyr Glu  
 165 170 175  
 gga acg agg cgt cga gaa gca act acg gac cct gcg tgg ttc gac gtt 576  
 Gly Thr Arg Arg Arg Glu Ala Thr Thr Asp Pro Ala Trp Phe Asp Val  
 180 185 190  
 gca cgt cgc ctg caa cct gaa ggc gac ggc ccc tac act tgg tgg acc 624  
 Ala Arg Arg Leu Gln Pro Glu Gly Asp Gly Pro Tyr Thr Trp Trp Thr  
 195 200 205  
 tac cgc gga aaa gcc ttc gac acc ggc gcc gga tgg cgc atc gac tac 672  
 Tyr Arg Gly Lys Ala Phe Asp Thr Gly Ala Gly Trp Arg Ile Asp Tyr  
 210 215 220  
 caa gca gca acc gca gcg atg ctc gaa cgc gca gaa cgc tcc tgg gta 720  
 Gln Ala Ala Thr Ala Ala Met Leu Glu Arg Ala Glu Arg Ser Trp Val  
 225 230 235 240  
 gac aaa gcc gct gca tac gat ttg cgc tgg tca gat cac tca cca ctg 768  
 Asp Lys Ala Ala Ala Tyr Asp Leu Arg Trp Ser Asp His Ser Pro Leu  
 245 250 255  
 aac gtg atc tac tcc taaaatgctg ctgacaattc tat 806  
 Asn Val Ile Tyr Ser  
 260

&lt;210&gt; 210

&lt;211&gt; 261

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

<400> 210  
 Val Arg Ala Ser Glu Lys Asp Thr Ala Thr Ala Leu Gln Pro Ala Leu  
 1 5 10 15  
 Asp Asn Gly Trp His Tyr Ile Gly Ala Pro Ala Ala Ala Lys Gly Arg  
 20 25 30  
 Ala Gly Val Gly Ile Leu Ser Arg His Glu Leu Glu Asp Val Asn Ile  
 35 40 45  
 Gly Phe Gly Ser Phe Leu Asp Ser Gly Arg Tyr Ile Glu Ala Thr Ile  
 50 55 60  
 Lys Asp Thr Thr Leu Asp Val Pro Val Thr Val Ala Ser Leu Tyr Leu  
 65 70 75 80  
 Pro Ser Gly Ser Ala Gly Thr Asp Lys Gln Asp Glu Lys Tyr Arg Phe  
 85 90 95  
 Leu Asp Glu Phe Glu Gly Phe Leu Asp Gln Arg Ala Lys Glu Arg Ser  
 100 105 110  
 His Met Val Ile Gly Gly Asp Trp Asn Ile Cys His Arg Arg Glu Asp  
 115 120 125  
 Leu Lys Asn Trp Lys Thr Asn Gln Lys Lys Ser Gly Phe Leu Pro Asp  
 130 135 140  
 Glu Arg Ala Phe Met Asp Ser Val Phe Gly Thr Phe Pro Asp Glu Ala  
 145 150 155 160  
 Thr Gln Val Ala Gly Ala Gly Asp Phe Phe Gly Ala Val Asp Tyr Glu  
 165 170 175  
 Gly Thr Arg Arg Arg Glu Ala Thr Thr Asp Pro Ala Trp Phe Asp Val  
 180 185 190  
 Ala Arg Arg Leu Gln Pro Glu Gly Asp Gly Pro Tyr Thr Trp Trp Thr  
 195 200 205  
 Tyr Arg Gly Lys Ala Phe Asp Thr Gly Ala Gly Trp Arg Ile Asp Tyr  
 210 215 220  
 Gln Ala Ala Thr Ala Ala Met Leu Glu Arg Ala Glu Arg Ser Trp Val  
 225 230 235 240  
 Asp Lys Ala Ala Ala Tyr Asp Leu Arg Trp Ser Asp His Ser Pro Leu  
 245 250 255  
 Asn Val Ile Tyr Ser  
 260

<210> 211  
 <211> 1035  
 <212> DNA  
 <213> *Corynebacterium glutamicum*

<220>  
 <221> CDS  
 <222> (101)..(1012)



&lt;223&gt; FRXA02883

&lt;400&gt; 211

tgccatcgtg gtgtggttcc ccatggtggc cttgcgtaaa cgcacataaa cggggttggc 60

ggatggagga tttcccaag caccactag tgtgacaagc atg agt ttt cac atc 115  
 Met Ser Phe His Ile  
 1 5

aca tcc gtc aat gtc aac ggc att agg gca cgc gtc aaa cag cga agc 163  
 Thr Ser Val Asn Val Asn Gly Ile Arg Ala Ala Val Lys Gln Arg Ser  
 10 15 20

gaa aca aac cta ggt ttc ctt ccg tgg ctt gaa gaa act cgc ccg gac 211  
 Glu Thr Asn Leu Gly Phe Leu Pro Trp Leu Glu Glu Thr Arg Pro Asp  
 25 30 35

gtt gtc ctc ctc caa gaa gtc cgc gca agc gaa aaa gac acc gcc acc 259  
 Val Val Leu Leu Gln Glu Val Arg Ala Ser Glu Lys Asp Thr Ala Thr  
 40 45 50

gca ctg caa ccc gcc tta gat aac gga tgg cac tac att ggt gcc cca 307  
 Ala Leu Gln Pro Ala Leu Asp Asn Gly Trp His Tyr Ile Gly Ala Pro  
 55 60 65

gca gct gcc aag gga cgt gcc ggt gtc ggc att ttg tct agg cat gaa 355  
 Ala Ala Ala Lys Gly Arg Ala Gly Val Gly Ile Leu Ser Arg His Glu  
 70 75 80 85

ctt gaa gat gtg aac atc ggt ttt gga tct ttc ctt gac tcc gcc cgc 403  
 Leu Glu Asp Val Asn Ile Gly Phe Gly Ser Phe Leu Asp Ser Gly Arg  
 90 95 100

tac att gaa gca acc atc aaa gac acc acc ctg gat gtg cca gta acc 451  
 Tyr Ile Glu Ala Thr Ile Lys Asp Thr Thr Leu Asp Val Pro Val Thr  
 105 110 115

gtg gca tct ctt tac ctc ccc tca ggt tca cgc ggc acc gac aag cag 499  
 Val Ala Ser Leu Tyr Leu Pro Ser Gly Ser Ala Gly Thr Asp Lys Gln  
 120 125 130

gat gaa aag tac cgc ttc ctc gat gaa ttc gaa ggg ttc ctg gac cag 547  
 Asp Glu Lys Tyr Arg Phe Leu Asp Glu Phe Glu Gly Phe Leu Asp Gln  
 135 140 145

cgc gct aaa gaa cgc tcc cac atg gtc atc ggt ggc gac tgg aac atc 595  
 Arg Ala Lys Glu Arg Ser His Met Val Ile Gly Gly Asp Trp Asn Ile  
 150 155 160 165

tgc cac cgc cgc gaa gac ctg aaa aac tgg aaa acc aac caa aag aaa 643  
 Cys His Arg Arg Glu Asp Leu Lys Asn Trp Lys Thr Asn Gln Lys Lys  
 170 175 180

tcc ggt ttc ctt ccc gac gaa cgc gca ttc atg gat tca gtc ttt ggc 691  
 Ser Gly Phe Leu Pro Asp Glu Arg Ala Phe Met Asp Ser Val Phe Gly  
 185 190 195

acc ttc cca gat gag gca acc cag gtt gca ggg gcc ggc gac ttc ttc 739  
 Thr Phe Pro Asp Glu Ala Thr Gln Val Ala Gly Ala Gly Asp Phe Phe  
 200 205 210

ggt gcc gtg gac tat gaa gga acg agg cgt cga gaa gca act acg gac 787  
 Gly Ala Val Asp Tyr Glu Gly Thr Arg Arg Arg Glu Ala Thr Thr Asp  
 215 220 225

cct gcg tgg ttc gac gtt gca cgt cgc ctg caa cct gaa ggc gac ggc 835  
 Pro Ala Trp Phe Asp Val Ala Arg Arg Leu Gln Pro Glu Gly Asp Gly  
 230 235 240 245

ccc tac act tgg tgg acc tac cgc gga aaa gcc ttc gac acc ggc gcc 883  
 Pro Tyr Thr Trp Trp Thr Tyr Arg Gly Lys Ala Phe Asp Thr Gly Ala  
 250 255 260

gga tgg cgc atc gac tac caa gca gca acc gca gcg atg ctc gaa cgc 931  
 Gly Trp Arg Ile Asp Tyr Gln Ala Ala Thr Ala Ala Met Leu Glu Arg  
 265 270 275

gca gaa cgc tcc tgg gta gac aaa gcc gct gca tac gat ttg cgc tgg 979  
 Ala Glu Arg Ser Trp Val Asp Lys Ala Ala Ala Tyr Asp Leu Arg Trp  
 280 285 290

tca gat cac tca cca ctg aac gtg atc tac tcc taaatgctg ctgacaattc 1032  
 Ser Asp His Ser Pro Leu Asn Val Ile Tyr Ser  
 295 300

tat 1035

<210> 212  
 <211> 304  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 212  
 Met Ser Phe His Ile Thr Ser Val Asn Val Asn Gly Ile Arg Ala Ala  
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 Val Lys Gln Arg Ser Glu Thr Asn Leu Gly Phe Leu Pro Trp Leu Glu  
 20 25 30  
 Glu Thr Arg Pro Asp Val Val Leu Leu Gln Glu Val Arg Ala Ser Glu  
 35 40 45  
 Lys Asp Thr Ala Thr Ala Leu Gln Pro Ala Leu Asp Asn Gly Trp His  
 50 55 60  
 Tyr Ile Gly Ala Pro Ala Ala Ala Lys Gly Arg Ala Gly Val Gly Ile  
 65 70 75 80  
 Leu Ser Arg His Glu Leu Glu Asp Val Asn Ile Gly Phe Gly Ser Phe  
 85 90 95  
 Leu Asp Ser Gly Arg Tyr Ile Glu Ala Thr Ile Lys Asp Thr Thr Leu  
 100 105 110  
 Asp Val Pro Val Thr Val Ala Ser Leu Tyr Leu Pro Ser Gly Ser Ala  
 115 120 125  
 Gly Thr Asp Lys Gln Asp Glu Lys Tyr Arg Phe Leu Asp Glu Phe Glu  
 130 135 140  
 Gly Phe Leu Asp Gln Arg Ala Lys Glu Arg Ser His Met Val Ile Gly



gat ccc gta ggt tcc aga gac ctc gat caa gct gtg ctg att gag gag 307  
 Asp Pro Val Gly Ser Arg Asp Leu Asp Gln Ala Val Leu Ile Glu Glu  
 55 60 65

atc gac agc gga ttt cgg gtg cat tac gcg att gca gat gtc gca gcc 355  
 Ile Asp Ser Gly Phe Arg Val His Tyr Ala Ile Ala Asp Val Ala Ala  
 70 75 80 85

ttc gtg gag ccg ggc agt gaa ttg gaa aag att tcc ctt cac cgc ggg 403  
 Phe Val Glu Pro Gly Ser Glu Leu Glu Lys Ile Ser Leu His Arg Gly  
 90 95 100

cag act att tat ctg ccg gat tcc cca gcg cga ctg cac cct gag gaa 451  
 Gln Thr Ile Tyr Leu Pro Asp Ser Pro Ala Arg Leu His Pro Glu Glu  
 105 110 115

tta tcc gaa gat gcg gca agc ctg ctg gag gga caa acg aga cca gcg 499  
 Leu Ser Glu Asp Ala Ala Ser Leu Leu Glu Gly Gln Thr Arg Pro Ala  
 120 125 130

gtt gtg tgg tgg att gat cta gat gaa cgt ggc gaa gtc aca gcc acc 547  
 Val Val Trp Ser Ile Asp Leu Asp Glu Arg Gly Glu Val Thr Ala Thr  
 135 140 145

aag gtg cgt cgc ggg ttg gtg aaa tcc ccg gcg cgt ttg gat tat gat 595  
 Lys Val Arg Arg Gly Leu Val Lys Ser Arg Ala Arg Leu Asp Tyr Asp  
 150 155 160 165

cag gct caa ata gat gcc gag aat ggt ccg ttg cat ccg tgg ata agc 643  
 Gln Ala Gln Ile Asp Ala Glu Asn Gly Arg Leu His Pro Ser Ile Ser  
 170 175 180

tta ttg ccc aag gtc ggg cag ctg agg cag gaa agc gcg cta ccg cgc 691  
 Leu Leu Pro Lys Val Gly Gln Leu Arg Gln Glu Ser Ala Leu Arg Arg  
 185 190 195

gaa gcc gtg aat ctt tct att ccc agc cag cga gtg gtg aaa gtg ccc 739  
 Glu Ala Val Asn Leu Ser Ile Pro Ser Gln Arg Val Val Lys Val Pro  
 200 205 210

aat gat gac gcc ggt gaa cac tat gaa att gtc atc gag cca cgc ccg 787  
 Asn Asp Asp Ala Gly Glu His Tyr Glu Ile Val Ile Glu Pro Arg Pro  
 215 220 225

cac atc atg gat tac aat tcc gag att tcc ctg ctc aca gcc atg gta 835  
 His Ile Met Asp Tyr Asn Ser Glu Ile Ser Leu Leu Thr Gly Met Val  
 230 235 240 245

gcg ggg gag atg atg gtg aaa gcg ggg cac ggt ttg ctg cgt aca ctc 883  
 Ala Gly Glu Met Met Val Lys Ala Gly His Gly Leu Leu Arg Thr Leu  
 250 255 260

gcc ccg gcg acc aaa gaa tcc gaa gct act ttc aga tca gag gcg caa 931  
 Ala Pro Ala Thr Lys Glu Ser Glu Ala Thr Phe Arg Ser Glu Ala Gln  
 265 270 275

gcc ctt ggt ttt gag atc gcg ccc gaa caa ccc atc ggt gag ttt ctt 979  
 Ala Leu Gly Phe Glu Ile Ala Pro Glu Gln Pro Ile Gly Glu Phe Leu  
 280 285 290

caa agt gtg gat ccc aat acg ccc aaa ggg atg gcc att cag agg gaa 1027  
Gln Ser Val Asp Pro Asn Thr Pro Lys Gly Met Ala Ile Gln Arg Glu  
295 300 305

gca cag aaa ctc ttg cgg ggc tcc gcc agc gtg aaa aat ggg 1075  
Ala Gln Lys Leu Leu Arg Gly Ser Gly Tyr Ala Ser Val Lys Asn Gly  
310 315 320 325

gac tcg gaa gtg cat tcc ggt gtt ggt ggt tac tat gct cac gtc acc 1123  
Asp Ser Glu Val His Ser Gly Val Gly Gly Tyr Tyr Ala His Val Thr  
330 335 340

gca ccg ctg cgc cga ctt atc gac cgt ttc gcc acc gaa cat tgc ctt 1171  
Ala Pro Leu Arg Arg Leu Ile Asp Arg Phe Ala Thr Glu His Cys Leu  
345 350 355

gcg att gcc tcc gga acg gac gtt cct gaa tgg gtg acc agg gtg gaa 1219  
Ala Ile Ala Ser Gly Thr Asp Val Pro Glu Trp Val Thr Arg Val Glu  
360 365 370

gag caa gtt ctc gac acc atg aaa tac tcc tcc att ttg gcc agc caa 1267  
Glu Gln Val Leu Asp Thr Met Lys Tyr Ser Ser Ile Leu Ala Ser Gln  
375 380 385

gtg gat aat gcc tgc ctc gac ctc aca gaa gcc acc gtg ttg aaa tac 1315  
Val Asp Asn Ala Cys Leu Asp Leu Thr Glu Ala Thr Val Leu Lys Tyr  
390 395 400 405

tgg gag ggc caa aac ttc aac gcg gtg gtt gta gcg agc gaa cct gaa 1363  
Trp Glu Gly Gln Asn Phe Asn Ala Val Val Val Ala Ser Glu Pro Glu  
410 415 420

aag aac tct gct cga ctt ttt gtg tac aaa ccg cca gtg ttg gca aag 1411  
Lys Asn Ser Ala Arg Leu Phe Val Tyr Lys Pro Pro Val Leu Ala Lys  
425 430 435

tgt att ggc gcc cca gaa cag gga aca aac caa gat gtc aca ctg gtg 1459  
Cys Ile Gly Ala Pro Glu Gln Gly Thr Asn Gln Asp Val Thr Leu Val  
440 445 450

act gcg aac ttg aag aag cgt gaa gtt ttg ttt gcg tgg ccg gct gac 1507  
Thr Ala Asn Leu Lys Lys Arg Glu Val Leu Phe Ala Trp Pro Ala Asp  
455 460 465

taagcatgca ggctgggttaa gta 1530

&lt;210&gt; 214

&lt;211&gt; 469

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 214

Met Lys Leu Tyr Ala Ala Val Leu Asp Phe Glu Pro Val Ala Gln Glu  
1 5 10 15Phe Gly Val Glu Arg Gly Phe Asp Pro His Ile His Asp Glu Ala Ala  
20 25 30Ser Ser Val Asp Arg Tyr Ala Gln Glu Arg Glu Asp Leu Leu His Met  
35 40 45

Pro Phe Val Thr Ile Asp Pro Val Gly Ser Arg Asp Leu Asp Gln Ala  
 50 55 60  
 Val Leu Ile Glu Glu Ile Asp Ser Gly Phe Arg Val His Tyr Ala Ile  
 65 70 75 80  
 Ala Asp Val Ala Ala Phe Val Glu Pro Gly Ser Glu Leu Glu Lys Ile  
 85 90 95  
 Ser Leu His Arg Gly Gln Thr Ile Tyr Leu Pro Asp Ser Pro Ala Arg  
 100 105 110  
 Leu His Pro Glu Glu Leu Ser Glu Asp Ala Ala Ser Leu Leu Glu Gly  
 115 120 125  
 Gln Thr Arg Pro Ala Val Val Trp Ser Ile Asp Leu Asp Glu Arg Gly  
 130 135 140  
 Glu Val Thr Ala Thr Lys Val Arg Arg Gly Leu Val Lys Ser Arg Ala  
 145 150 155 160  
 Arg Leu Asp Tyr Asp Gln Ala Gln Ile Asp Ala Glu Asn Gly Arg Leu  
 165 170 175  
 His Pro Ser Ile Ser Leu Leu Pro Lys Val Gly Gln Leu Arg Gln Glu  
 180 185 190  
 Ser Ala Leu Arg Arg Glu Ala Val Asn Leu Ser Ile Pro Ser Gln Arg  
 195 200 205  
 Val Val Lys Val Pro Asn Asp Asp Ala Gly Glu His Tyr Glu Ile Val  
 210 215 220  
 Ile Glu Pro Arg Pro His Ile Met Asp Tyr Asn Ser Glu Ile Ser Leu  
 225 230 235 240  
 Leu Thr Gly Met Val Ala Gly Glu Met Met Val Lys Ala Gly His Gly  
 245 250 255  
 Leu Leu Arg Thr Leu Ala Pro Ala Thr Lys Glu Ser Glu Ala Thr Phe  
 260 265 270  
 Arg Ser Glu Ala Gln Ala Leu Gly Phe Glu Ile Ala Pro Glu Gln Pro  
 275 280 285  
 Ile Gly Glu Phe Leu Gln Ser Val Asp Pro Asn Thr Pro Lys Gly Met  
 290 295 300  
 Ala Ile Gln Arg Glu Ala Gln Lys Leu Leu Arg Gly Ser Gly Tyr Ala  
 305 310 315 320  
 Ser Val Lys Asn Gly Asp Ser Glu Val His Ser Gly Val Gly Gly Tyr  
 325 330 335  
 Tyr Ala His Val Thr Ala Pro Leu Arg Arg Leu Ile Asp Arg Phe Ala  
 340 345 350  
 Thr Glu His Cys Leu Ala Ile Ala Ser Gly Thr Asp Val Pro Glu Trp  
 355 360 365

Val Thr Arg Val Glu Glu Gln Val Leu Asp Thr Met Lys Tyr Ser Ser  
 370 375 380

Ile Leu Ala Ser Gln Val Asp Asn Ala Cys Leu Asp Leu Thr Glu Ala  
 385 390 395 400

Thr Val Leu Lys Tyr Trp Glu Gly Gln Asn Phe Asn Ala Val Val Val  
 405 410 415

Ala Ser Glu Pro Glu Lys Asn Ser Ala Arg Leu Phe Val Tyr Lys Pro  
 420 425 430

Pro Val Leu Ala Lys Cys Ile Gly Ala Pro Glu Gln Gly Thr Asn Gln  
 435 440 445

Asp Val Thr Leu Val Thr Ala Asn Leu Lys Lys Arg Glu Val Leu Phe  
 450 455 460

Ala Trp Pro Ala Asp  
 465

<210> 215  
 <211> 519  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(496)  
 <223> RXA02077

<400> 215  
 ccagcagccc tgaatctgat gctccaaga tgcgcgcttc aattgtcagc cgttacggcc 60  
 tggcagatat cgctcgcgaa attgatcttg gcaaccacat atg ctg ggc aaa ggc 115  
 Met Leu Gly Lys Gly  
 1 5

gaa ttg ctc acc gaa ggt cgc agt aag gat tcc att ctt gcg gac acc 163  
 Glu Leu Leu Thr Glu Gly Arg Ser Lys Asp Ser Ile Leu Ala Asp Thr  
 10 15 20

aca gag gcg ttg ttc ggc gcg att ttc cgc cag cac ggt ttt gaa acc 211  
 Thr Glu Ala Leu Phe Gly Ala Ile Phe Arg Gln His Gly Phe Glu Thr  
 25 30 35

gcc cgc gac gta att ttg cgc ctg ttt gcc tac aag atc gat aac gca 259  
 Ala Arg Asp Val Ile Leu Arg Leu Phe Ala Tyr Lys Ile Asp Asn Ala  
 40 45 50

tcg gcc agg ggc att cac cag gac tgg aag acc acg ctg cag gag gaa 307  
 Ser Ala Arg Gly Ile His Gln Asp Trp Lys Thr Thr Leu Gln Glu Glu  
 55 60 65

ctt gct cag cgc aag cgc ccc atg gct gaa tat tcc gcc acc tca gtc 355  
 Leu Ala Gln Arg Lys Arg Pro Met Ala Glu Tyr Ser Ala Thr Ser Val  
 70 75 80 85

ggt ccg gat cac gat cta gtg ttc acc gcc atc gtg acg ctg gaa ggt 403  
 Gly Pro Asp His Asp Leu Val Phe Thr Ala Ile Val Thr Leu Glu Gly

	90	95	100	
gaa gaa atg ggt cgg gga gaa ggc ccg aac aag ctg gcc gag cag				451
Glu Glu Met Gly Arg Gly Glu Gly Pro Asn Lys Lys Leu Ala Glu Gln				
	105	110	115	
gaa gca cgc cac cag gca ttc cga aag ctt cgg gag tcc cgt gcc				496
Glu Ala Ala His Gln Ala Phe Arg Lys Leu Arg Glu Ser Arg Ala				
	120	125	130	
tgaactgcct gaagttgagg tgg				519

&lt;210&gt; 216

&lt;211&gt; 132

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 216

Met Leu Gly Lys Gly Glu Leu Leu Thr Glu Gly Arg Ser Lys Asp Ser			
	1	5	10
			15

Ile Leu Ala Asp Thr Thr Glu Ala Leu Phe Gly Ala Ile Phe Arg Gln			
	20	25	30

His Gly Phe Glu Thr Ala Arg Asp Val Ile Leu Arg Leu Phe Ala Tyr			
	35	40	45

Lys Ile Asp Asn Ala Ser Ala Arg Gly Ile His Gln Asp Trp Lys Thr			
	50	55	60

Thr Leu Gln Glu Glu Leu Ala Gln Arg Lys Arg Pro Met Ala Glu Tyr			
	65	70	75
			80

Ser Ala Thr Ser Val Gly Pro Asp His Asp Leu Val Phe Thr Ala Ile			
	85	90	95

Val Thr Leu Glu Gly Glu Glu Met Gly Arg Gly Glu Gly Pro Asn Lys			
	100	105	110

Lys Leu Ala Glu Gln Glu Ala Ala His Gln Ala Phe Arg Lys Leu Arg			
	115	120	125

Glu Ser Arg Ala	
	130

&lt;210&gt; 217

&lt;211&gt; 1332

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1309)

&lt;223&gt; RXN01563

&lt;400&gt; 217

gacctcaccg cgcattgtga agcgttcgca gcagtgcttg cctctgtgtgc tggacttccc 60

ccagagggcg tcaccgaact acgaaggttag attggacacc atg gtt tcc gat ctc 115



	Met	Val	Ser	Asp	Leu	
	1				5	
ctt caa ccc cgc gac ggc att ccg cct ttg cta tct acc cct ggt gag						163
Leu Gln Pro Arg Asp Gly Ile Pro Pro Leu Leu Ser Thr Pro Gly Glu						
	10				20	
ttc act gct gcg gca gat ctc ttg gct agc gga act ggg ccc ttc gcc						211
Phe Thr Ala Ala Ala Asp Leu Leu Ala Ser Gly Thr Gly Pro Phe Ala						
	25				35	
att gat acg gaa cgc gcg tcc ggt ttt aga tac gat gac cgc gca ttt						259
Ile Asp Thr Glu Arg Ala Ser Gly Phe Arg Tyr Asp Asp Arg Ala Phe						
	40				50	
ttg att cag atc cgg cgc cgt ggc agc gga act ctc cta ttc gac ccg						307
Leu Ile Gln Ile Arg Arg Gly Ser Gly Thr Leu Phe Asp Pro						
	55				65	
gag cag ttc cgt cct gaa tta act cag gcg tta aag ccg gtg ctc aat						355
Glu Gln Phe Arg Pro Glu Leu Thr Gln Ala Leu Lys Pro Val Leu Asn						
	70				80	85
ggg caa gag tgg atc att cac gca gca agc acc gat ttg ccg agc ctt						403
Gly Gln Glu Trp Ile Ile His Ala Ala Ser Thr Asp Leu Pro Ser Leu						
	90				95	100
gcg tgg ctt gat ctt cac ccc gga tta ctc ttt gat aca gaa ctt gct						451
Ala Trp Leu Asp Leu His Pro Gly Leu Leu Phe Asp Thr Glu Leu Ala						
	105				110	115
ggc cgc tta gcc gga ttt gat cac gtt aat ctc gct gcc atg gtg gaa						499
Gly Arg Leu Ala Gly Phe Asp His Val Asn Leu Ala Ala Met Val Glu						
	120				125	130
cag att ttt gat ctc cac ttg ctc aaa ggc cac cgt tcg gaa gat tgg						547
Gln Ile Phe Asp Leu His Leu Leu Lys Gly His Arg Ser Glu Asp Trp						
	135				140	145
tcc aag cgt cct ctg ccg gaa tct tgg ctc aac tac gca gca ctc gat						595
Ser Lys Arg Pro Leu Pro Glu Ser Trp Leu Asn Tyr Ala Ala Leu Asp						
	150				155	160
gtg gag atg ctg ctg gag ett gcc gat gtc atg gct gaa atc ctg gat						643
Val Glu Met Leu Leu Glu Leu Ala Asp Val Met Ala Glu Ile Leu Asp						
	170				175	180
cag cag gga aaa ctc ccc tgg gct gaa cag gaa ttt gtc cat att gtg						691
Gln Gln Gly Lys Leu Pro Trp Ala Glu Gln Glu Phe Val His Ile Val						
	185				190	195
gat caa ttc gcc acg atg acc gaa cct tcc gaa acg tcc tgg cag gac						739
Asp Gln Phe Ala Thr Met Thr Glu Pro Ser Glu Thr Ser Trp Gln Asp						
	200				205	210
ctt aaa ggg ctg tcc act ctc aaa cga cca gac caa tta gtt gtg gcc						787
Leu Lys Gly Leu Ser Thr Leu Lys Arg Pro Asp Gln Leu Val Val Ala						
	215				220	225
cgt gaa atg tgg ttg gaa cgc gac tct ttc gca gcc tcc cgc gac ctg						835
Arg Glu Met Trp Leu Glu Arg Asp Ser Phe Ala Ala Ser Arg Asp Leu						

230	235	240	245	
gcg ccc ggt aaa gtg ctg tcc aac aaa gtc atc gtg gaa gtc gcc cgt				883
Ala Pro Gly Lys Val Leu Ser Asn Lys Val Ile Val Glu Val Ala Arg	250	255	260	
gtt ctc ccc cgc acc ccg gca gaa tta gcg cag gtc aag gga ttc ccc				931
Val Leu Pro Arg Thr Pro Ala Glu Leu Ala Gln Val Lys Gly Phe Pro	265	270	275	
ggg cga tcc cag ggt gcc acc aaa cgc tgg ttc cgc atc atc acc cgg				979
Gly Arg Ser Gln Gly Ala Thr Lys Arg Trp Phe Arg Ile Ile Thr Arg	280	285	290	
gcg ctc aaa tcc cct cgc agg aac tgg cca aag cct cag cag cgc aag				1027
Ala Leu Lys Ser Pro Arg Arg Asn Trp Pro Lys Pro Gln Gln Arg Lys	295	300	305	
gac ggc atc ccc gat cgt cgc gcg tgg gcg tcc tac tac cca gaa gag				1075
Asp Gly Ile Pro Asp Arg Arg Ala Trp Ala Ser Tyr Tyr Pro Glu Glu	310	315	320	325
cac gaa gtg ctc caa gag att aga gcg ctt atc gac gac ctc gcc gcc				1123
His Glu Val Leu Gln Glu Ile Arg Ala Leu Ile Asp Asp Leu Ala Ala	330	335	340	
gat atc aac gtt ccc ggc gag aat atc ctt cag cct tca act ctg cga				1171
Asp Ile Asn Val Pro Gly Glu Asn Ile Leu Gln Pro Ser Thr Leu Arg	345	350	355	
gta gct gtg tgg atg gct aaa cac acc ggc gag atc cat aat gct gaa				1219
Val Ala Val Trp Met Ala Lys His Thr Gly Glu Ile His Asn Ala Glu	360	365	370	
aca ctc aac gct gta ctt cgc gat tat ggt gcc cgc cag tgg caa att				1267
Thr Leu Asn Ala Val Leu Arg Asp Tyr Gly Ala Arg Gln Trp Gln Ile	375	380	385	
gac cag act ttt ccg att ctg tcc gcc aac ttg ctg aag ctc				1309
Asp Gln Thr Phe Pro Ile Leu Ser Ala Asn Leu Leu Lys Leu	390	395	400	
taaacctaaa gcccgcggt aag				1332
<210> 218				
<211> 403				
<212> PRT				
<213> Corynebacterium glutamicum				
<400> 218				
Met Val Ser Asp Leu Leu Gln Pro Arg Asp Gly Ile Pro Pro Leu Leu				
1	5	10	15	
Ser Thr Pro Gly Glu Phe Thr Ala Ala Ala Asp Leu Leu Ala Ser Gly				
20	25	30		
Thr Gly Pro Phe Ala Ile Asp Thr Glu Arg Ala Ser Gly Phe Arg Tyr				
35	40	45		
Asp Asp Arg Ala Phe Leu Ile Gln Ile Arg Arg Arg Gly Ser Gly Thr				

50	55	60
Leu Leu Phe Asp Pro Glu Gln Phe Arg Pro Glu Leu Thr Gln Ala Leu 65 70 75 80		
Lys Pro Val Leu Asn Gly Gln Glu Trp Ile Ile His Ala Ala Ser Thr 85 90 95		
Asp Leu Pro Ser Leu Ala Trp Leu Asp Leu His Pro Gly Leu Leu Phe 100 105 110		
Asp Thr Glu Leu Ala Gly Arg Leu Ala Gly Phe Asp His Val Asn Leu 115 120 125		
Ala Ala Met Val Glu Gln Ile Phe Asp Leu His Leu Leu Lys Gly His 130 135 140		
Arg Ser Glu Asp Trp Ser Lys Arg Pro Leu Pro Glu Ser Trp Leu Asn 145 150 155 160		
Tyr Ala Ala Leu Asp Val Glu Met Leu Leu Glu Leu Ala Asp Val Met 165 170 175		
Ala Glu Ile Leu Asp Gln Gln Gly Lys Leu Pro Trp Ala Glu Gln Glu 180 185 190		
Phe Val His Ile Val Asp Gln Phe Ala Thr Met Thr Glu Pro Ser Glu 195 200 205		
Thr Ser Trp Gln Asp Leu Lys Gly Leu Ser Thr Leu Lys Arg Pro Asp 210 215 220		
Gln Leu Val Val Ala Arg Glu Met Trp Leu Glu Arg Asp Ser Phe Ala 225 230 235 240		
Ala Ser Arg Asp Leu Ala Pro Gly Lys Val Leu Ser Asn Lys Val Ile 245 250 255		
Val Glu Val Ala Arg Val Leu Pro Arg Thr Pro Ala Glu Leu Ala Gln 260 265 270		
Val Lys Gly Phe Pro Gly Arg Ser Gln Gly Ala Thr Lys Arg Trp Phe 275 280 285		
Arg Ile Ile Thr Arg Ala Leu Lys Ser Pro Arg Arg Asn Trp Pro Lys 290 295 300		
Pro Gln Gln Arg Lys Asp Gly Ile Pro Asp Arg Arg Ala Trp Ala Ser 305 310 315 320		
Tyr Tyr Pro Glu Glu His Glu Val Leu Gln Glu Ile Arg Ala Leu Ile 325 330 335		
Asp Asp Leu Ala Ala Asp Ile Asn Val Pro Gly Glu Asn Ile Leu Gln 340 345 350		
Pro Ser Thr Leu Arg Val Ala Val Trp Met Ala Lys His Thr Gly Glu 355 360 365		
Ile His Asn Ala Glu Thr Leu Asn Ala Val Leu Arg Asp Tyr Gly Ala 370 375 380		

Arg Gln Trp Gln Ile Asp Gln Thr Phe Pro Ile Leu Ser Ala Asn Leu  
 385 390 395 400

Leu Lys Leu

<210> 219  
 <211> 833  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (1)..(810)  
 <223> FRXA01563

<400> 219  
 cag att ttt gat ctc cac ttg ctc aaa ggc cac ggt tcg gaa gat tgg 48  
 Gln Ile Phe Asp Leu His Leu Leu Lys Gly His Gly Ser Glu Asp Trp  
 1 5 10 15  
 tcc aag cgt cct ctg ccg gaa tct tgg ctc aac tac gca gca ctc gat 96  
 Ser Lys Arg Pro Leu Pro Glu Ser Trp Leu Asn Tyr Ala Ala Leu Asp  
 20 25 30  
 gtg gag atg ctg ctg gag ctt gcc gat gtc atg gct gaa atc ctg gat 144  
 Val Glu Met Leu Leu Glu Leu Ala Asp Val Met Ala Glu Ile Leu Asp  
 35 40 45  
 cag cag gga aaa ctc ccc tgg gct gaa cag gaa ttt gtc cat att gtg 192  
 Gln Gln Gly Lys Leu Pro Trp Ala Glu Gln Glu Phe Val His Ile Val  
 50 55 60  
 gat caa ttc gcc acg atg acc gaa cct tcc gaa acg tcc tgg cag gac 240  
 Asp Gln Phe Ala Thr Met Thr Glu Pro Ser Glu Thr Ser Trp Gln Asp  
 65 70 75 80  
 ctt aaa ggg ctg tcc act ctc aaa cga cca gac caa tta gtt gtg gcc 288  
 Leu Lys Gly Leu Ser Thr Leu Lys Arg Pro Asp Gln Leu Val Val Ala  
 85 90 95  
 cgt gaa atg tgg ttg gaa cgc gac tct ttc gca gcc tcc cgc gac ctg 336  
 Arg Glu Met Trp Leu Glu Arg Asp Ser Phe Ala Ala Ser Arg Asp Leu  
 100 105 110  
 gcg ccc ggt aaa gtg ctg tcc aac aaa gtc atc gtg gaa gtc gcc cgt 384  
 Ala Pro Gly Lys Val Leu Ser Asn Lys Val Ile Val Glu Val Ala Arg  
 115 120 125  
 gtt ctc ccc cgc acc ccg gca gaa tta gcg cag gtc aag gga ttc ccc 432  
 Val Leu Pro Arg Thr Pro Ala Glu Leu Ala Gln Val Lys Gly Phe Pro  
 130 135 140  
 ggt cga tcc cag ggt gcc acc aaa cgc tgg ttc cgc atc atc acc cgg 480  
 Gly Arg Ser Gln Gly Ala Thr Lys Arg Trp Phe Arg Ile Ile Thr Arg  
 145 150 155 160  
 gcg ctc aaa tcc cct cgc agg aac tgg cca aag cct cag cag cgc aag 528  
 Ala Leu Lys Ser Pro Arg Arg Asn Trp Pro Lys Pro Gln Gln Arg Lys

165	170	175	
gac ggc atc ccc gat cgt cgc gcg tgg gcg tcc tac tac cca gaa gag			576
Asp Gly Ile Pro Asp Arg Arg Ala Trp Ala Ser Tyr Tyr Pro Glu Glu			
180	185	190	
cac gaa gtg ctc caa gag att aga gcg ctt atc gac gac ctc gcc gcc			624
His Glu Val Leu Gln Glu Ile Arg Ala Leu Ile Asp Asp Leu Ala Ala			
195	200	205	
gat atc aac gtt ccc ggc gag aat atc ctt cag cct tca act ctg cga			672
Asp Ile Asn Val Pro Gly Glu Asn Ile Leu Gln Pro Ser Thr Leu Arg			
210	215	220	
gta gct gtg tgg atg gct aaa cac acc ggc gag atc cat aat gct gaa			720
Val Ala Val Trp Met Ala Lys His Thr Gly Glu Ile His Asn Ala Glu			
225	230	240	
aca ctc aac gct gta ctt cgc gat tat ggt gcc cgc cag tgg caa att			768
Thr Leu Asn Ala Val Leu Arg Asp Tyr Gly Ala Arg Gln Trp Gln Ile			
245	250	255	
gac cag act ttt ccg att ctg tcc gcc aac ttg ctg aag ctc			810
Asp Gln Thr Phe Pro Ile Leu Ser Ala Asn Leu Leu Lys Leu			
260	265	270	
taaacctaaa gcccgcggt aag			833
<210> 220			
<211> 270			
<212> PRT			
<213> Corynebacterium glutamicum			
<400> 220			
Gln Ile Phe Asp Leu His Leu Leu Lys Gly His Gly Ser Glu Asp Trp			
1	5	10	15
Ser Lys Arg Pro Leu Pro Glu Ser Trp Leu Asn Tyr Ala Ala Leu Asp			
20	25	30	
Val Glu Met Leu Leu Glu Leu Ala Asp Val Met Ala Glu Ile Leu Asp			
35	40	45	
Gln Gln Gly Lys Leu Pro Trp Ala Glu Gln Glu Phe Val His Ile Val			
50	55	60	
Asp Gln Phe Ala Thr Met Thr Glu Pro Ser Glu Thr Ser Trp Gln Asp			
65	70	75	80
Leu Lys Gly Leu Ser Thr Leu Lys Arg Pro Asp Gln Leu Val Val Ala			
85	90	95	
Arg Glu Met Trp Leu Glu Arg Asp Ser Phe Ala Ala Ser Arg Asp Leu			
100	105	110	
Ala Pro Gly Lys Val Leu Ser Asn Lys Val Ile Val Glu Val Ala Arg			
115	120	125	
Val Leu Pro Arg Thr Pro Ala Glu Leu Ala Gln Val Lys Gly Phe Pro			
130	135	140	

Gly Arg Ser Gln Gly Ala Thr Lys Arg Trp Phe Arg Ile Ile Thr Arg  
145 150 155 160

Ala Leu Lys Ser Pro Arg Arg Asn Trp Pro Lys Pro Gln Gln Arg Lys  
165 170 175

Asp Gly Ile Pro Asp Arg Arg Ala Trp Ala Ser Tyr Tyr Pro Glu Glu  
180 185 190

His Glu Val Leu Gln Glu Ile Arg Ala Leu Ile Asp Asp Leu Ala Ala  
195 200 205

Asp Ile Asn Val Pro Gly Glu Asn Ile Leu Gln Pro Ser Thr Leu Arg  
210 215 220

Val Ala Val Trp Met Ala Lys His Thr Gly Glu Ile His Asn Ala Glu  
225 230 235 240

Thr Leu Asn Ala Val Leu Arg Asp Tyr Gly Ala Arg Gln Trp Gln Ile  
245 250 255

Asp Gln Thr Phe Pro Ile Leu Ser Ala Asn Leu Leu Lys Leu  
260 265 270

<210> 221

<211> 454

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(454)

<223> FRXA01713

<400> 221

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ccagagggcg tcaccgaact acgaaggttag attggacacc atg gtt tcc gat ctc 115  
Met Val Ser Asp Leu  
1 5

ctt caa ccc cgc gac ggc att ccg cct ttg cta tct acc cct ggt gag 163  
Leu Gln Pro Arg Asp Gly Ile Pro Pro Leu Leu Ser Thr Pro Gly Glu  
10 15 20

ttc act gct gcg gca gat ctc ttg gct agc gga act ggg ccc ttc gcc 211  
Phe Thr Ala Ala Ala Asp Leu Leu Ala Ser Gly Thr Gly Pro Phe Ala  
25 30 35

att gat acg gaa cgc gcg tcc ggt ttt aga tac gat gac cgc gca ttt 259  
Ile Asp Thr Glu Arg Ala Ser Gly Phe Arg Tyr Asp Asp Arg Ala Phe  
40 45 50

ttg att cag atc cgg cgc cgt ggc agc gga act ctc cta ttc gac ccg 307  
Leu Ile Gln Ile Arg Arg Gly Ser Gly Thr Leu Leu Phe Asp Pro  
55 60 65

gag cag ttc cgt cct gaa tta act cag gcg tta aag ccg gtg ctc aat 355  
Glu Gln Phe Arg Pro Glu Leu Thr Gln Ala Leu Lys Pro Val Leu Asn

70	75	80	85	
ggg caa gag tgg atc att cac gca gca agc acc gat ttg ccg agc ctt				403
Gly Gln Glu Trp Ile Ile His Ala Ala Ser Thr Asp Leu Pro Ser Leu	90	95	100	
gcg tgg ctt gat ctt cac ccc gga tta ctc ttt gat aca gaa ctt gct				451
Ala Trp Leu Asp Leu His Pro Gly Leu Leu Phe Asp Thr Glu Leu Ala	105	110	115	
ggc				454
Gly				

&lt;210&gt; 222

&lt;211&gt; 118

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 222

Met Val Ser Asp Leu Leu Gln Pro Arg Asp Gly Ile Pro Pro Leu Leu			
1	5	10	15

Ser Thr Pro Gly Glu Phe Thr Ala Ala Ala Asp Leu Leu Ala Ser Gly			
20	25	30	

Thr Gly Pro Phe Ala Ile Asp Thr Glu Arg Ala Ser Gly Phe Arg Tyr			
35	40	45	

Asp Asp Arg Ala Phe Leu Ile Gln Ile Arg Arg Arg Gly Ser Gly Thr			
50	55	60	

Leu Leu Phe Asp Pro Glu Gln Phe Arg Pro Glu Leu Thr Gln Ala Leu			
65	70	75	80

Lys Pro Val Leu Asn Gly Gln Glu Trp Ile Ile His Ala Ala Ser Thr			
85	90	95	

Asp Leu Pro Ser Leu Ala Trp Leu Asp Leu His Pro Gly Leu Leu Phe			
100	105	110	

Asp Thr Glu Leu Ala Gly	
115	

&lt;210&gt; 223

&lt;211&gt; 2412

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(2389)

&lt;223&gt; RXA02369

&lt;400&gt; 223

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cattgctcaa tcgtggagat aagaaaatag gagtgtcgct	gtg cca aat aac aag	115
	Val Pro Asn Asn Lys	

	1	5	
gca gta gaa gca gaa atc tct ccc tcg gct gtg ctg gcc gcg gaa ttt			163
Ala Val Glu Ala Glu Ile Ser Pro Ser Ala Val Leu Ala Ala Glu Phe	10	15	20
gat cga gat tca ttg agc gaa aaa acc cgc gta cat caa ctg gcc aaa			211
Asp Arg Asp Ser Leu Ser Glu Lys Thr Arg Val His Gln Leu Ala Lys	25	30	35
cga ctt gga atg gtt tcc aag gac gtc gtt gtt gcg ctc gat ggc atc			259
Arg Leu Gly Met Val Ser Lys Asp Val Val Val Ala Leu Asp Gly Ile	40	45	50
ggc ctg gtc aag gtt gcg cag tca aac ctg agc aaa gaa gaa gta gaa			307
Gly Leu Val Lys Val Ala Gln Ser Asn Leu Ser Lys Glu Glu Val Glu	55	60	65
aag ctt ctc gac gcc ctg tct cag ccc gta ctc aac gct gcc cca gct			355
Lys Leu Leu Asp Ala Leu Ser Gln Pro Val Leu Asn Ala Ala Pro Ala	70	75	80
gcc gtc ccc gac gtt gaa ccg gtg gag aag att cgt cga cgc gtt gag			403
Ala Val Pro Asp Val Glu Pro Val Glu Lys Ile Arg Arg Arg Val Glu	90	95	100
aag aat gtg gaa aat gaa atc cac caa atc gaa gaa aaa gta gag cgc			451
Lys Asn Val Glu Asn Glu Ile His Gln Ile Glu Glu Lys Val Glu Arg	105	110	115
gaa ctc gcg gca gtc gcg caa cct act gac ttc gag gcg gca gcc cgc			499
Glu Leu Ala Ala Val Ala Gln Pro Thr Asp Phe Glu Ala Ala Ala Arg	120	125	130
gaa gaa gcc act gca gaa ctg ctg gaa gat atc gtc cca gag atc acc			547
Glu Glu Ala Thr Ala Glu Leu Leu Glu Asp Ile Val Pro Glu Ile Thr	135	140	145
ccg gcg ccg gtg gaa gca tct gtg tac acg ccg atc ttt gtg gca cct			595
Pro Ala Pro Val Glu Ala Ser Val Tyr Thr Pro Ile Phe Val Ala Pro	150	155	160
gca gtt gta cct act gaa aac gtc caa gac acc gac gat gaa cag gtc			643
Ala Val Val Pro Thr Glu Asn Val Gln Asp Thr Asp Asp Glu Gln Val	170	175	180
cgc gaa cgc acg gcg ccg aag cgc cgt ggg cgt cgt ggc acc ggc cgc			691
Arg Glu Arg Thr Ala Arg Lys Arg Arg Gly Arg Arg Gly Thr Gly Arg	185	190	195
gga cgt gga gct gaa gct gaa acc gtc acc gaa gtg agt gag gag gcg			739
Gly Arg Gly Ala Glu Ala Glu Thr Val Thr Glu Val Ser Glu Glu Ala	200	205	210
tcg aca agc gaa gta gaa gag gta aac gag cca atc gga att aag ggc			787
Ser Thr Ser Glu Val Glu Glu Val Asn Glu Pro Ile Gly Ile Lys Gly	215	220	225
tcc act cgc ttg gag gcg caa cgc cgc cgt cgc acg gaa atg cgc gaa			835
Ser Thr Arg Leu Glu Ala Gln Arg Arg Arg Arg Thr Glu Met Arg Glu	230	235	240



gaa aac aaa aaa cgc cgc cat gtg gtc agc acc cag gag ttc atg gaa 883  
 Glu Asn Lys Lys Arg Arg His Val Val Ser Thr Gln Glu Phe Met Glu  
 250 255 260

cgc cgt gaa tgc atg gaa cgt cgc atg att gtg cgc gag cgc caa cgc 931  
 Arg Arg Glu Ser Met Glu Arg Arg Met Ile Val Arg Glu Arg Gln Arg  
 265 270 275

cac gat cac cca ggt ctg gtc act cag gtt ggt gtg ctg gaa gac gat 979  
 His Asp His Pro Gly Leu Val Thr Gln Val Gly Val Leu Glu Asp Asp  
 280 285 290

cag ctg gtt gag cag ttt gtt acc tct gat cgc cag atg tct atg gtg 1027  
 Gln Leu Val Glu Gln Phe Val Thr Ser Asp Ala Gln Met Ser Met Val  
 295 300 305

ggc aat att tat ctg ggc cgc gtt caa aat gtg ctg cca agc atg gaa 1075  
 Gly Asn Ile Tyr Leu Gly Arg Val Gln Asn Val Leu Pro Ser Met Glu  
 310 315 320 325

gct gcc ttc att gac att gga aaa ggt cgc aac ggt gtg ttg tat gcc 1123  
 Ala Ala Phe Ile Asp Ile Gly Lys Gly Arg Asn Gly Val Leu Tyr Ala  
 330 335 340

ggc gaa gtc gac tgg aaa gct gct gga ctt ggc gga cgt gga cgt cgc 1171  
 Gly Glu Val Asp Trp Lys Ala Ala Gly Leu Gly Gly Arg Gly Arg Arg  
 345 350 355

att gag cag cgc ctg aaa gcc ggc gac cag gtt ctc gtc cag gtc tcc 1219  
 Ile Glu Gln Ala Leu Lys Ala Gly Asp Gln Val Leu Val Gln Val Ser  
 360 365 370

aag gat cca ttg ggc cat aag ggt cgc cgt ttg acc acc caa att tcc 1267  
 Lys Asp Pro Leu Gly His Lys Gly Ala Arg Leu Thr Thr Gln Ile Ser  
 375 380 385

ctg cgc gga cgt tac ctg gtg tac gtt cca ggt ggt cgc agc gct ggc 1315  
 Leu Ala Gly Arg Tyr Leu Val Tyr Val Pro Gly Gly Arg Ser Ala Gly  
 390 395 400 405

att tcc cgc aaa ctg cct gga cct gag cgc aag cgt ctg aag gaa atc 1363  
 Ile Ser Arg Lys Leu Pro Gly Pro Glu Arg Lys Arg Leu Lys Glu Ile  
 410 415 420

ctt ggc cgc gtt gtc cca cgc cag ggt gga acc atc atc cga act gct 1411  
 Leu Gly Arg Val Val Pro Ala Gln Gly Gly Thr Ile Ile Arg Thr Ala  
 425 430 435

gct gaa ggt gtg tgc gaa gaa aac atc gca gct gac gtg aac cgt ctg 1459  
 Ala Glu Gly Val Ser Glu Glu Asn Ile Ala Ala Asp Val Asn Arg Leu  
 440 445 450

cac acc ctg tgg gag cag atc aag gaa cgc act cgc gag gaa aag aag 1507  
 His Thr Leu Trp Glu Gln Ile Lys Glu Arg Thr Ala Glu Glu Lys Lys  
 455 460 465

tcc cgc ggt tct aag cgc atc acc atg tat gaa gag cca gac atg ctg 1555  
 Ser Arg Gly Ser Lys Pro Ile Thr Met Tyr Glu Glu Pro Asp Met Leu  
 470 475 480 485

gtg aag gtg atc cgt gac ctc ttc aat gaa gat ttc acc tca ctg atc 1603  
Val Lys Val Ile Arg Asp Leu Phe Asn Glu Asp Phe Thr Ser Leu Ile  
490 495 500

gtt gac ggc gac cgt gcc tgg aac acc gtg cgt gcc tac atc caa tca 1651  
Val Asp Gly Asp Arg Ala Trp Asn Thr Val Arg Ala Tyr Ile Gln Ser  
505 510 515

gtc gct cct gat ttg gtg tcc cgc gtg gaa cac ttc aat cgc gca gac 1699  
Val Ala Pro Asp Leu Val Ser Arg Val Glu His Phe Asn Arg Ala Asp  
520 525 530

ttt gac ggc aag gat gct ttc gaa gca ttc gac ctg aac acc cag ctt 1747  
Phe Asp Gly Lys Asp Ala Phe Glu Ala Phe Asp Leu Asn Thr Gln Leu  
535 540 545

gag gaa gcg ctg tcc cga aag gtg aac ctg cca tgc ggt gga tgc ctg 1795  
Glu Glu Ala Leu Ser Arg Lys Val Asn Leu Pro Ser Gly Gly Ser Leu  
550 555 560 565

atc atc gac cgc acc gaa gcc atg acg gtg atc gat gtg aac acc gga 1843  
Ile Ile Asp Arg Thr Glu Ala Met Thr Val Ile Asp Val Asn Thr Gly  
570 575 580

cgc tac acc ggc aag ggt ggt ggc aac ttg gaa gaa acc gtc acg ctc 1891  
Arg Tyr Thr Gly Lys Gly Gly Asn Leu Glu Thr Val Thr Leu  
585 590 595

aac aac att gaa gct gcc gaa gaa atc gtg cgc caa atg cgc ctg cgg 1939  
Asn Asn Ile Glu Ala Ala Glu Glu Ile Val Arg Gln Met Arg Leu Arg  
600 605 610

gat ctc ggt ggc atg atc gtt gtc gac ttc atc gat atg gtg ctg cca 1987  
Asp Leu Gly Gly Met Ile Val Val Asp Phe Ile Asp Met Val Leu Pro  
615 620 625

gaa aac caa gaa ttg gtc ctg cgc cga ctc aat gaa gcg cta gaa aac 2035  
Glu Asn Gln Glu Leu Val Leu Arg Arg Leu Asn Glu Ala Leu Glu Asn  
630 635 640 645

gat cgc acc cgc cac caa gtc tct gag gta acc tca ctg gga ctt gtt 2083  
Asp Arg Thr Arg His Gln Val Ser Glu Val Thr Ser Leu Gly Leu Val  
650 655 660

cag atg acc cgc aaa cgc atc ggc gcg ggc ctg ctg gaa acc ttc tct 2131  
Gln Met Thr Arg Lys Arg Ile Gly Ala Gly Leu Leu Glu Thr Phe Ser  
665 670 675

tca ccg tgt gag cac tgt gaa ggc cga ggc atc atc gtt cat gtt gat 2179  
Ser Pro Cys Glu His Cys Glu Gly Arg Gly Ile Ile Val His Val Asp  
680 685 690

cca gta gac acc gtt gac gag cgc gtt gag gcg aaa gcg gaa gag cgt 2227  
Pro Val Asp Thr Val Asp Glu Arg Val Glu Ala Lys Ala Glu Glu Arg  
695 700 705

agc cgt cgt cac cag cgt tcc aat agc act aac aag gca gct gcg gag 2275  
Ser Arg Arg His Gln Arg Ser Asn Ser Thr Asn Lys Ala Ala Glu  
710 715 720 725

cac ccg atg gtt gtt gcc atg cgt gat ctc gtg gaa agc gat gaa cac 2323

His Pro Met Val Val Ala Met Arg Asp Leu Val Glu Ser Asp Glu His  
730 735 740

gat ctg gat caa gaa ttt gag gaa ctc gct gca tca atg atc gtt ctc 2371  
Asp Leu Asp Gln Glu Phe Glu Glu Leu Ala Ala Ser Met Ile Val Leu  
745 750 755

gat gac tcc gat cta tta tgatgtggac aacgacaagc tcg 2412  
Asp Asp Ser Asp Leu Leu  
760

<210> 224

<211> 763

<212> PRT

<213> Corynebacterium glutamicum

<400> 224

Val Pro Asn Asn Lys Ala Val Glu Ala Glu Ile Ser Pro Ser Ala Val  
1 5 10 15

Leu Ala Ala Glu Phe Asp Arg Asp Ser Leu Ser Glu Lys Thr Arg Val  
20 25 30

His Gln Leu Ala Lys Arg Leu Gly Met Val Ser Lys Asp Val Val Val  
35 40 45

Ala Leu Asp Gly Ile Gly Leu Val Lys Val Ala Gln Ser Asn Leu Ser  
50 55 60

Lys Glu Glu Val Glu Lys Leu Leu Asp Ala Leu Ser Gln Pro Val Leu  
65 70 75 80

Asn Ala Ala Pro Ala Ala Val Pro Asp Val Glu Pro Val Glu Lys Ile  
85 90 95

Arg Arg Arg Val Glu Lys Asn Val Glu Asn Glu Ile His Gln Ile Glu  
100 105 110

Glu Lys Val Glu Arg Glu Leu Ala Ala Val Ala Gln Pro Thr Asp Phe  
115 120 125

Glu Ala Ala Ala Arg Glu Glu Ala Thr Ala Glu Leu Glu Asp Ile  
130 135 140

Val Pro Glu Ile Thr Pro Ala Pro Val Glu Ala Ser Val Tyr Thr Pro  
145 150 155 160

Ile Phe Val Ala Pro Ala Val Val Pro Thr Glu Asn Val Gln Asp Thr  
165 170 175

Asp Asp Glu Gln Val Arg Glu Arg Thr Ala Arg Lys Arg Arg Gly Arg  
180 185 190

Arg Gly Thr Gly Arg Gly Arg Gly Ala Glu Ala Glu Thr Val Thr Glu  
195 200 205

Val Ser Glu Glu Ala Ser Thr Ser Glu Val Glu Glu Val Asn Glu Pro  
210 215 220

Ile Gly Ile Lys Gly Ser Thr Arg Leu Glu Ala Gln Arg Arg Arg Arg

225	230	235	240
Thr Glu Met Arg Glu Asn Lys Lys Arg Arg His Val Val Ser Thr	245	250	255
Gln Glu Phe Met Glu Arg Arg Glu Ser Met Glu Arg Arg Met Ile Val	260	265	270
Arg Glu Arg Gln Arg His Asp His Pro Gly Leu Val Thr Gln Val Gly	275	280	285
Val Leu Glu Asp Asp Gln Leu Val Glu Gln Phe Val Thr Ser Asp Ala	290	295	300
Gln Met Ser Met Val Gly Asn Ile Tyr Leu Gly Arg Val Gln Asn Val	305	310	315
Leu Pro Ser Met Glu Ala Ala Phe Ile Asp Ile Gly Lys Gly Arg Asn	325	330	335
Gly Val Leu Tyr Ala Gly Glu Val Asp Trp Lys Ala Ala Gly Leu Gly	340	345	350
Gly Arg Gly Arg Arg Ile Glu Gln Ala Leu Lys Ala Gly Asp Gln Val	355	360	365
Leu Val Gln Val Ser Lys Asp Pro Leu Gly His Lys Gly Ala Arg Leu	370	375	380
Thr Thr Gln Ile Ser Leu Ala Gly Arg Tyr Leu Val Tyr Val Pro Gly	385	390	395
Gly Arg Ser Ala Gly Ile Ser Arg Lys Leu Pro Gly Pro Glu Arg Lys	405	410	415
Arg Leu Lys Glu Ile Leu Gly Arg Val Val Pro Ala Gln Gly Thr	420	425	430
Ile Ile Arg Thr Ala Ala Glu Gly Val Ser Glu Glu Asn Ile Ala Ala	435	440	445
Asp Val Asn Arg Leu His Thr Leu Trp Glu Gln Ile Lys Glu Arg Thr	450	455	460
Ala Glu Glu Lys Lys Ser Arg Gly Ser Lys Pro Ile Thr Met Tyr Glu	465	470	475
Glu Pro Asp Met Leu Val Lys Val Ile Arg Asp Leu Phe Asn Glu Asp	485	490	495
Phe Thr Ser Leu Ile Val Asp Gly Asp Arg Ala Trp Asn Thr Val Arg	500	505	510
Ala Tyr Ile Gln Ser Val Ala Pro Asp Leu Val Ser Arg Val Glu His	515	520	525
Phe Asn Arg Ala Asp Phe Asp Gly Lys Asp Ala Phe Glu Ala Phe Asp	530	535	540
Leu Asn Thr Gln Leu Glu Glu Ala Leu Ser Arg Lys Val Asn Leu Pro	545	550	555
			560

Ser Gly Gly Ser Leu Ile Ile Asp Arg Thr Glu Ala Met Thr Val Ile  
565 570 575

Asp Val Asn Thr Gly Arg Tyr Thr Gly Lys Gly Gly Asn Leu Glu  
580 585 590

Glu Thr Val Thr Leu Asn Asn Ile Glu Ala Ala Glu Glu Ile Val Arg  
595 600 605

Gln Met Arg Leu Arg Asp Leu Gly Gly Met Ile Val Val Asp Phe Ile  
610 615 620

Asp Met Val Leu Pro Glu Asn Gln Glu Leu Val Leu Arg Arg Leu Asn  
625 630 635 640

Glu Ala Leu Glu Asn Asp Arg Thr Arg His Gln Val Ser Glu Val Thr  
645 650 655

Ser Leu Gly Leu Val Gln Met Thr Arg Lys Arg Ile Gly Ala Gly Leu  
660 665 670

Leu Glu Thr Phe Ser Ser Pro Cys Glu His Cys Glu Gly Arg Gly Ile  
675 680 685

Ile Val His Val Asp Pro Val Asp Thr Val Asp Glu Arg Val Glu Ala  
690 695 700

Lys Ala Glu Glu Arg Ser Arg Arg His Gln Arg Ser Asn Ser Thr Asn  
705 710 715 720

Lys Ala Ala Ala Glu His Pro Met Val Val Ala Met Arg Asp Leu Val  
725 730 735

Glu Ser Asp Glu His Asp Leu Asp Gln Glu Phe Glu Glu Leu Ala Ala  
740 745 750

Ser Met Ile Val Leu Asp Asp Ser Asp Leu Leu  
755 760

<210> 225

<211> 915

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(892)

<223> RXN02370

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caagaatttg aggaactcgc tgcacatgat atcgttctcg atg act ccg atc tat 115  
Met Thr Pro Ile Tyr  
1 5

gat gat gtg gac aac gac aag ctc gac gag cct gag cgc att ctt gct 163  
Asp Asp Val Asp Asn Asp Lys Leu Asp Glu Pro Glu Arg Ile Leu Ala  
10 15 20

gaa tcc acc gtg gaa ccg gag gaa gga cca cgc atg agg gcc cgc cgt 211  
 Glu Ser Thr Val Glu Pro Glu Glu Gly Pro Arg Met Arg Ala Arg Arg  
 25 30 35

caa cgt cag gaa tct gct gcg gat gat att gcc gcg att gca gct gct 259  
 Gln Arg Gln Glu Ser Ala Ala Asp Asp Ile Ala Ala Ile Ala Ala Ala  
 40 45 50

gcc gtg gac att gct tct gaa gaa gac cct gat gag cct tcg gga tcg 307  
 Ala Val Asp Ile Ala Ser Glu Glu Asp Pro Asp Glu Pro Ser Gly Ser  
 55 60 65

tcg tat gtg tct gac ttt gag gca gag cct att gca cct gta gtt gag 355  
 Ser Tyr Val Ser Asp Phe Glu Ala Glu Pro Ile Ala Pro Val Val Glu  
 70 75 80 85

aag gct gct gaa cct gtg gct gag cca acc gct gat tat gaa aag gca 403  
 Lys Ala Ala Glu Pro Val Ala Glu Pro Thr Ala Asp Tyr Glu Lys Ala  
 90 95 100

cgt gcc gaa ttt gag gca agc cca cgc agg cgc cgc aag act cgt gcc 451  
 Arg Ala Glu Phe Glu Ala Ser Pro Arg Arg Arg Arg Lys Thr Arg Gly  
 105 110 115

aat tca cgt tcg gat cat gct cca aag cca gag gat ttc gca cct gta 499  
 Asn Ser Arg Ser Asp His Ala Pro Lys Pro Glu Asp Phe Ala Pro Val  
 120 125 130

gtt gaa gag gtt gct gag act cca gtg aag aca cct gcg cgg aag gct 547  
 Val Glu Glu Val Ala Glu Thr Pro Val Lys Thr Pro Ala Arg Lys Ala  
 135 140 145

cca cgc cgt aac cgt cca agt gag ctc agt tcc ggt gcg ccg tcc tct 595  
 Pro Arg Arg Asn Arg Pro Ser Glu Leu Ser Ser Gly Ala Pro Ser Ser  
 150 155 160 165

gca cca tcg acc agg aac cgt cgc cgc gca gtg cgc cgt caa ctg gtg 643  
 Ala Pro Ser Thr Arg Asn Arg Arg Ala Val Arg Arg Gln Leu Val  
 170 175 180

gaa gct cct gag acc gtc gtt gag ata gca cct gaa gca gca cca gaa 691  
 Glu Ala Pro Glu Thr Val Val Glu Ile Ala Pro Glu Ala Ala Pro Glu  
 185 190 195

cag gtt gca gag cct cag gtt gaa ttc gac cag cca gac aac cgc cga 739  
 Gln Val Ala Glu Pro Gln Val Glu Phe Asp Gln Pro Asp Asn Arg Arg  
 200 205 210

aag cgt cgt cgt gct gtg cgc gtg aca gcg gcg ccg gtg gag aag aag 787  
 Lys Arg Arg Arg Ala Val Arg Val Thr Ala Ala Pro Val Glu Lys Lys  
 215 220 225

gtg gcg tcg aca agc aat gcg cgg gcg ccg aag aag gaa cct cag gcg 835  
 Val Ala Ser Thr Ser Asn Ala Arg Ala Pro Lys Lys Glu Pro Gln Ala  
 230 235 240 245

gcg agc acc acc aac cca ggc cgc cgt agg cgg gct acc cga cga ggc 883  
 Ala Ser Thr Thr Asn Pro Gly Arg Arg Arg Arg Ala Thr Arg Arg Gly  
 250 255 260

cca cga agc taggggtataa gggcggtttg tgt  
Pro Arg Ser

<210> 226  
<211> 264  
<212> PRT  
<213> *Corynebacterium glutamicum*

<400> 226  
Met Thr Pro Ile Tyr Asp Asp Val Asp Asn Asp Lys Leu Asp Glu Pro  
1 5 10 15  
Glu Arg Ile Leu Ala Glu Ser Thr Val Glu Pro Glu Glu Gly Pro Arg  
20 25 30  
Met Arg Ala Arg Arg Gln Arg Gln Glu Ser Ala Ala Asp Asp Ile Ala  
35 40 45  
Ala Ile Ala Ala Ala Val Asp Ile Ala Ser Glu Glu Asp Pro Asp  
50 55 60  
Glu Pro Ser Gly Ser Ser Tyr Val Ser Asp Phe Glu Ala Glu Pro Ile  
65 70 75 80  
Ala Pro Val Val Glu Lys Ala Ala Glu Pro Val Ala Glu Pro Thr Ala  
85 90 95  
Asp Tyr Glu Lys Ala Arg Ala Glu Phe Glu Ala Ser Pro Arg Arg Arg  
100 105 110  
Arg Lys Thr Arg Gly Asn Ser Arg Ser Asp His Ala Pro Lys Pro Glu  
115 120 125  
Asp Phe Ala Pro Val Val Glu Glu Val Ala Glu Thr Pro Val Lys Thr  
130 135 140  
Pro Ala Arg Lys Ala Pro Arg Arg Asn Arg Pro Ser Glu Leu Ser Ser  
145 150 155 160  
Gly Ala Pro Ser Ser Ala Pro Ser Thr Arg Asn Arg Arg Arg Ala Val  
165 170 175  
Arg Arg Gln Leu Val Glu Ala Pro Glu Thr Val Val Glu Ile Ala Pro  
180 185 190  
Glu Ala Ala Pro Glu Gln Val Ala Glu Pro Gln Val Glu Phe Asp Gln  
195 200 205  
Pro Asp Asn Arg Arg Lys Arg Arg Arg Ala Val Arg Val Thr Ala Ala  
210 215 220  
Pro Val Glu Lys Lys Val Ala Ser Thr Ser Asn Ala Arg Ala Pro Lys  
225 230 235 240  
Lys Glu Pro Gln Ala Ala Ser Thr Thr Asn Pro Gly Arg Arg Arg Arg  
245 250 255  
Ala Thr Arg Arg Gly Pro Arg Ser  
260

<210> 227  
 <211> 915  
 <212> DNA  
 <213> *Corynebacterium glutamicum*

<220>  
 <221> CDS  
 <222> (101)..(892)  
 <223> FRXA02370

<400> 227  
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 caagaatttg aggaactcgc tgcataatg atcgttctcg atg act ccg atc tat 115  
 Met Thr Pro Ile Tyr  
 1 5  
 tat gat gtg gac aac gac aag ctc gac gag cct gag cgc att ctt gct 163  
 Tyr Asp Val Asp Asn Asp Lys Leu Asp Glu Pro Glu Arg Ile Leu Ala  
 10 15 20  
 gaa tcc acc gtg gaa ccg gag gaa gga cca cgc atg agg gcc cgc cgt 211  
 Glu Ser Thr Val Glu Pro Glu Glu Gly Pro Arg Met Arg Ala Arg Arg  
 25 30 35  
 caa cgt cag gaa tct gct gcg gat gat att gcc gcg att gca gct gct 259  
 Gln Arg Gln Glu Ser Ala Ala Asp Asp Ile Ala Ala Ile Ala Ala Ala  
 40 45 50  
 gcc gtg gac att gct tct gaa gaa gac cct gat gag cct tcg gga tcg 307  
 Ala Val Asp Ile Ala Ser Glu Glu Asp Pro Asp Glu Pro Ser Gly Ser  
 55 60 65  
 tcg tat gtg tct gac ttt gag gca gag cct att gca cct gta gtt gag 355  
 Ser Tyr Val Ser Asp Phe Glu Ala Glu Pro Ile Ala Pro Val Val Glu  
 70 75 80 85  
 aag gct gct gaa cct gtg gct gag cca acc gct gat tat gaa aag gca 403  
 Lys Ala Ala Glu Pro Val Ala Glu Pro Thr Ala Asp Tyr Glu Lys Ala  
 90 95 100  
 cgt gcc gaa ttt gag gca agc cca cgc agg cgc cgc aag act cgt gcc 451  
 Arg Ala Glu Phe Glu Ala Ser Pro Arg Arg Arg Arg Lys Thr Arg Gly  
 105 110 115  
 aat tca cgt tcg gat cat gct cca aag cca gag gat ttc gca cct gta 499  
 Asn Ser Arg Ser Asp His Ala Pro Lys Pro Glu Asp Phe Ala Pro Val  
 120 125 130  
 gtt gaa gag gtt gct gag act cca gtg aag aca cct gcg cgg aag gct 547  
 Val Glu Glu Val Ala Glu Thr Pro Val Lys Thr Pro Ala Arg Lys Ala  
 135 140 145  
 cca cgc cgt aac cgt cca agt gag ctc agt tcc ggt gcg ccg tcc tct 595  
 Pro Arg Arg Asn Arg Pro Ser Glu Leu Ser Ser Gly Ala Pro Ser Ser  
 150 155 160 165  
 gca cca tcg acc agg aac cgt cgc cgc gca gtg cgc cgt caa ctg gtg 643  
 Ala Pro Ser Thr Arg Asn Arg Arg Arg Ala Val Arg Arg Gln Leu Val



170	175	180	
gaa gct cct gag acc gtc gtt gag ata gca cct gaa gca gca cca gaa Glu Ala Pro Glu Thr Val Val Glu Ile Ala Pro Glu Ala Ala Pro Glu			691
185	190	195	
cag gtt gca gag cct cag gtt gaa ttc gac cag cca gac aac cgc cga Gln Val Ala Glu Pro Gln Val Glu Phe Asp Gln Pro Asp Asn Arg Arg			739
200	205	210	
aag cgt cgt cgt gct gtg cgc gtg aca gcg gcg ccg gtg gag aag aag Lys Arg Arg Arg Ala Val Arg Val Thr Ala Ala Pro Val Glu Lys Lys			787
215	220	225	
gtg gcg tgc aca agc aat gcg gcg gcg ccg aag aag gaa cct cag gcg Val Ala Ser Thr Ser Asn Ala Arg Ala Pro Lys Lys Glu Pro Gln Ala			835
230	235	240	245
gcg agc acc acc aac cca ggc cgc cgt agg gcg gct acc cga cga ggc Ala Ser Thr Thr Asn Pro Gly Arg Arg Arg Arg Ala Thr Arg Arg Gly			883
250	255	260	
cca cga agc tagggataa gggcggtttg tgt			915
Pro Arg Ser			

&lt;210&gt; 228

&lt;211&gt; 264

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 228

Met Thr Pro Ile Tyr Tyr Asp Val Asp Asn Asp Lys Leu Asp Glu Pro		
1	5	15

Glu Arg Ile Leu Ala Glu Ser Thr Val Glu Pro Glu Glu Gly Pro Arg		
20	25	30

Met Arg Ala Arg Arg Gln Arg Gln Glu Ser Ala Ala Asp Asp Ile Ala		
35	40	45

Ala Ile Ala Ala Ala Val Asp Ile Ala Ser Glu Glu Asp Pro Asp		
50	55	60

Glu Pro Ser Gly Ser Ser Tyr Val Ser Asp Phe Glu Ala Glu Pro Ile		
65	70	80

Ala Pro Val Val Glu Lys Ala Ala Glu Pro Val Ala Glu Pro Thr Ala		
85	90	95

Asp Tyr Glu Lys Ala Arg Ala Glu Phe Glu Ala Ser Pro Arg Arg Arg		
100	105	110

Arg Lys Thr Arg Gly Asn Ser Arg Ser Asp His Ala Pro Lys Pro Glu		
115	120	125

Asp Phe Ala Pro Val Val Glu Glu Val Ala Glu Thr Pro Val Lys Thr		
130	135	140

Pro Ala Arg Lys Ala Pro Arg Arg Asn Arg Pro Ser Glu Leu Ser Ser

atc gtg atc tcc gcc caa gac atc gac cga ttt ggc atc caa cac gca 355  
Ile Val Ile Ser Ala Gln Asp Ile Asp Arg Phe Gly Ile Gln His Ala  
70 75 80 85

aac atc tcc ggc atg cga cga gcc gta gcc gcc cta ggc acc caa ccc 403  
 Asn Ile Ser Gly Met Arg Arg Ala Val Ala Ala Leu Gly Thr Gln Pro  
 90 95 100

ggc tac gta ctt acc gac gcc atg aaa gtc ccc ggc ttc aca gtc cca 451  
 Gly Tyr Val Leu Thr Asp Ala Met Lys Val Pro Gly Phe Thr Val Pro  
 105 110 115

tac cta ccc atc atc ggc gga gac gcc tcc gcc cga tgc atc gcc gcc 499  
 Tyr Leu Pro Ile Ile Gly Gly Asp Ala Ser Ala Arg Cys Ile Ala Ala  
 120 125 130

gca agt gta tta gcc aaa caa acc cgc gac gac atc atg acc gac atg 547  
 Ala Ser Val Leu Ala Lys Gln Thr Arg Asp Asp Ile Met Thr Asp Met  
 135 140 145

gcc aac gac tac ccg cac tac ggt ctc gaa att cac aaa ggc tac agt 595  
 Ala Asn Asp Tyr Pro His Tyr Gly Leu Glu Ile His Lys Gly Tyr Ser  
 150 155 160 165

acg aag atc cac atg gat gcg gtg cgc cac cac gcc gca agt ccc gag 643  
 Thr Lys Ile His Met Asp Ala Val Arg His His Gly Ala Ser Pro Glu  
 170 175 180

cac aga tat agt tat gca aat gtg gcc aag gca cac caa gaa tgg cta 691  
 His Arg Tyr Ser Tyr Ala Asn Val Ala Lys Ala His Gln Glu Trp Leu  
 185 190 195

cac gct gca gat aat gac acg acg gaa ggt gga gca tgagcgctga 737  
 His Ala Ala Asp Asn Asp Thr Thr Glu Gly Gly Ala  
 200 205

agaactcgac aac 750

<210> 230  
 <211> 209  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 230  
 Leu Ser Arg Asn Gly Leu Gly Pro Val Ala Gly Val Asp Glu Ala Gly  
 1 5 10 15

Arg Gly Ala Cys Cys Gly Pro Ile Ser Ile Ala Ala Cys Ile Leu Pro  
 20 25 30

Asp Lys Pro Ile Gln Glu Leu Ala Ala Leu Thr Asp Ser Lys Lys Leu  
 35 40 45

Ser Ala Ser Thr Arg Glu Lys Leu Met Pro Leu Ile Lys Lys His Ala  
 50 55 60

Leu Ala Trp Ser Val Ile Val Ile Ser Ala Gln Asp Ile Asp Arg Phe  
 65 70 75 80

Gly Ile Gln His Ala Asn Ile Ser Gly Met Arg Arg Ala Val Ala Ala  
 85 90 95

Leu Gly Thr Gln Pro Gly Tyr Val Leu Thr Asp Ala Met Lys Val Pro  
 100 105 110

Gly Phe Thr Val Pro Tyr Leu Pro Ile Ile Gly Gly Asp Ala Ser Ala  
115 120 125

Arg Cys Ile Ala Ala Ser Val Leu Ala Lys Gln Thr Arg Asp Asp  
130 135 140

Ile Met Thr Asp Met Ala Asn Asp Tyr Pro His Tyr Gly Leu Glu Ile  
145 150 155 160

His Lys Gly Tyr Ser Thr Lys Ile His Met Asp Ala Val Arg His His  
165 170 175

Gly Ala Ser Pro Glu His Arg Tyr Ser Tyr Ala Asn Val Ala Lys Ala  
180 185 190

His Gln Glu Trp Leu His Ala Ala Asp Asn Asp Thr Thr Glu Gly Gly  
195 200 205

Ala

<210> 231  
<211> 807  
<212> DNA  
<213> Corynebacterium glutamicum

<220>  
<221> CDS  
<222> (101)..(784)  
<223> RXN01786

<400> 231  
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Met Arg Ala Ala Lys  
1 5

atc acc cgt gga ttt act tcc aac cct gca ggc agc gtg ctt gta gaa 163  
Ile Thr Arg Gly Phe Thr Ser Asn Pro Ala Gly Ser Val Leu Val Glu  
10 15 20

ttc ggc aat act cgt gtc atg tgc acc gct tct gtg gaa ttg ggt gtg 211  
Phe Gly Asn Thr Arg Val Met Cys Thr Ala Ser Val Glu Leu Gly Val  
25 30 35

cct cgt ttc aag cgt gat tca ggt gaa ggc tgg ttg acc gca gag tac 259  
Pro Arg Phe Lys Arg Asp Ser Gly Glu Gly Trp Leu Thr Ala Glu Tyr  
40 45 50

gcg atg ctt cct gct gcg act gcg gag cgt aac cgt cgt gaa tcc atg 307  
Ala Met Leu Pro Ala Ala Thr Ala Glu Arg Asn Arg Arg Glu Ser Met  
55 60 65

gcc ggc aag gtc aag gga cgc act cat gaa att tct cgt ctg att ggt 355  
Ala Gly Lys Val Lys Gly Arg Thr His Glu Ile Ser Arg Leu Ile Gly  
70 75 80 85

cgt tct ttg cgt gca gct gtg gat ctt tcc cag ctg ggt gag aac acc 403

Arg	Ser	Leu	Arg	Ala	Val	Asp	Leu	Ser	Gln	Leu	Gly	Glu	Asn	Thr	100	
90																95
att	gcg	att	gac	tcg	gat	gtt	ctg	caa	gct	gac	ggc	ggc	act	cgt	act	451
Ile	Ala	Ile	Asp	Cys	Asp	Val	Leu	Gln	Ala	Asp	Gly	Gly	Thr	Arg	Thr	
105																110
gca	tcg	atc	acc	ggc	gcg	tat	gtg	gcg	ctg	gct	gat	gcc	atc	aag	gtt	499
Ala	Ser	Ile	Thr	Gly	Ala	Tyr	Val	Ala	Leu	Ala	Asp	Ala	Ile	Lys	Val	
120																125
ctg	cag	gag	cgc	ggg	gtt	gtt	cca	ggc	agc	cca	ctt	ctt	gca	cca	gtt	547
Leu	Gln	Glu	Arg	Gly	Val	Val	Pro	Gly	Ser	Pro	Leu	Leu	Ala	Pro	Val	
135																140
gct	gct	gtt	tcc	gtt	ggc	ctg	gtc	gac	ggc	aat	gta	tcg	ctt	gac	ttg	595
Ala	Ala	Val	Ser	Val	Gly	Leu	Val	Asp	Gly	Asn	Val	Cys	Leu	Asp	Leu	
150																155
cca	tat	gaa	gaa	gat	tcc	cgc	gcc	gat	gtt	gac	ctc	aac	gtt	gtt	atg	643
Pro	Tyr	Glu	Glu	Asp	Ser	Arg	Ala	Asp	Val	Asp	Leu	Asn	Val	Val	Met	
170																175
acc	gaa	cac	ggc	gaa	ttc	gtg	gaa	att	cag	ggc	acc	ggc	gaa	gaa	act	691
Thr	Glu	His	Gly	Glu	Phe	Val	Glu	Ile	Gln	Gly	Thr	Gly	Glu	Glu	Thr	
185																190
acc	ttc	acc	cgc	gcg	cag	ctc	aac	gac	atg	ctt	gac	cac	gct	gaa	aag	739
Thr	Phe	Thr	Arg	Ala	Gln	Leu	Asn	Asp	Met	Leu	Asp	His	Ala	Glu	Lys	
200																205
ggc	tcg	cgc	gaa	ttg	gtt	gct	gcc	caa	aaa	gct	gca	ctg	gga	atc		784
Gly	Cys	Arg	Glu	Leu	Val	Ala	Ala	Gln	Lys	Ala	Ala	Leu	Gly	Ile		
215																220
taaaaccaca acagaggttaa gga																807
<210> 232																
<211> 228																
<212> PRT																
<213> Corynebacterium glutamicum																
<400> 232																
Met	Arg	Ala	Ala	Lys	Ile	Thr	Arg	Gly	Phe	Thr	Ser	Asn	Pro	Ala	Gly	
1																5
Ser Val Leu Val Glu Phe Gly Asn Thr Arg Val Met Cys Thr Ala Ser																
20																25
Val Glu Leu Gly Val Pro Arg Phe Lys Arg Asp Ser Gly Glu Gly Trp																
35																40
Leu Thr Ala Glu Tyr Ala Met Leu Pro Ala Ala Thr Ala Glu Arg Asn																
50																55
Arg Arg Glu Ser Met Ala Gly Lys Val Lys Gly Arg Thr His Glu Ile																
65																70
Ser Arg Leu Ile Gly Arg Ser Leu Arg Ala Ala Val Asp Leu Ser Gln																
85																90
95																

Leu Gly Glu Asn Thr Ile Ala Ile Asp Cys Asp Val Leu Gln Ala Asp  
100 105 110

Gly Gly Thr Arg Thr Ala Ser Ile Thr Gly Ala Tyr Val Ala Leu Ala  
115 120 125

Asp Ala Ile Lys Val Leu Gln Glu Arg Gly Val Val Pro Gly Ser Pro  
130 135 140

Leu Leu Ala Pro Val Ala Ala Val Ser Val Gly Leu Val Asp Gly Asn  
145 150 155 160

Val Cys Leu Asp Leu Pro Tyr Glu Glu Asp Ser Arg Ala Asp Val Asp  
165 170 175

Leu Asn Val Val Met Thr Glu His Gly Glu Phe Val Glu Ile Gln Gly  
180 185 190

Thr Gly Glu Glu Thr Thr Phe Thr Arg Ala Gln Leu Asn Asp Met Leu  
195 200 205

Asp His Ala Glu Lys Gly Cys Arg Glu Leu Val Ala Ala Gln Lys Ala  
210 215 220

Ala Leu Gly Ile  
225

<210> 233

<211> 541

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(541)

<223> PRXA01786

<400> 233

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ttccagcttt tctcgttttg atggccgcgc acaggatcag atg cgt gcc gcc aaa 115  
Met Arg Ala Ala Lys  
1 5

atc acc cgt gga ttt act tcc aac cct gca ggc agc gtg ctt gta gaa 163  
Ile Thr Arg Gly Phe Thr Ser Asn Pro Ala Gly Ser Val Leu Val Glu  
10 15 20

ttc ggc aat act cgt gtc atg tgc acc gct tct gtg gaa ttg ggt gtg 211  
Phe Gly Asn Thr Arg Val Met Cys Thr Ala Ser Val Glu Leu Gly Val  
25 30 35

cct cgt ttc aag cgt gat tca ggt gaa ggc tgg ttg acc gca gag tac 259  
Pro Arg Phe Lys Arg Asp Ser Gly Glu Gly Trp Leu Thr Ala Glu Tyr  
40 45 50

gcg atg ctt cct gct gcg act gcg gag cgt aac cgt cgt gaa tcc atg 307  
Ala Met Leu Pro Ala Ala Thr Ala Glu Arg Asn Arg Arg Glu Ser Met  
55 60 65

gcc ggc aag gtc aag gga cgc act cat gaa att tct cgt ctg att ggt 355  
 Ala Gly Lys Val Lys Gly Arg Thr His Glu Ile Ser Arg Leu Ile Gly  
 70 75 80 85

cgt tct ttg cgt gca gct gtg gat ctt tcc cag ctg ggt gag aac acc 403  
 Arg Ser Leu Arg Ala Ala Val Asp Leu Ser Gln Leu Gly Glu Asn Thr  
 90 95 100

att gcg att gac tgc gat gtt ctg caa gct gac ggc ggt act cgt act 451  
 Ile Ala Ile Asp Cys Asp Val Leu Gln Ala Asp Gly Gly Thr Arg Thr  
 105 110 115

gca tgc atc acc ggt gcg tat gtg gcg ctg gct gat gcc atc aag gtt 499  
 Ala Ser Ile Thr Gly Ala Tyr Val Ala Leu Ala Asp Ala Ile Lys Val  
 120 125 130

ctg cag gag cgc ggg gtt gtt cca ggc agc cca ctt ctt gca 541  
 Leu Gln Glu Arg Gly Val Val Pro Gly Ser Pro Leu Leu Ala  
 135 140 145

<210> 234

<211> 147

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 234

Met Arg Ala Ala Lys Ile Thr Arg Gly Phe Thr Ser Asn Pro Ala Gly  
 1 5 10 15

Ser Val Leu Val Glu Phe Gly Asn Thr Arg Val Met Cys Thr Ala Ser  
 20 25 30

Val Glu Leu Gly Val Pro Arg Phe Lys Arg Asp Ser Gly Glu Gly Trp  
 35 40 45

Leu Thr Ala Glu Tyr Ala Met Leu Pro Ala Ala Thr Ala Glu Arg Asn  
 50 55 60

Arg Arg Glu Ser Met Ala Gly Lys Val Lys Gly Arg Thr His Glu Ile  
 65 70 75 80

Ser Arg Leu Ile Gly Arg Ser Leu Arg Ala Ala Val Asp Leu Ser Gln  
 85 90 95

Leu Gly Glu Asn Thr Ile Ala Ile Asp Cys Asp Val Leu Gln Ala Asp  
 100 105 110

Gly Gly Thr Arg Thr Ala Ser Ile Thr Gly Ala Tyr Val Ala Leu Ala  
 115 120 125

Asp Ala Ile Lys Val Leu Gln Glu Arg Gly Val Val Pro Gly Ser Pro  
 130 135 140

Leu Leu Ala  
 145

<210> 235

<211> 741

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(718)

&lt;223&gt; RXN00163

&lt;400&gt; 235

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cactgggaat ctaaaaccac aacagagtta aggcacccgg atg aaa ctt ctt ctt 115  
 Met Lys Leu Leu Leu  
 1 5

gca tcc aac aac gca aag aaa ctc aaa gaa ctc cag cgg att ttg gat 163  
 Ala Ser Asn Asn Ala Lys Lys Leu Lys Glu Leu Gln Arg Ile Leu Asp  
 10 15 20

caa gca ggc ctg gat tcc gtt gaa ttg ctt gcg ctg cgt gat gtc gag 211  
 Gln Ala Gly Leu Asp Ser Val Glu Leu Ala Leu Arg Asp Val Glu  
 25 30 35

gca tac gac gag ccg atc gaa gac ggc cgc act ttt gcc gac aac gca 259  
 Ala Tyr Asp Glu Pro Ile Glu Asp Gly Arg Thr Phe Ala Asp Asn Ala  
 40 45 50

cag atc aaa gcg cgc gcc ggg gta acc cac aca ggc atc gcc acg atc 307  
 Gln Ile Lys Ala Arg Ala Gly Val Thr His Thr Gly Ile Ala Thr Ile  
 55 60 65

gcc gat gat tcc ggc atc gct gtc gaa gaa ctc aac gga atg ccc ggc 355  
 Ala Asp Asp Ser Gly Ile Ala Val Glu Glu Leu Asn Gly Met Pro Gly  
 70 75 80 85

gtt ttg tcc gca cgc tgg tcc ggc gca cac ggc aac gac acc gcc aac 403  
 Val Leu Ser Ala Arg Trp Ser Gly Ala His Gly Asn Asp Thr Ala Asn  
 90 95 100

aac gag ctg ctt ctt gcc caa atg gaa cat gtt ccc gac gag cgc cgc 451  
 Asn Glu Leu Leu Leu Ala Gln Met Glu His Val Pro Asp Glu Arg Arg  
 105 110 115

aac gca gcc ttc gtg tcc gta tgc gtg ctt gca ctt ccg gac gcc caa 499  
 Asn Ala Ala Phe Val Ser Val Cys Val Leu Ala Leu Pro Asp Gly Gln  
 120 125 130

gaa ttt gtt cag gaa ggc cgt tgg gaa ggc caa ctc cta cgc gga cct 547  
 Glu Phe Val Gln Glu Gly Arg Trp Glu Gly Gln Leu Leu Arg Gly Pro  
 135 140 145

aag ggc gaa aac ggt ttc gga tac gat cca ctg ttc att cca gca gag 595  
 Lys Gly Glu Asn Gly Phe Gly Tyr Asp Pro Leu Phe Ile Pro Ala Glu  
 150 155 160 165

gaa atc gat gga caa gga cgc agc tcc gct gaa ctt tcc gca gag gaa 643  
 Glu Ile Asp Gly Gln Gly Arg Ser Ser Ala Glu Leu Ser Ala Glu Glu  
 170 175 180

aag gac gct ttg tcc cac cga ggt caa gcg ctg cgc gga ttg gtt gag 691  
 Lys Asp Ala Leu Ser His Arg Gly Gln Ala Leu Arg Gly Leu Val Glu



	185		190		195	
aag atc gca cag gta gct gcg gct agc taaggcctta agggaaacta						738
Lys Ile Ala Gln Val Ala Ala Ala Ser						
200			205			

aaa						741
-----	--	--	--	--	--	-----

<210> 236  
 <211> 206  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 236	
Met Lys Leu Leu Leu Ala Ser Asn Asn Ala Lys Lys Leu Lys Glu Leu	
1	5 10 15

Gln Arg Ile Leu Asp Gln Ala Gly Leu Asp Ser Val Glu Leu Leu Ala	
20	25 30

Leu Arg Asp Val Glu Ala Tyr Asp Glu Pro Ile Glu Asp Gly Arg Thr	
35	40 45

Phe Ala Asp Asn Ala Gln Ile Lys Ala Arg Ala Gly Val Thr His Thr	
50	55 60

Gly Ile Ala Thr Ile Ala Asp Asp Ser Gly Ile Ala Val Glu Glu Leu	
65	70 75 80

Asn Gly Met Pro Gly Val Leu Ser Ala Arg Trp Ser Gly Ala His Gly	
85	90 95

Asn Asp Thr Ala Asn Asn Glu Leu Leu Leu Ala Gln Met Glu His Val	
100	105 110

Pro Asp Glu Arg Arg Asn Ala Ala Phe Val Ser Val Cys Val Leu Ala	
115	120 125

Leu Pro Asp Gly Gln Glu Phe Val Gln Glu Gly Arg Trp Glu Gly Gln	
130	135 140

Leu Leu Arg Gly Pro Lys Gly Glu Asn Gly Phe Gly Tyr Asp Pro Leu	
145	150 155 160

Phe Ile Pro Ala Glu Glu Ile Asp Gly Gln Gly Arg Ser Ser Ala Glu	
165	170 175

Leu Ser Ala Glu Glu Lys Asp Ala Leu Ser His Arg Gly Gln Ala Leu	
180	185 190

Arg Gly Leu Val Glu Lys Ile Ala Gln Val Ala Ala Ala Ser	
195	200 205

<210> 237  
 <211> 641  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>

<221> CDS  
 <222> (58) .. (618)  
 <223> FRXA00163

<400> 237

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                                     Leu
                                     1

gat caa gca ggc ctg gat tcc gtt gaa ttg ctt gcg ctg cgt gat gtc 108
Asp Gln Ala Gly Leu Asp Ser Val Glu Leu Leu Ala Leu Arg Asp Val
                    5                      10                      15

gag gca tac gac gag cgc atc gaa gac ggc cgc act ttt gcc gac aac 156
Glu Ala Tyr Asp Glu Pro Ile Glu Asp Gly Arg Thr Phe Ala Asp Asn
                20                      25                      30

gca cag atc aaa gcg cgc gcc ggg gta acc cac aca ggc atc gcc acg 204
Ala Gln Ile Lys Ala Arg Ala Gly Val Thr His Thr Gly Ile Ala Thr
                35                      40                      45

atc gcc gat gat tcc ggc atc gct gtc gaa gaa ctc aac gga atg ccc 252
Ile Ala Asp Asp Ser Gly Ile Ala Val Glu Glu Leu Asn Gly Met Pro
                50                      55                      60                      65

ggc gtt ttg tcc gca cgc tgg tcc ggc gca cac ggc aac gac acc gcc 300
Gly Val Leu Ser Ala Arg Trp Ser Gly Ala His Gly Asn Asp Thr Ala
                70                      75                      80

aac aac gag ctg ctt ctt gcc caa atg gaa cat gtt ccc gac gag cgc 348
Asn Asn Glu Leu Leu Leu Ala Gln Met Glu His Val Pro Asp Glu Arg
                85                      90                      95

cgc aac gca gcc ttc gtg tcc gta tgc gtg ctt gca ctt cgc gac ggc 396
Arg Asn Ala Ala Phe Val Ser Val Cys Val Leu Ala Leu Pro Asp Gly
                100                      105                      110

caa gaa ttt gtt cag gaa ggc cgt tgg gaa ggc caa ctc cta cgc gga 444
Gln Glu Phe Val Gln Glu Gly Arg Trp Glu Gly Gln Leu Leu Arg Gly
                115                      120                      125

cct aag ggc gaa aac ggt ttc gga tac gat cca ctg ttc att cca gca 492
Pro Lys Gly Glu Asn Gly Phe Gly Tyr Asp Pro Leu Phe Ile Pro Ala
                130                      135                      140                      145

gag gaa atc gat gga caa gga cgc agc tcc gct gaa ctt tcc gca gag 540
Glu Glu Ile Asp Gly Gln Gly Arg Ser Ser Ala Glu Leu Ser Ala Glu
                150                      155                      160

gaa aag gac gct ttg tcc cac cga ggt caa gcg ctg cgc gga ttg gtt 588
Glu Lys Asp Ala Leu Ser His Arg Gly Gln Ala Leu Arg Gly Leu Val
                165                      170                      175

gag aag atc gca cag gta gct gcg gct agc taaggcctta aggaaaaacta 638
Glu Lys Ile Ala Gln Val Ala Ala Ala Ser
                180                      185

aaa 641

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<210> 238

&lt;211&gt; 187

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 238

Leu Asp Gln Ala Gly Leu Asp Ser Val Glu Leu Leu Ala Leu Arg Asp  
 1 5 10 15

Val Glu Ala Tyr Asp Glu Pro Ile Glu Asp Gly Arg Thr Phe Ala Asp  
 20 25 30

Asn Ala Gln Ile Lys Ala Arg Ala Gly Val Thr His Thr Gly Ile Ala  
 35 40 45

Thr Ile Ala Asp Asp Ser Gly Ile Ala Val Glu Glu Leu Asn Gly Met  
 50 55 60

Pro Gly Val Leu Ser Ala Arg Trp Ser Gly Ala His Gly Asn Asp Thr  
 65 70 75 80

Ala Asn Asn Glu Leu Leu Leu Ala Gln Met Glu His Val Pro Asp Glu  
 85 90 95

Arg Arg Asn Ala Ala Phe Val Ser Val Cys Val Leu Ala Leu Pro Asp  
 100 105 110

Gly Gln Glu Phe Val Gln Glu Gly Arg Trp Glu Gly Gln Leu Leu Arg  
 115 120 125

Gly Pro Lys Gly Glu Asn Gly Phe Gly Tyr Asp Pro Leu Phe Ile Pro  
 130 135 140

Ala Glu Glu Ile Asp Gly Gln Gly Arg Ser Ser Ala Glu Leu Ser Ala  
 145 150 155 160

Glu Glu Lys Asp Ala Leu Ser His Arg Gly Gln Ala Leu Arg Gly Leu  
 165 170 175

Val Glu Lys Ile Ala Gln Val Ala Ala Ser  
 180 185

&lt;210&gt; 239

&lt;211&gt; 432

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(409)

&lt;223&gt; RXA01424

&lt;400&gt; 239

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gatgaggaaa gggcgctcgcg ctggcagtaa aactgtcggt gtg cac ctg tgg gat 115  
 Val His Leu Trp Asp  
 1 5

agt gcc gaa tcg ttg gat ggc acc gaa aaa cag ggc gaa gtc gcc tca 163  
 Ser Ala Glu Ser Leu Asp Gly Thr Glu Lys Gln Gly Glu Val Ala Ser

	10	15	20	
ttc ggt ggt ccg cgg ttc ggc ctt gtc gtt tct aag gcc gtc gga aat				211
Phe Gly Gly Pro Arg Phe Gly Leu Val Val Ser Lys Ala Val Gly Asn				
	25	30	35	
gcg gtg gtt cgt cac cgc acc tcc cga cgg ctt cgt cat atc tgt gca				259
Ala Val Val Arg His Arg Thr Ser Arg Arg Leu Arg His Ile Cys Ala				
	40	45	50	
agc att gca gaa aaa tca cca gag cta ctc tcc ccc act cat cac gtg				307
Ser Ile Ala Glu Lys Ser Pro Glu Leu Leu Ser Pro Thr His His Val				
	55	60	65	
gtg atc cgc gcg ttg gcg ggg gct ggg aat gca acc tcg gcg gaa ctt				355
Val Ile Arg Ala Leu Ala Gly Ala Gly Asn Ala Thr Ser Ala Glu Leu				
	70	75	80	85
gaa cga gac atc cgc tac ggg ttg ggg aaa gct agc cgt gtg cgc acc				403
Glu Arg Asp Ile Arg Tyr Gly Leu Gly Lys Ala Ser Arg Val Arg Thr				
	90	95	100	
aac aag tgatgacatcct ttcgacatcc cag				432
ASN Lys				

&lt;210&gt; 240

&lt;211&gt; 103

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 240

Val His Leu Trp Asp Ser Ala Glu Ser Leu Asp Gly Thr Glu Lys Gln			
1	5	10	15

Gly Glu Val Ala Ser Phe Gly Gly Pro Arg Phe Gly Leu Val Val Ser			
20	25	30	

Lys Ala Val Gly Asn Ala Val Val Arg His Arg Thr Ser Arg Arg Leu			
35	40	45	

Arg His Ile Cys Ala Ser Ile Ala Glu Lys Ser Pro Glu Leu Leu Ser			
50	55	60	

Pro Thr His His Val Val Ile Arg Ala Leu Ala Gly Ala Gly Asn Ala			
65	70	75	80

Thr Ser Ala Glu Leu Glu Arg Asp Ile Arg Tyr Gly Leu Gly Lys Ala			
85	90	95	

Ser Arg Val Arg Thr Asn Lys	
100	

&lt;210&gt; 241

&lt;211&gt; 615

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

<400> 242  
Met Gln Asn Ser Lys Lys Thr Leu Gly Gly Val Leu Gly Val Ile Val

1 5 10 15  
 Val Leu Ala Ala Ala Trp Phe Gly Ile Asp Leu Ser Thr Ser Gly Glu  
 20 25 30  
 Ala Thr Ser Gln Ala Ser Ser Ser Ala Thr Thr Thr Thr Ile Thr Ser  
 35 40 45  
 Ser Asn Thr Pro Thr Ser Glu Ser Ile Ser Ser Asn Ser Asp Leu Asp  
 50 55 60  
 Gly Asp Ser Cys Ser Met Ser Glu Leu Pro Gln Glu Ala Asp Glu Val  
 65 70 75 80  
 Val Asp Asp Ile Leu Ala Gly Gly Pro Phe Asp Tyr Pro Asp Asn Asp  
 85 90 95  
 Gly Val Arg Phe Gly Asn Tyr Glu Gly Val Leu Pro Lys Glu Ser Ser  
 100 105 110  
 Asn Tyr Tyr Arg Glu Tyr Thr Val Glu Thr Pro Gly Leu Ser His Arg  
 115 120 125  
 Gly Pro Leu Arg Ile Val Thr Gly Gly Ser Asn Pro Thr Asp Pro Glu  
 130 135 140  
 Val Trp Tyr Tyr Thr Ser Asp His Tyr Glu Thr Phe Cys Ala Ile Thr  
 145 150 155 160  
 Asp Ala Glu Asn

&lt;210&gt; 243

&lt;211&gt; 2100

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(2077)

&lt;223&gt; RXN00724

&lt;400&gt; 243

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tccgcacca tgtgcgcaaa tactccacca cggctctggc gtg gga att ggt gat 115  
 Val Gly Ile Gly Asp  
 1 5

gcc act gag ggc gat ctt gtt acc atc gtg ggt cag gtc gcc ttt gcc 163  
 Ala Thr Glu Gly Asp Leu Val Thr Ile Val Gly Gln Val Ala Phe Ala  
 10 15 20

aag cag tcc tat acc cag tcc ggc aag atg ctg tac aag gtt aca gtc 211  
 Lys Gln Ser Tyr Thr Gln Ser Gly Lys Met Leu Tyr Lys Val Thr Val  
 25 30 35

tgg act gag acg gaa cgc atc ggc att tcc ttc ttc gga gcc aag cac 259  
 Leu Thr Glu Thr Glu Arg Ile Gly Ile Ser Phe Phe Gly Ala Lys His  
 40 45 50

att ccg cgt ctt ctc cca gaa ggc act cgt gcg ctt ttt acc ggc aag 307  
 Ile Pro Arg Leu Leu Pro Glu Gly Thr Arg Ala Leu Phe Thr Gly Lys  
 55 60 65

gtg aag ttt ttt cgc aac gaa cct cag cta tct cat cca gag ttc att 355  
 Val Lys Phe Phe Arg Asn Glu Pro Gln Leu Ser His Pro Glu Phe Ile  
 70 75 80 85

gtg atc cca gat cct gga tca ggc cgc cga ctc acc gcc act ggc ggt 403  
 Val Ile Pro Asp Pro Gly Ser Gly Arg Arg Leu Thr Ala Thr Gly Gly  
 90 95 100

atg aaa tct ctg gct gcc tac ggc gat gtg gaa gaa gtg gca ctt cgt 451  
 Met Lys Ser Leu Ala Ala Tyr Gly Asp Val Glu Glu Val Ala Leu Arg  
 105 110 115

ttg gtg gat cgc gaa tac atc ccg atc tat gcc ggc acc gcc acc atg 499  
 Leu Val Asp Arg Glu Tyr Ile Pro Ile Tyr Ala Gly Thr Ala Thr Met  
 120 125 130

act acc tgg cgg atc atg gct gca gtg caa cgg gta ctg gaa acc atg 547  
 Thr Thr Trp Arg Ile Met Ala Ala Val Gln Arg Val Leu Glu Thr Met  
 135 140 145

ccg gtg atc aaa gaa cca ctg agc gtg gtg ccc gaa ggc atg ccc agt 595  
 Pro Val Ile Lys Glu Pro Leu Ser Val Val Pro Glu Gly Met Pro Ser  
 150 155 160 165

ttc gac gag gcc atc cgc ggc att cac gat cca ggc cat gaa tct ccc 643  
 Phe Asp Glu Ala Ile Arg Gly Ile His Asp Pro Gly His Glu Ser Pro  
 170 175 180

agc acg ttt atc aac cgt ctg aaa tac aac gaa gca cta tcg ctg gcc 691  
 Ser Thr Phe Ile Asn Arg Leu Lys Tyr Asn Glu Ala Leu Ser Leu Ala  
 185 190 195

acg gtg atg gcg atc ccg cgt gcc gat acc aag aac cgc aaa gca cca 739  
 Thr Val Met Ala Ile Arg Arg Ala Asp Thr Lys Asn Arg Lys Ala Pro  
 200 205 210

ccc atg ccg cgc gca ctc aaa ggg cat cag cac atg ctc atc gat gca 787  
 Pro Met Pro Arg Ala Leu Lys Gly His Gln His Met Leu Ile Asp Ala  
 215 220 225

ctc aac ttt cag ctc aca gtg gga cag aag caa gtg atc cgt gag atc 835  
 Leu Asn Phe Gln Leu Thr Val Gly Gln Lys Gln Val Ile Arg Glu Ile  
 230 235 240 245

agc gcg gac att gaa caa cgc gtt ccc atg tct cgt ctg ctc caa ggt 883  
 Ser Ala Asp Ile Glu Gln Arg Val Pro Met Ser Arg Leu Leu Gln Gly  
 250 255 260

gag gtt ggt tcg ggt aaa acc atc gtg tcg ttg atc gcg atg ctg cag 931  
 Glu Val Gly Ser Gly Lys Thr Ile Val Ser Leu Ile Ala Met Leu Gln  
 265 270 275

gca att gat tcc ggt agg cag tgc gcc atg ctc gcc ccg acg gaa gtg 979  
 Ala Ile Asp Ser Gly Arg Gln Cys Ala Met Leu Ala Pro Thr Glu Val  
 280 285 290

ttg gcc acc cag cat gcc cgc agc ctg agc aaa act ctc gac gac gca Leu Ala Thr Gln His Ala Arg Ser Leu Ser Lys Thr Leu Asp Asp Ala 295 300 305	1027
ggc ctt gat atc aat gtt gtg ctc ttg act ggc tcg atg ccc acg gga Gly Leu Asp Ile Asn Val Val Leu Leu Thr Gly Ser Met Pro Thr Gly 310 315 320 325	1075
gcc aag aag gag gct ctg ctg gaa atc atc tcc ggt gac gca gac att Ala Lys Lys Glu Ala Leu Leu Glu Ile Ile Ser Gly Asp Ala Asp Ile 330 335 340	1123
gtg gtc ggc acg cat cgc ctg atc cag gac acc gtg gag ttc ttc gac Val Val Gly Thr His Ala Leu Ile Gln Asp Thr Val Glu Phe Phe Asp 345 350 355	1171
ctt ggc ctc gtg gtg gtg gat gag cag cac cgt ttc ggc gtg gag caa Leu Gly Leu Val Val Val Asp Glu Gln His Arg Phe Gly Val Glu Gln 360 365 370	1219
cgc gat caa ctg cgg acc aag ggc agg gaa ggc ctg acc ccg cac cta Arg Asp Gln Leu Arg Thr Lys Gly Arg Glu Gly Leu Thr Pro His Leu 375 380 385	1267
ttg gtt atg act gcg acc cca att ccg cgc acc atc gcc atg acg gtg Leu Val Met Thr Ala Thr Pro Ile Pro Arg Thr Ile Ala Met Thr Val 390 395 400 405	1315
ttc ggc gac ttg gcg gtg tcc acg ttg cgt gaa ctt cca ggc ggg cgc Phe Gly Asp Leu Ala Val Ser Thr Leu Arg Glu Leu Pro Gly Gly Arg 410 415 420	1363
cgg ccg att caa acc tcg gtg ata ccc gat cac aaa cct ggc tgg gtt Arg Pro Ile Gln Thr Ser Val Ile Pro Asp His Lys Pro Gly Trp Val 425 430 435	1411
aaa cgc ggt tgg gaa cgc atc ggt gag gaa gtc ctc gcc gga cgc caa Lys Arg Gly Trp Glu Arg Ile Gly Glu Glu Val Leu Ala Gly Arg Gln 440 445 450	1459
gcc tat gtg gtg tgt ccg cgc att gaa ggc gaa ggc ggc gtg ctg gaa Ala Tyr Val Val Cys Pro Arg Ile Glu Gly Glu Gly Gly Val Leu Glu 455 460 465	1507
atc cac gcc tat ctt tcc gaa cag gta tat cca gga ttg aat gtt gga Ile His Ala Tyr Leu Ser Glu Gln Val Tyr Pro Gly Leu Asn Val Gly 470 475 480 485	1555
atg ctg cac ggt cgc atg gac acg gat ctc aaa gat tcg gtc atg cag Met Leu His Gly Arg Met Asp Thr Asp Leu Lys Asp Ser Val Met Gln 490 495 500	1603
gaa ttc gcc caa ggt gag atc gat att ttg gtc gcc acc acg gtc att Glu Phe Ala Gln Gly Glu Ile Asp Ile Leu Val Ala Thr Thr Val Ile 505 510 515	1651
gag gtc ggt att gac gtt gcc aac gcc acc gtc atg ctc atc cgc gag Glu Val Gly Ile Asp Val Ala Asn Ala Thr Val Met Leu Ile Arg Glu 520 525 530	1699
gcg gaa cgc ttc ggc gtt tcc cag atc cac cag ctg cgc ggc cgt gtt	1747



Ala Glu Arg Phe Gly Val Ser Gln Ile His Gln Leu Arg Gly Arg Val  
535 540 545

ggc cgt ggg cag cac gat tcc ctc tgc ctg ctg cac acc acc ttc gac 1795  
Gly Arg Gly Gln His Asp Ser Leu Cys Leu Leu His Thr Thr Phe Asp  
550 555 560 565

gag gac tcc cca caa ggc caa cgc ctc gcc gca att tcc acc aca acc 1843  
Glu Asp Ser Pro Gln Gly Gln Arg Leu Ala Ala Ile Ser Thr Thr Thr  
570 575 580

gac ggt ttt caa ctc tct gaa ctt gat ttg cag gta cgc caa gaa ggc 1891  
Asp Gly Phe Gln Leu Ser Glu Leu Asp Leu Gln Val Arg Gln Glu Gly  
585 590 595

gac gtg ttg ggc acc cgc cag tcc ggc agc gac acc aaa ctc cgt cac 1939  
Asp Val Leu Gly Thr Arg Gln Ser Gly Ser Asp Thr Lys Leu Arg His  
600 605 610

ctc tgg ttt atc agc gac caa aaa atc atc gag cgt gcg ctt atc gac 1987  
Leu Ser Phe Ile Ser Asp Gln Lys Ile Ile Glu Arg Ala Leu Ile Asp  
615 620 625

gcc acc gag ctg gtt gcc gcc agc cgt tcc agg gcg ctt gag ctg gtc 2035  
Ala Thr Glu Leu Val Ala Ala Ser Arg Ser Arg Ala Leu Glu Leu Val  
630 635 640 645

arg gac atc gca atg atc aac cag gaa tac ctg gaa aag agc 2077  
Ser Asp Ile Ala Met Ile Asn Gln Glu Tyr Leu Glu Lys Ser  
650 655

tgatattgat aggggttaag tca 2100

<210> 244

<211> 659

<212> PRT

<213> Corynebacterium glutamicum

<400> 244

Val Gly Ile Gly Asp Ala Thr Glu Gly Asp Leu Val Thr Ile Val Gly  
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Gln Val Ala Phe Ala Lys Gln Ser Tyr Thr Gln Ser Gly Lys Met Leu  
20 25 30

Tyr Lys Val Thr Val Leu Thr Glu Thr Glu Arg Ile Gly Ile Ser Phe  
35 40 45

Phe Gly Ala Lys His Ile Pro Arg Leu Leu Pro Glu Gly Thr Arg Ala  
50 55 60

Leu Phe Thr Gly Lys Val Lys Phe Phe Arg Asn Glu Pro Gln Leu Ser  
65 70 75 80

His Pro Glu Phe Ile Val Ile Pro Asp Pro Gly Ser Gly Arg Arg Leu  
85 90 95

Thr Ala Thr Gly Gly Met Lys Ser Leu Ala Ala Tyr Gly Asp Val Glu  
100 105 110

Glu Val Ala Leu Arg Leu Val Asp Arg Glu Tyr Ile Pro Ile Tyr Ala  
 115 120 125  
 Gly Thr Ala Thr Met Thr Thr Trp Arg Ile Met Ala Ala Val Gln Arg  
 130 135 140  
 Val Leu Glu Thr Met Pro Val Ile Lys Glu Pro Leu Ser Val Val Pro  
 145 150 155 160  
 Glu Gly Met Pro Ser Phe Asp Glu Ala Ile Arg Gly Ile His Asp Pro  
 165 170 175  
 Gly His Glu Ser Pro Ser Thr Phe Ile Asn Arg Leu Lys Tyr Asn Glu  
 180 185 190  
 Ala Leu Ser Leu Ala Thr Val Met Ala Ile Arg Arg Ala Asp Thr Lys  
 195 200 205  
 Asn Arg Lys Ala Pro Pro Met Pro Arg Ala Leu Lys Gly His Gln His  
 210 215 220  
 Met Leu Ile Asp Ala Leu Asn Phe Gln Leu Thr Val Gly Gln Lys Gln  
 225 230 235 240  
 Val Ile Arg Glu Ile Ser Ala Asp Ile Glu Gln Arg Val Pro Met Ser  
 245 250 255  
 Arg Leu Leu Gln Gly Glu Val Gly Ser Gly Lys Thr Ile Val Ser Leu  
 260 265 270  
 Ile Ala Met Leu Gln Ala Ile Asp Ser Gly Arg Gln Cys Ala Met Leu  
 275 280 285  
 Ala Pro Thr Glu Val Leu Ala Thr Gln His Ala Arg Ser Leu Ser Lys  
 290 295 300  
 Thr Leu Asp Asp Ala Gly Leu Asp Ile Asn Val Val Leu Leu Thr Gly  
 305 310 315 320  
 Ser Met Pro Thr Gly Ala Lys Lys Glu Ala Leu Leu Glu Ile Ile Ser  
 325 330 335  
 Gly Asp Ala Asp Ile Val Val Gly Thr His Ala Leu Ile Gln Asp Thr  
 340 345 350  
 Val Glu Phe Phe Asp Leu Gly Leu Val Val Val Asp Glu Gln His Arg  
 355 360 365  
 Phe Gly Val Glu Gln Arg Asp Gln Leu Arg Thr Lys Gly Arg Glu Gly  
 370 375 380  
 Leu Thr Pro His Leu Leu Val Met Thr Ala Thr Pro Ile Pro Arg Thr  
 385 390 395 400  
 Ile Ala Met Thr Val Phe Gly Asp Leu Ala Val Ser Thr Leu Arg Glu  
 405 410 415  
 Leu Pro Gly Gly Arg Arg Pro Ile Gln Thr Ser Val Ile Pro Asp His  
 420 425 430  
 Lys Pro Gly Trp Val Lys Arg Gly Trp Glu Arg Ile Gly Glu Glu Val

435                      440                      445  
 Leu Ala Gly Arg Gln Ala Tyr Val Val Cys Pro Arg Ile Glu Gly Glu  
 450                      455                      460  
 Gly Gly Val Leu Glu Ile His Ala Tyr Leu Ser Glu Gln Val Tyr Pro  
 465                      470                      475                      480  
 Gly Leu Asn Val Gly Met Leu His Gly Arg Met Asp Thr Asp Leu Lys  
 485                      490                      495  
 Asp Ser Val Met Gln Glu Phe Ala Gln Gly Glu Ile Asp Ile Leu Val  
 500                      505                      510  
 Ala Thr Thr Val Ile Glu Val Gly Ile Asp Val Ala Asn Ala Thr Val  
 515                      520                      525  
 Met Leu Ile Arg Glu Ala Glu Arg Phe Gly Val Ser Gln Ile His Gln  
 530                      535                      540  
 Leu Arg Gly Arg Val Gly Arg Gly Gln His Asp Ser Leu Cys Leu Leu  
 545                      550                      555                      560  
 His Thr Thr Phe Asp Glu Asp Ser Pro Gln Gly Gln Arg Leu Ala Ala  
 565                      570                      575  
 Ile Ser Thr Thr Thr Asp Gly Phe Gln Leu Ser Glu Leu Asp Leu Gln  
 580                      585                      590  
 Val Arg Gln Glu Gly Asp Val Leu Gly Thr Arg Gln Ser Gly Ser Asp  
 595                      600                      605  
 Thr Lys Leu Arg His Leu Ser Phe Ile Ser Asp Gln Lys Ile Ile Glu  
 610                      615                      620  
 Arg Ala Leu Ile Asp Ala Thr Glu Leu Val Ala Ala Ser Arg Ser Arg  
 625                      630                      635                      640  
 Ala Leu Glu Leu Val Ser Asp Ile Ala Met Ile Asn Gln Glu Tyr Leu  
 645                      650                      655  
 Glu Lys Ser

<210> 245  
 <211> 1604  
 <212> DNA  
 <213> *Corynebacterium glutamicum*

<220>  
 <221> CDS  
 <222> (1)..(1581)  
 <223> RXN01979

<400> 245  
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 Leu Gly His Asp Phe Arg Pro Asp Tyr Arg Arg Ile Arg Asp Leu Leu  
 1                      5                      10                      15  
 gcg gga ctt gcg ccc aat att ccc gtg cta gca acc aca gcc acc gcc 96

Ala Gly Leu Ala Pro Asn Ile Pro Val Leu Ala Thr Thr Ala Thr Ala	20	25	30	
aat gac cgc gtg gtt gaa gat gtc cgt gcc caa cta gaa gat gcc aca				144
Asn Asp Arg Val Val Glu Asp Val Arg Ala Gln Leu Glu Asp Gly Thr	35	40	45	
ggg ttg ttt cgt ggt ggg ata gac cgt gaa tcc ctt tac cta tca gtg				192
Gly Leu Phe Arg Gly Gly Ile Asp Arg Glu Ser Leu Tyr Leu Ser Val	50	55	60	
gtg aac ctg ctc aac ccc acc gaa cgc cca gct tgg ctt gcc acc cac				240
Val Asn Leu Leu Asn Pro Thr Glu Arg Pro Ala Trp Leu Ala Thr His	65	70	75	80
ctc aaa gaa ctg acg ggt tgc ggc atc att tac tgc ctc act gtg tca				288
Leu Lys Glu Leu Thr Gly Ser Gly Ile Ile Tyr Cys Leu Thr Val Ser	85	90	95	
gct gca cat gat ctt gcc gat gca ctt aat tct gtt gga tgg aat gtt				336
Ala Ala His Asp Leu Ala Asp Ala Leu Asn Ser Val Gly Trp Asn Val	100	105	110	
gcc gcg tac acc ggt cga acc gaa gca gga gag cgc gaa cgt tta gaa				384
Ala Ala Tyr Thr Gly Arg Thr Glu Ala Gly Glu Arg Glu Arg Leu Glu	115	120	125	
cat gcc ttg atc aac aac gag atc aaa gca cta gta gca acc tct gca				432
His Ala Leu Ile Asn Asn Glu Ile Lys Ala Leu Val Ala Thr Ser Ala	130	135	140	
ctg gga atg ggc ttt gac aaa cct gac ctt gga ttt gtt gtg cac atg				480
Leu Gly Met Gly Phe Asp Lys Pro Asp Leu Gly Phe Val Val His Met	145	150	155	160
ggc agc ccc agc tca ccg gtg tct tat tac cag cag att ggt cgc gcc				528
Gly Ser Pro Ser Ser Pro Val Ser Tyr Tyr Gln Gln Ile Gly Arg Ala	165	170	175	
ggg cgc ggc acc gct cgt gcc gat gtc atc ctg ctg cca gga act gaa				576
Gly Arg Gly Thr Ala Arg Ala Asp Val Ile Leu Leu Pro Gly Thr Glu	180	185	190	
gac aaa gag atc tgg gag tac ttt gca tca gta tgc ttc cca cgc gaa				624
Asp Lys Glu Ile Trp Glu Tyr Phe Ala Ser Val Ser Phe Pro Arg Glu	195	200	205	
gag gta gtc cgc caa ctg ctt gcg gtg tta acc gat gag gcg caa tcc				672
Glu Val Val Arg Gln Leu Leu Ala Val Leu Thr Asp Glu Ala Gln Ser	210	215	220	
act gtc aaa ttg gaa tca caa gta gat ctt tcc cga tca cgc ctt gaa				720
Thr Val Lys Leu Glu Ser Gln Val Asp Leu Ser Arg Ser Arg Leu Glu	225	230	235	240
caa gta ctt aaa gtg cta gac gta gat gcc gca gtc aaa cgt gta cgt				768
Gln Val Leu Lys Val Leu Asp Val Asp Gly Ala Val Lys Arg Val Arg	245	250	255	
ggc gga tgg gtc tcc acc ggg caa gag tgg atc tac gat gcg gaa cgc				816
Gly Gly Trp Val Ser Thr Gly Gln Glu Trp Ile Tyr Asp Ala Glu Arg				

260	265	270	
tac gca gga ctt gaa caa gca agg aaa att gaa cag caa agc atg gtg Tyr Ala Gly Leu Glu Gln Ala Arg Lys Ile Glu Gln Ser Met Val 275 280 285			864
aac tac cag aac acc act gag tgc cgc atg ctg tac ctc cgc aaa gaa Asn Tyr Gln Asn Thr Thr Glu Cys Arg Met Leu Tyr Leu Arg Lys Glu 290 295 300			912
cta gac gat gtg gag gca act act ccg tgc ggg cgc tgc gac aat tgc Leu Asp Asp Val Glu Ala Thr Thr Pro Cys Gly Arg Cys Asp Asn Cys 305 310 315 320			960
acg ggc aaa acg tgg ggg ctc gac acc gat gcc tgc atc act ttg aaa Thr Gly Lys Thr Trp Gly Leu Asp Thr Asp Ala Ser Ile Thr Leu Lys 325 330 335			1008
gtg gac caa cag ctt caa aca ccc gga gtg aaa ata gcc cca cga aaa Val Asp Gln Gln Leu Gln Thr Pro Gly Val Lys Ile Ala Pro Arg Lys 340 345 350			1056
atg tgg ccg act ggc att agt gtc aga gga aaa atc gca ggg cta gaa Met Trp Pro Thr Gly Ile Ser Val Arg Gly Lys Ile Ala Gly Leu Glu 355 360 365			1104
gaa gga cga gca ctg gga cga ctc aat gac att gcc cgt gga cct gca Glu Gly Arg Ala Leu Gly Arg Leu Asn Asp Ile Ala Arg Gly Pro Ala 370 375 380			1152
cta aag gcc ctg ctg gac agc gga gct tat tct gat gat cca tgg atg Leu Lys Ala Leu Leu Asp Ser Gly Ala Tyr Ser Asp Asp Pro Trp Met 385 390 395 400			1200
gca cgc atc atc gaa gtg ctg aaa aac tgg gat tgg acc aac cgg cct Ala Arg Ile Ile Glu Val Leu Lys Asn Trp Asp Trp Thr Asn Arg Pro 405 410 415			1248
gcc aac gtg gtc gct ctc gcc aat acc aac ttt gga tca act gag atg Ala Asn Val Val Ala Leu Gly Asn Thr Asn Phe Gly Ser Thr Glu Met 420 425 430			1296
atc atc cag gta gct caa tca atc gca cgc gtg gga cga atg aac ttt Ile Ile Gln Val Ala Gln Ser Ile Ala Ala Val Gly Arg Met Asn Phe 435 440 445			1344
gcg ggt gta ctt ccc gcc gcg ccg ggt gct gaa gaa gtc atg gct cag Ala Gly Val Leu Pro Ala Ala Pro Gly Ala Glu Glu Val Met Ala Gln 450 455 460			1392
aat tcc gca tac cga gta gaa gcc cta ttg aaa caa tgg gac tgg tgc Asn Ser Ala Tyr Arg Val Glu Ala Leu Leu Lys Gln Trp Asp Trp Ser 465 470 475 480			1440
caa ggc ttg caa cta gtt ccc ggt ccc att ttg ctg gtg aca gac ctt Gln Gly Leu Gln Leu Val Pro Gly Pro Ile Leu Leu Val Thr Asp Leu 485 490 495			1488
att gat act ggc tgg tgc gtg aca gtt gca gga aat ggc att gcg cag Ile Asp Thr Gly Trp Ser Val Thr Val Ala Gly Asn Gly Ile Ala Gln 500 505 510			1536

cgg acc tca gag aag gtg ctg cgg ttc gct tta gcg agt agg gga 1581  
 Arg Thr Ser Glu Lys Val Leu Pro Phe Ala Leu Ala Ser Arg Gly  
 515 520 525

taggtgctct gggacgagag caa 1604

<210> 246  
 <211> 527  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 246  
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 20 25 30  
 Asn Asp Arg Val Val Glu Asp Val Arg Ala Gln Leu Glu Asp Gly Thr  
 35 40 45  
 Gly Leu Phe Arg Gly Gly Ile Asp Arg Glu Ser Leu Tyr Leu Ser Val  
 50 55 60  
 Val Asn Leu Leu Asn Pro Thr Glu Arg Pro Ala Trp Leu Ala Thr His  
 65 70 75 80  
 Leu Lys Glu Leu Thr Gly Ser Gly Ile Ile Tyr Cys Leu Thr Val Ser  
 85 90 95  
 Ala Ala His Asp Leu Ala Asp Ala Leu Asn Ser Val Gly Trp Asn Val  
 100 105 110  
 Ala Ala Tyr Thr Gly Arg Thr Glu Ala Gly Glu Arg Glu Arg Leu Glu  
 115 120 125  
 His Ala Leu Ile Asn Asn Glu Ile Lys Ala Leu Val Ala Thr Ser Ala  
 130 135 140  
 Leu Gly Met Gly Phe Asp Lys Pro Asp Leu Gly Phe Val Val His Met  
 145 150 155 160  
 Gly Ser Pro Ser Ser Pro Val Ser Tyr Tyr Gln Gln Ile Gly Arg Ala  
 165 170 175  
 Gly Arg Gly Thr Ala Arg Ala Asp Val Ile Leu Leu Pro Gly Thr Glu  
 180 185 190  
 Asp Lys Glu Ile Trp Glu Tyr Phe Ala Ser Val Ser Phe Pro Arg Glu  
 195 200 205  
 Glu Val Val Arg Gln Leu Leu Ala Val Leu Thr Asp Glu Ala Gln Ser  
 210 215 220  
 Thr Val Lys Leu Glu Ser Gln Val Asp Leu Ser Arg Ser Arg Leu Glu  
 225 230 235 240  
 Gln Val Leu Lys Val Leu Asp Val Asp Gly Ala Val Lys Arg Val Arg  
 245 250 255

Gly Gly Trp Val Ser Thr Gly Gln Glu Trp Ile Tyr Asp Ala Glu Arg  
 260 265 270  
 Tyr Ala Gly Leu Glu Gln Ala Arg Lys Ile Glu Gln Gln Ser Met Val  
 275 280 285  
 Asn Tyr Gln Asn Thr Thr Glu Cys Arg Met Leu Tyr Leu Arg Lys Glu  
 290 295 300  
 Leu Asp Asp Val Glu Ala Thr Thr Pro Cys Gly Arg Cys Asp Asn Cys  
 305 310 315 320  
 Thr Gly Lys Thr Trp Gly Leu Asp Thr Asp Ala Ser Ile Thr Leu Lys  
 325 330 335  
 Val Asp Gln Gln Leu Gln Thr Pro Gly Val Lys Ile Ala Pro Arg Lys  
 340 345 350  
 Met Trp Pro Thr Gly Ile Ser Val Arg Gly Lys Ile Ala Gly Leu Glu  
 355 360 365  
 Glu Gly Arg Ala Leu Gly Arg Leu Asn Asp Ile Ala Arg Gly Pro Ala  
 370 375 380  
 Leu Lys Ala Leu Leu Asp Ser Gly Ala Tyr Ser Asp Asp Pro Trp Met  
 385 390 395 400  
 Ala Arg Ile Ile Glu Val Leu Lys Asn Trp Asp Trp Thr Asn Arg Pro  
 405 410 415  
 Ala Asn Val Val Ala Leu Gly Asn Thr Asn Phe Gly Ser Thr Glu Met  
 420 425 430  
 Ile Ile Gln Val Ala Gln Ser Ile Ala Ala Val Gly Arg Met Asn Phe  
 435 440 445  
 Ala Gly Val Leu Pro Ala Ala Pro Gly Ala Glu Glu Val Met Ala Gln  
 450 455 460  
 Asn Ser Ala Tyr Arg Val Glu Ala Leu Leu Lys Gln Trp Asp Trp Ser  
 465 470 475 480  
 Gln Gly Leu Gln Leu Val Pro Gly Pro Ile Leu Leu Val Thr Asp Leu  
 485 490 495  
 Ile Asp Thr Gly Trp Ser Val Thr Val Ala Gly Asn Gly Ile Ala Gln  
 500 505 510  
 Arg Thr Ser Glu Lys Val Leu Pro Phe Ala Leu Ala Ser Arg Gly  
 515 520 525  
  
 <210> 247  
 <211> 3888  
 <212> DNA  
 <213> *Corynebacterium glutamicum*  
  
 <220>  
 <221> CDS  
 <222> (101)..(3865)

&lt;223&gt; RXN01770

&lt;400&gt; 247

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acacctccac tttttctact ttttaagaaag ccacattctc atg cca att atc att 115  
 Met Pro Ile Ile Ile  
 1 5

gat aac ctc aat tct gac gac gac tcc acc atc ggc act gcc acc gaa 163  
 Asp Asn Leu Asn Ser Asp Asp Asp Ser Thr Ile Gly Thr Ala Thr Glu  
 10 15 20

tac aac cct gac act gac gcc gat tta ctt gat gct att aac gct gat 211  
 Tyr Asn Pro Asp Thr Asp Ala Asp Leu Leu Asp Ala Ile Asn Ala Asp  
 25 30 35

gct gac ctt gat ggc gac gcc acc atc agc act aac gcg aca gaa gaa 259  
 Ala Asp Leu Asp Gly Asp Ala Thr Ile Ser Thr Asn Ala Thr Glu Glu  
 40 45 50

ggt gta gac gca gca gct gaa aaa cct aag aaa aag cgt aaa gcc cct 307  
 Gly Val Asp Ala Ala Ala Glu Lys Pro Lys Lys Lys Arg Lys Ala Pro  
 55 60 65

gct ctg aag cct aaa gga ctc acg gca aag ttc ttc cac cgt gat ctt 355  
 Ala Leu Lys Pro Lys Gly Leu Thr Ala Lys Phe Phe His Arg Asp Leu  
 70 75 80 85

act ggc gta ggt ggt agg acc ggt cgc ctc aac aag aac gta cac ccg 403  
 Thr Gly Val Gly Gly Arg Thr Gly Arg Leu Asn Lys Asn Val His Pro  
 90 95 100

acc aac cca gat ctg tcc tac cag cca gtc tct gat gtc tac acc cca 451  
 Thr Asn Pro Asp Leu Ser Tyr Gln Pro Val Ser Asp Val Tyr Thr Pro  
 105 110 115

caa tca gca gat cac aag ggt att aag acc cgc tac atc ctt acc cat 499  
 Gln Ser Ala Asp His Lys Gly Ile Lys Thr Arg Tyr Ile Leu Thr His  
 120 125 130

cca acc ccc gct gtt gtt ctc agt gag tcc atc agc aac gcg ttt cat 547  
 Pro Thr Pro Ala Val Val Leu Ser Glu Ser Ile Ser Asn Ala Phe His  
 135 140 145

gtc tct acc ctg cgt cgc aac aat aat gtc aac aac tct gat tcg gaa 595  
 Val Ser Thr Leu Arg Arg Asn Asn Asn Val Asn Asn Ser Asp Ser Glu  
 150 155 160 165

ttg gct gcc tgg ccg tac ctc tac caa ctc gat att ccg cag ctg gac 643  
 Leu Ala Ala Trp Pro Tyr Leu Tyr Gln Leu Asp Ile Pro Gln Leu Asp  
 170 175 180

cag atg att aat gtc gct gac atc tgt gat tac cat ttc cac gga tat 691  
 Gln Met Ile Asn Val Ala Asp Ile Cys Asp Tyr His Phe His Gly Tyr  
 185 190 195

aac ctg tgg gtg gat ttt acc ccg cag act atc gct cta cga tcc ggt 739  
 Asn Leu Trp Val Asp Phe Thr Pro Gln Thr Ile Ala Leu Arg Ser Gly  
 200 205 210



aag acg gta ctc gat gac ggt acc acc gcc tct gat aac acc act cat 787  
 Lys Thr Val Leu Asp Asp Gly Thr Thr Ala Ser Asp Asn Thr Thr His  
 215 220 225  
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 Asn Pro Ile Ser Thr Pro Ser Ile Lys Arg Ile Gly Ala Val Thr Asp  
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 Lys Ser Tyr Gln Leu Cys Glu Arg Val Val Ala Gln Ala Lys Leu Ile  
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Asp Ala Leu Asn Ser Ile Val Ser Gln Leu Pro Val Pro Asp Lys Asp 455 460 465	
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ggg gct ggt acc ggt aaa tcc acc gtg att ctg gaa cgc att gag tac Gly Ala Gly Thr Gly Lys Ser Thr Val Ile Leu Glu Arg Ile Glu Tyr 505 510 515	1651
ttg tgc gct gca ggc acc aac cct gaa gag att gct gtg ctg tct ttt Leu Cys Ala Ala Gly Thr Asn Pro Glu Glu Ile Ala Val Leu Ser Phe 520 525 530	1699
act aat gct gcc gcc gat aac atc aca gca aaa aat gac aag gtg acc Thr Asn Ala Ala Ala Asp Asn Ile Thr Ala Lys Asn Asp Lys Val Thr 535 540 545	1747
tct atg acc atc tcc aag atg gtt cat gag att tac gca cac aat ttc Ser Met Thr Ile Ser Lys Met Val His Glu Ile Tyr Ala His Asn Phe 550 555 560 565	1795
cct gat cat gag atc tcc acc atc gac acc att atc aat acg ctt gat Pro Asp His Glu Ile Ser Thr Thr Ile Asp Thr Ile Ile Asn Thr Leu Asp 570 575 580	1843
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aca gcg ttg agc atc ttc atg gaa tcc cat atc gag gcg ttc atc tgc Thr Ala Leu Ser Ile Phe Met Glu Ser His Ile Glu Ala Phe Ile Ser 615 620 625	1987
gtg ttg gat cag atc aag cag act tct ctt gag ctg gaa atc atc atc Val Leu Asp Gln Ile Lys Gln Thr Ser Leu Glu Leu Glu Ile Ile Ile 630 635 640 645	2035
tgc tac ctg ctc ttg gat aag ctg atc gag cct cat gca tgc cgc aag Cys Tyr Leu Leu Leu Asp Lys Leu Ile Glu Pro His Ala Ser Pro Lys 650 655 660	2083
tac ctc att att gat gag gtg cag gac aac tgc gtc ttc gag ttc gtc Tyr Leu Ile Ile Asp Glu Val Gln Asp Asn Ser Val Phe Glu Phe Val 665 670 675	2131
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695	700	705	
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acc acc aat tac cgt tcc aac cag gaa att ctt gac ttc gct aat atc Thr Thr Asn Tyr Arg Ser Asn Gln Glu Ile Leu Asp Phe Ala Asn Ile 730 735 740			2323
cac ctc tcg gat att gaa gct aac cag ttc gca ggt att cag ctc tac His Leu Ser Asp Ile Glu Ala Asn Gln Phe Ala Gly Ile Gln Leu Tyr 745 750 755			2371
gcc aac tct ttt gat gca cct act gcg gac agc ttc aaa gaa aag gtt Ala Asn Ser Phe Asp Ala Pro Thr Ala Asp Ser Phe Lys Glu Lys Val 760 765 770			2419
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ttg aac aat gag caa acc att gtg ctt gct cat tct ggt cgt gaa att Leu Asn Asn Glu Gln Thr Ile Val Leu Ala His Ser Gly Arg Glu Ile 810 815 820			2563
cgt gca gcg cag caa gcg cta gcc gag atg tac ccc agc atc acg gtg Arg Ala Ala Gln Gln Ala Leu Ala Glu Met Tyr Pro Ser Ile Thr Val 825 830 835			2611
cgt aac ttg cag tcc gat aag ggt ttc aac aac acg gta ttt tcg acc Arg Asn Leu Gln Ser Asp Lys Gly Phe Asn Asn Thr Val Phe Ser Thr 840 845 850			2659
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gcc gca ttt acc ttt acc agc caa gtc acc gct cat cta gat aag ttg Ala Ala Phe Thr Phe Thr Ser Gln Val Thr Ala His Leu Asp Lys Leu 870 875 880 885			2755
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gct gca tgg tgg cgt gaa aat gag cgt gac atc cag ggt tgg gtg cag Ala Ala Trp Trp Arg Glu Asn Glu Arg Asp Ile Gln Gly Trp Val Gln 905 910 915			2851
caa act cag tcc ggt gcg atc acc aac gaa gag ttc ttc tac cgt ctt Gln Thr Gln Ser Gly Ala Ile Thr Asn Glu Glu Phe Phe Tyr Arg Leu 920 925 930			2899
cgt cag tgc att ctt gac tat gaa atc agg aat aac cga gca cgt cag Arg Gln Cys Ile Leu Asp Tyr Glu Ile Arg Asn Asn Arg Ala Arg Gln 935 940 945			2947

tcc atg ctc aat gcg cgc aac aac gct aac aag gag gct gtc gca cag 2995  
 Ser Met Leu Asn Ala Arg Asn Asn Ala Asn Lys Glu Ala Val Ala Gln  
 950 955 960 965

gag aaa cca ctg ctc atg gtc tcc acc att cac agt gca aag ggt ctg 3043  
 Glu Lys Pro Leu Leu Met Val Ser Thr Ile His Ser Ala Lys Gly Leu  
 970 975 980

gaa ttc gat aat gtc atc gtg ctt caa aaa cca agc tcc gat gca gag 3091  
 Glu Phe Asp Asn Val Ile Val Leu Gln Lys Pro Ser Ser Asp Ala Glu  
 985 990 995

atg acc gaa gaa ggt aag cgc gca acc tat gtg gcg ctg acc cgt gca 3139  
 Met Thr Glu Glu Gly Lys Arg Ala Thr Tyr Val Ala Leu Thr Arg Ala  
 1000 1005 1010

aaa aag cgt gaa ctc att att gct ggt tct act cgc gca tac cca cgc 3187  
 Lys Lys Arg Glu Leu Ile Ile Ala Gly Ser Thr Arg Ala Tyr Pro Arg  
 1015 1020 1025

atc gtc acc gat tat gag caa atc gtt gat ctt ctt gaa aag cgc gat 3235  
 Ile Val Thr Asp Tyr Glu Gln Ile Val Asp Leu Leu Glu Lys Arg Asp  
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gag gag cgc aaa att aag gag gaa gag gct gca gca ctc gcc acc ctt 3283  
 Glu Glu Arg Lys Ile Lys Glu Glu Glu Ala Ala Leu Ala Thr Leu  
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gaa gct gaa cag gag acg cgc gcc ctt gct gct gct gag gcg cag gct 3331  
 Glu Ala Glu Gln Glu Thr Arg Ala Leu Ala Ala Ala Glu Ala Gln Ala  
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 Gln Ala Leu Leu Glu His Asn Pro Trp Leu Arg Asp Leu Ser Asp  
 1080 1085 1090

gaa gaa gtc act gct cta act gag caa gag atc atc aac aat gtt gag 3427  
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cca gcc cta cag att gaa gaa gag gag gaa gag gct cgt gca ctc gct 3475  
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 Thr Val Ala Ala Asp Pro Val Glu Pro Thr Ile Val Ala Ala Gln Pro 1205  
 1190 1195 1200

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 Glu Val Asp Asp Asn Leu Val Tyr Ser Thr Ser Thr Pro Asn Ser His 1220  
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 Ser Asp Val Ile Ala Val Asn Ser Asp Thr Ser Glu Asn Ala Val 1235  
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aat cca gtt ctg tcc gat att gag gca ctc cga gca att ttc aac aac 3859  
 Asn Pro Val Leu Ser Asp Ile Glu Ala Leu Arg Ala Ile Phe Asn Asn 1250  
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 Gln Asp 1255

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&lt;211&gt; 1255

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 248

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Gly Thr Ala Thr Glu Tyr Asn Pro Asp Thr Asp Ala Asp Leu Leu Asp  
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Ala Ile Asn Ala Asp Ala Asp Leu Asp Gly Asp Ala Thr Ile Ser Thr  
 35 40 45

Asn Ala Thr Glu Glu Gly Val Asp Ala Ala Ala Glu Lys Pro Lys Lys  
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Lys Arg Lys Ala Pro Ala Leu Lys Pro Lys Gly Leu Thr Ala Lys Phe  
 65 70 75 80

Phe His Arg Asp Leu Thr Gly Val Gly Gly Arg Thr Gly Arg Leu Asn  
 85 90 95

Lys Asn Val His Pro Thr Asn Pro Asp Leu Ser Tyr Gln Pro Val Ser  
 100 105 110

Asp Val Tyr Thr Pro Gln Ser Ala Asp His Lys Gly Ile Lys Thr Arg  
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Tyr Ile Leu Thr His Pro Thr Pro Ala Val Val Leu Ser Glu Ser Ile  
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Ser Asn Ala Phe His Val Ser Thr Leu Arg Arg Asn Asn Asn Val Asn  
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Asn Ser Asp Ser Glu Leu Ala Ala Trp Pro Tyr Leu Tyr Gln Leu Asp  
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Ile Pro Gln Leu Asp Gln Met Ile Asn Val Ala Asp Ile Cys Asp Tyr

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 Asn Asp Lys Val Thr Ser Met Thr Ile Ser Lys Met Val His Glu Ile  
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 Tyr Ala His Asn Phe Pro Asp His Glu Ile Ser Thr Ile Asp Thr Ile  
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 Ile Asn Thr Leu Asp Ile Glu Tyr Gly Asp Gln Met Val Thr Ser Asp  
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 595 600 605  
 Gly Asn Ala Asn Leu Thr Ala Leu Ser Ile Phe Met Glu Ser His Ile  
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 Glu Ala Phe Ile Ser Val Leu Asp Gln Ile Lys Gln Thr Ser Leu Glu  
 625 630 635 640  
 Leu Glu Ile Ile Ile Cys Tyr Leu Leu Leu Asp Lys Leu Ile Glu Pro  
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 His Ala Ser Pro Lys Tyr Leu Ile Ile Asp Glu Val Gln Asp Asn Ser  
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 Ser Ala Asn Pro Lys Ala Leu Asn Ser Leu Glu Ala Ser Gly Val Phe  
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 Gly Thr Tyr Arg Leu Thr Thr Asn Tyr Arg Ser Asn Gln Glu Ile Leu  
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 Asp Phe Ala Asn Ile His Leu Ser Asp Ile Glu Ala Asn Gln Phe Ala  
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 Gly Ile Gln Leu Tyr Ala Asn Ser Phe Asp Ala Pro Thr Ala Asp Ser  
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 Phe Lys Glu Lys Val Glu Leu Asp Met His His Val Ser Lys Gln Ser  
 770 775 780  
 Glu Phe Thr Asp Ser Ile Pro Tyr Phe Met Glu Ser Asn Lys Ala Arg  
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 Phe Asp Ala Ala Ile Leu Asn Asn Glu Gln Thr Ile Val Leu Ala His  
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 Ser Gly Arg Glu Ile Arg Ala Ala Gln Gln Ala Leu Ala Glu Met Tyr  
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Pro Ser Ile Thr Val Arg Asn Leu Gln Ser Asp Lys Gly Phe Asn Asn  
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 Thr Val Phe Ser Thr Phe Ile Lys Asp Phe Trp Phe Glu Val Thr Ala  
 850 855 860  
 Val Asp Pro Ala His Ala Ala Phe Thr Phe Thr Ser Gln Val Thr Ala  
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 His Leu Asp Lys Leu Val Arg Gly Lys Arg Glu Gln Met Glu Asp Arg  
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 Val Ile Arg Ser Met Ala Ala Trp Trp Arg Glu Asn Glu Arg Asp Ile  
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 Phe Phe Tyr Arg Leu Arg Gln Cys Ile Leu Asp Tyr Glu Ile Arg Asn  
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 Asn Arg Ala Arg Gln Ser Met Leu Asn Ala Arg Asn Asn Ala Asn Lys  
 945 950 955 960  
 Glu Ala Val Ala Gln Glu Lys Pro Leu Leu Met Val Ser Thr Ile His  
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 Ser Ala Lys Gly Leu Glu Phe Asp Asn Val Ile Val Leu Gln Lys Pro  
 980 985 990  
 Ser Ser Asp Ala Glu Met Thr Glu Glu Gly Lys Arg Ala Thr Tyr Val  
 995 1000 1005  
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1155 1160 1165

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Asp Leu Glu Val Thr Thr Val Ala Ala Asp Pro Val Glu Pro Thr Ile  
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Val Lys Ala Phe Leu  
1 5

tcc tcc cct gca gcc ttg ggc gaa aca gtg tcc aat cgc etc aaa aag 163  
Ser Ser Pro Ala Ala Leu Gly Glu Thr Val Ser Asn Arg Leu Lys Lys  
10 15 20

gcc tct gca cca gaa gaa aaa cgc gcc cta gaa acc ctt tca caa ctt 211  
Ala Ser Ala Pro Glu Glu Lys Arg Ala Leu Glu Thr Leu Ser Gln Leu  
25 30 35

aat tct gcg atc acc ccg cag acc tca cag aag tac caa tct cta ctg 259  
Asn Ser Ala Ile Thr Pro Gln Thr Ser Gln Lys Tyr Gln Ser Leu Leu  
40 45 50

agc tac etc ggt gac atc gga gtg aag aag aac tcc gat acc cgc gtg 307  
Ser Tyr Leu Gly Asp Ile Gly Val Lys Lys Asn Ser Asp Thr Arg Val  
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Val Ile Phe Ser Glu Arg Val Ala Thr Leu His Trp Leu Gln Glu Asn  
70 75 80 85

ctc atc cgt gat etc aag atg cca ccc aac tct att gct gtt atg cac 403  
Leu Ile Arg Asp Leu Lys Met Pro Pro Asn Ser Ile Ala Val Met His  
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 Gly Gly Leu Pro Asp Gln Glu Gln Met Arg Leu Val Asp Glu Phe Lys  
 105 110 115

aag acg gat tct ccc atc cgc atc atg atc acc ggc gat gtt gcc tca 499  
 Lys Thr Asp Ser Pro Ile Arg Ile Met Ile Thr Gly Asp Val Ala Ser  
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 Glu Gly Val Asn Leu His Thr Leu Cys His Asn Leu Val His Tyr Asp  
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 Ile Pro Trp Ser Leu Ile Arg Ile Gln Gln Arg Asn Gly Arg Ile Asp  
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cgt tat ggt caa acc cac aac cct tcc atc gtt acc ttc ttg ctc gat 643  
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ccc gcc gag gat tcc aaa gta ggt gaa gtc cat gtg ctg gag agg ctc 691  
 Pro Ala Glu Asp Ser Lys Val Gly Glu Val His Val Leu Glu Arg Leu  
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 Met Glu Arg Glu His Glu Ala His Ser Leu Leu Gly Asp Ala Ala Ser  
 200 205 210

ctc atg ggc aag cac tct gag cgt ttg gaa gaa gaa acc atc cgc gaa 787  
 Leu Met Gly Lys His Ser Glu Arg Leu Glu Glu Glu Thr Ile Arg Glu  
 215 220 225

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 230 235 240 245

gaa gtc cta gaa aac cca gca gcc cta gat gat att gat tgg ttg cta 883  
 Glu Val Leu Glu Asn Pro Ala Gly Leu Asp Asp Ile Asp Trp Leu Leu  
 250 255 260

gcc caa atc gcc caa gcc gat gcc aag gca gaa aca gaa gca gaa gca 931  
 Ala Gln Ile Ala Gln Ala Asp Ala Lys Ala Glu Thr Glu Ala Glu Ala  
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gaa aca gaa aac caa aca gca cca gat gca gct tcc aat agc acg cag 979  
 Glu Thr Glu Asn Gln Thr Ala Pro Asp Ala Ala Ser Asn Ser Thr Gln  
 280 285 290

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 His Ala Gln Arg Arg Leu Tyr Ala Gln Glu Ser Ser Phe Leu Tyr Asp  
 295 300 305

tgc ctc ctc gaa ggt ttc aat aac gta ccg gag gat tcc atc aac cgc 1075  
 Cys Leu Leu Glu Gly Phe Asn Asn Val Pro Glu Asp Ser Ile Asn Arg  
 310 315 320 325

ggt ggc gtg ggg ttc aaa aaa cac gat aat gac atc gtg gag ctc acc 1123  
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 330 335 340

ccc acc gat gat ctg cgc cgt cgt cta gat ttc ctc ccg cag gat tat 1171  
Pro Thr Asp Asp Leu Arg Arg Arg Leu Asp Phe Leu Pro Gln Asp Tyr  
345 350 355

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360 365 370

atg cgt gcc caa gaa cgc ctc aac gct gcg cgc act ggt gaa gat gcc 1267  
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375 380 385

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Ser Thr Trp Pro Ser Ala His Tyr Leu Gly Pro Leu His Pro Val Thr  
390 395 400 405

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Pro Ala Ala Ser Gly Lys Val Thr Glu Pro Thr Val Leu Leu Met Ser  
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Ala Leu Pro Asp Asp Ile Glu Gln Leu Ile Ser Leu Ala Val Gln Ala  
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gcc cgc gcc gag atc cgt cca tta atg atc gcc gcc cgc gct cag gct 1651  
Ala Arg Gly Glu Ile Arg Pro Leu Met Ile Ala Ala Arg Ala Gln Ala  
505 510 515

caa act cgc gtt gag cat tgg gct aag cga gcc gaa gcc tgg aat aac 1699  
Gln Thr Arg Val Glu His Trp Ala Lys Arg Ala Glu Ala Trp Asn Asn  
520 525 530

aaa cga agt gcc gca gcg tcc acg tcc cgt acc gcg cga act gca aaa 1747  
Lys Arg Ser Gly Ala Ala Ser Thr Ser Arg Thr Ala Arg Thr Ala Lys  
535 540 545

ttg att gag gag cag cag aaa ttg agt aat gct ctc gag cca gac cgt 1795  
Leu Ile Glu Glu Gln Gln Lys Leu Ser Asn Ala Leu Glu Pro Asp Arg  
550 555 560 565

gaa ctt att agg cct ttg gcc gtc att ctt ccg cag ccc gca act ttg 1843  
Glu Leu Ile Arg Pro Leu Ala Val Ile Leu Pro Gln Pro Ala Thr Leu  
570 575 580

aac acc gag gtt taacacaatg agtgcatttg att 1878

Asn Thr Glu Val  
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<210> 250

<211> 585

<212> PRT

<213> Corynebacterium glutamicum

<400> 250

Val Lys Ala Phe Leu Ser Ser Pro Ala Ala Leu Gly Glu Thr Val Ser  
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Asn Arg Leu Lys Lys Ala Ser Ala Pro Glu Glu Lys Arg Ala Leu Glu  
20 25 30

Thr Leu Ser Gln Leu Asn Ser Ala Ile Thr Pro Gln Thr Ser Gln Lys  
35 40 45

Tyr Gln Ser Leu Leu Ser Tyr Leu Gly Asp Ile Gly Val Lys Lys Asn  
50 55 60

Ser Asp Thr Arg Val Val Ile Phe Ser Glu Arg Val Ala Thr Leu His  
65 70 75 80

Trp Leu Gln Glu Asn Leu Ile Arg Asp Leu Lys Met Pro Pro Asn Ser  
85 90 95

Ile Ala Val Met His Gly Gly Leu Pro Asp Gln Glu Gln Met Arg Leu  
100 105 110

Val Asp Glu Phe Lys Lys Thr Asp Ser Pro Ile Arg Ile Met Ile Thr  
115 120 125

Gly Asp Val Ala Ser Glu Gly Val Asn Leu His Thr Leu Cys His Asn  
130 135 140

Leu Val His Tyr Asp Ile Pro Trp Ser Leu Ile Arg Ile Gln Gln Arg  
145 150 155 160

Asn Gly Arg Ile Asp Arg Tyr Gly Gln Thr His Asn Pro Ser Ile Val  
165 170 175

Thr Phe Leu Leu Asp Pro Ala Glu Asp Ser Lys Val Gly Glu Val His  
180 185 190

Val Leu Glu Arg Leu Met Glu Arg Glu His Glu Ala His Ser Leu Leu  
195 200 205

Gly Asp Ala Ala Ser Leu Met Gly Lys His Ser Glu Arg Leu Glu Glu  
210 215 220

Glu Thr Ile Arg Glu Val Leu Arg Gly Ala Gln Asn Phe Asn Asp Ala  
225 230 235 240

Val Ala Asp Pro Ala Glu Val Leu Glu Asn Pro Ala Gly Leu Asp Asp  
245 250 255

Ile Asp Trp Leu Leu Ala Gln Ile Ala Gln Ala Asp Ala Lys Ala Glu  
260 265 270

Thr Glu Ala Glu Ala Glu Thr Glu Asn Gln Thr Ala Pro Asp Ala Ala  
 275 280 285  
 Ser Asn Ser Thr Gln His Ala Gln Arg Arg Leu Tyr Ala Gln Glu Ser  
 290 295 300  
 Ser Phe Leu Tyr Asp Cys Leu Leu Glu Gly Phe Asn Asn Val Pro Glu  
 305 310 315 320  
 Asp Ser Ile Asn Arg Gly Gly Val Gly Phe Lys Lys His Asp Asn Asp  
 325 330 335  
 Ile Val Glu Leu Thr Pro Thr Asp Asp Leu Arg Arg Arg Leu Asp Phe  
 340 345 350  
 Leu Pro Gln Asp Tyr Val Ala Ala Arg Lys Val Lys Glu Asp Leu Leu  
 355 360 365  
 Leu Ala Ser Thr Leu Met Arg Gly Gln Glu Arg Leu Asn Ala Ala Arg  
 370 375 380  
 Thr Gly Glu Asp Gly Ser Thr Trp Pro Ser Ala His Tyr Leu Gly Pro  
 385 390 395 400  
 Leu His Pro Val Thr Ser Trp Ala Ala Asp Arg Ala Leu Ala Thr Met  
 405 410 415  
 Pro Arg Ser Glu Ile Pro Ala Ala Ser Gly Lys Val Thr Glu Pro Thr  
 420 425 430  
 Val Leu Leu Met Ser Thr Leu Ser Asn Arg Arg Gly Gln Ile Val Ser  
 435 440 445  
 Arg Ser Phe Val Ala Ser Ser Gly Pro Phe Asp Thr Glu Val Leu Ser  
 450 455 460  
 Asp Pro Ile Gln Trp Leu His Ser Ile Gly Leu Asp Glu Thr Ala Ile  
 465 470 475 480  
 Asn Pro Gly Thr Ala Ala Leu Pro Asp Asp Ile Glu Gln Leu Ile Ser  
 485 490 495  
 Leu Ala Val Gln Ala Ala Arg Gly Glu Ile Arg Pro Leu Met Ile Ala  
 500 505 510  
 Ala Arg Ala Gln Ala Gln Thr Arg Val Glu His Trp Ala Lys Arg Ala  
 515 520 525  
 Glu Ala Trp Asn Asn Lys Arg Ser Gly Ala Ala Ser Thr Ser Arg Thr  
 530 535 540  
 Ala Arg Thr Ala Lys Leu Ile Glu Glu Gln Gln Lys Leu Ser Asn Ala  
 545 550 555 560  
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 Gln Pro Ala Thr Leu Asn Thr Glu Val  
 580 585

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 <213> *Corynebacterium glutamicum*

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 <222> (101)..(1771)  
 <223> RXN02131

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 Val Ala Phe Gly Asp  
 1 5  
 gga cct tta atc gtc caa tcc gat aag aca gtc ctg cta gaa ata gat 163  
 Gly Pro Leu Ile Val Gln Ser Asp Lys Thr Val Leu Leu Glu Ile Asp  
 10 15 20  
 cac ccc caa gca ggc gaa gca cgc ata gct cta gca cct ttt gca gag 211  
 His Pro Gln Ala Gly Glu Ala Arg Ile Ala Leu Ala Pro Phe Ala Glu  
 25 30 35  
 ctc gag cgt gca ccc gag cat att cac acc tac cgc atc acc cct ctg 259  
 Leu Glu Arg Ala Pro Glu His Ile His Thr Tyr Arg Ile Thr Pro Leu  
 40 45 50  
 gcg ttg tgg aac gcg cgc acc gca ggc cac gac gcc gaa caa gtc gtg 307  
 Ala Leu Trp Asn Ala Arg Thr Ala Gly His Asp Ala Glu Gln Val Val  
 55 60 65  
 gac atg ctg gag cgt ttt tca cgc ttc ccc gtt cgg caa gcg ctc ctg 355  
 Asp Met Leu Glu Arg Phe Ser Arg Phe Pro Val Pro Gln Ala Leu Leu  
 70 75 80 85  
 atc gac atc gca gag acg atg tcc cgc tac gga cgt gtg cgc ctg cac 403  
 Ile Asp Ile Ala Glu Thr Met Ser Arg Tyr Gly Arg Val Arg Leu His  
 90 95 100  
 cgt cac ccc gca cac ggg ctg atc ctt gaa tct ggc gaa cct gcg atc 451  
 Arg His Pro Ala His Gly Leu Ile Leu Glu Ser Gly Glu Pro Ala Ile  
 105 110 115  
 ctg gtg gaa atc tcc cgg cac aaa aag atc aaa ccc atg ctg ggc gca 499  
 Leu Val Glu Ile Ser Arg His Lys Lys Ile Lys Pro Met Leu Gly Ala  
 120 125 130  
 caa gtg gat cct gaa acc atc gtg gtc cat cgg tca gaa cgc ggg cgc 547  
 Gln Val Asp Pro Glu Thr Ile Val Val His Pro Ser Glu Arg Gly Arg  
 135 140 145  
 ctc aag cag gaa ctg ctc aag gtc ggt tgg cca gcg gaa gat ctc gcg 595  
 Leu Lys Gln Glu Leu Leu Lys Val Gly Trp Pro Ala Glu Asp Leu Ala  
 150 155 160 165  
 gga tat gtg gac ggt gaa tcc cac ccc att ggt ctc tcc act gaa ttt 643  
 Gly Tyr Val Asp Gly Glu Ser His Pro Ile Gly Leu Ser Thr Glu Phe  
 170 175 180

gaa gac tgg tgc ctg cgc gat tat cag caa atg gca gcc gat tcc ttc 691  
 Glu Asp Trp Ser Leu Arg Asp Tyr Gln Gln Met Ala Ala Asp Ser Phe  
 185 190 195

tgg gaa ggc ggt tcc ggc gta gtc gtg ctg cct tgt ggc gcg ggt aaa 739  
 Trp Glu Gly Gly Ser Gly Val Val Val Leu Pro Cys Gly Ala Gly Lys  
 200 205 210

acc atg gtc ggt gca gcc tcc atg gct cgc gca cag gca acc acc ttg 787  
 Thr Met Val Gly Ala Ala Ser Met Ala Arg Ala Gln Ala Thr Thr Leu  
 215 220 225

atc ctt gtc acc aac acc gtg gcc ggc cga cag tgg aaa gac gaa ctt 835  
 Ile Leu Val Thr Asn Thr Val Ala Gly Arg Gln Trp Lys Asp Glu Leu  
 230 235 240 245

ctt cgc cgc acc aca ctc acc gaa gac gaa atc ggt gag tac tcc ggc 883  
 Leu Arg Arg Thr Thr Leu Thr Glu Asp Glu Ile Gly Glu Tyr Ser Gly  
 250 255 260

gaa cgc aaa gaa atc cga ccc gtc acc atc gcc acc tac caa gta gtc 931  
 Glu Arg Lys Glu Ile Arg Pro Val Thr Ile Ala Thr Tyr Thr Val Val  
 265 270 275

acc agg cgt acc aaa ggc gaa tac aaa gct ctc gag ctt ttt gat tcc 979  
 Thr Arg Arg Thr Lys Gly Glu Tyr Lys Lys Ala Leu Glu Leu Phe Asp Ser  
 280 285 290

cgc gac tgg ggc tta att att tac gac gaa gtc cat ctt ctt ccc gcc 1027  
 Arg Asp Trp Gly Leu Ile Ile Tyr Asp Glu Val His Leu Leu Pro Ala  
 295 300 305

ccc gtt ttc cgc atg acc tcc gac ctg caa tcc agg cga cgc ctc gga 1075  
 Pro Val Phe Arg Met Thr Ser Asp Leu Gln Ser Arg Arg Arg Leu Gly  
 310 315 320 325

ctg act gcc acc ctc gtg cgc gaa gac gga cga gaa ggc gat gtc ttc 1123  
 Leu Thr Ala Thr Leu Val Arg Glu Asp Gly Arg Glu Gly Asp Val Phe  
 330 335 340

agc ctg atc ggc ccc aag cgt tac gac gca cca tgg aaa gac ctc gag 1171  
 Ser Leu Ile Gly Pro Lys Arg Tyr Asp Ala Pro Trp Lys Asp Leu Glu  
 345 350 355

tcc caa ggg ttc atc gcc acc gcc gac tgc gta gaa atc cga tcc acc 1219  
 Ser Gln Gly Phe Ile Ala Thr Ala Asp Cys Val Glu Ile Arg Ser Thr  
 360 365 370

atg acc gat gct gag cgc atg gtg tac gcg act gcc gag tcg gca gat 1267  
 Met Thr Asp Ala Glu Arg Met Val Tyr Ala Thr Ala Glu Ser Ala Asp  
 375 380 385

cgt tac cgt cta gcc gcc act gcc cac act aag gtg gcc gtg gtg cgc 1315  
 Arg Tyr Arg Leu Ala Ala Thr Ala His Thr Lys Val Ala Val Val Arg  
 390 395 400 405

aaa ctc ctc gaa gag cac gct ggt aag ccc acg ctg atc atc ggc gca 1363  
 Lys Leu Leu Glu Glu His Ala Gly Lys Pro Thr Leu Ile Ile Gly Ala  
 410 415 420

tac ctc gat cag ttg gaa gaa cta ggt gca gaa ttc aac gca cca gtc 1411

Tyr Leu Asp Gln Leu Glu Glu Leu Gly Ala Glu Phe Asn Ala Pro Val  
425 430 435

atc gac ggc aaa acg ccc aac aaa aag cgt gaa gcc ctc ttt gat caa 1459  
Ile Asp Gly Lys Thr Pro Asn Lys Lys Arg Glu Ala Leu Phe Asp Gln  
440 445 450

ttc cgt tcc ggc tcg ctt tcc gta ctg gtt gtc tcc aaa gtg gcg aac 1507  
Phe Arg Ser Gly Ser Leu Ser Val Leu Val Val Ser Lys Val Ala Asn  
455 460 465

ttc tcc atc gac ctg ccc gaa gca tcc gta gcc atc cag gtc tct gga 1555  
Phe Ser Ile Asp Leu Pro Glu Ala Ser Val Ala Ile Gln Val Ser Gly  
470 475 480 485

aca ttc ggc agc cga caa gaa gaa gcc caa cgc tta gcc cgc ctc ctg 1603  
Thr Phe Gly Ser Arg Gln Glu Glu Ala Gln Arg Leu Gly Arg Leu Leu  
490 495 500

cga ccc aag cac gat ggc agc gaa gcc cac ttc tac tcc atc gtc agc 1651  
Arg Pro Lys His Asp Gly Ser Glu Ala His Phe Tyr Ser Ile Val Ser  
505 510 515

cgc gac acc ctc gac acc gaa tac gca gcc cac cgc cag cga ttc ctc 1699  
Arg Asp Thr Leu Asp Thr Glu Tyr Ala Ala His Arg Gln Arg Phe Leu  
520 525 530

gcc gaa caa ggc tac gca tac cgc atc ctc gac gcc gac gac atc ctc 1747  
Ala Glu Gln Gly Tyr Ala Tyr Arg Ile Leu Asp Ala Asp Asp Ile Leu  
535 540 545

ttc cca cta ccc aag aaa gag cta taacgtgcac aactctctct tcg 1794  
Phe Pro Leu Pro Lys Lys Glu Leu  
550 555

<210> 252

<211> 557

<212> PRT

<213> Corynebacterium glutamicum

<400> 252

Val Ala Phe Gly Asp Gly Pro Leu Ile Val Gln Ser Asp Lys Thr Val  
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Leu Leu Glu Ile Asp His Pro Gln Ala Gly Glu Ala Arg Ile Ala Leu  
20 25 30

Ala Pro Phe Ala Glu Leu Glu Arg Ala Pro Glu His Ile His Thr Tyr  
35 40 45

Arg Ile Thr Pro Leu Ala Leu Trp Asn Ala Arg Thr Ala Gly His Asp  
50 55 60

Ala Glu Gln Val Val Asp Met Leu Glu Arg Phe Ser Arg Phe Pro Val  
65 70 75 80

Pro Gln Ala Leu Leu Ile Asp Ile Ala Glu Thr Met Ser Arg Tyr Gly  
85 90 95

Arg Val Arg Leu His Arg His Pro Ala His Gly Leu Ile Leu Glu Ser



100	105	110
Gly Glu Pro Ala Ile Leu Val 115	Glu Ile Ser Arg His Lys 120	Lys Ile Lys 125
Pro Met Leu Gly Ala Gln Val 130	Asp Pro Glu Thr 135	Ile Val Val His Pro 140
Ser Glu Arg Gly Arg Leu Lys 145	Gln Glu Leu Leu Lys 150	Val Gly Trp Pro 155
Ala Glu Asp Leu Ala Gly Tyr 165	Val Asp Gly Glu Ser His 170	Pro Ile Gly 175
Leu Ser Thr Glu Phe Glu Asp 180	Trp Ser Leu Arg Asp Tyr 185	Gln Gln Met 190
Ala Ala Asp Ser Phe Trp Glu 195	Gly Gly Ser Gly Val Val 200	Val Val Leu Pro 205
Cys Gly Ala Gly Lys Thr Met 210	Val Gly Ala Ala Ser Met 215	Ala Arg Ala 220
Gln Ala Thr Thr Leu Ile Leu 225	Val Thr Asn Thr Val Ala 230	Gly Arg Gln 235
Trp Lys Asp Glu Leu Leu Arg 245	Arg Thr Thr Leu Thr Glu 250	Asp Gly Ile 255
Gly Glu Tyr Ser Gly Glu Arg 260	Lys Glu Ile Arg Pro Val 265	Thr Ile Ala 270
Thr Tyr Gln Val Val Thr Arg 275	Arg Thr Lys Gly Glu Tyr 280	Lys Ala Leu 285
Glu Leu Phe Asp Ser Arg Asp 290	Trp Gly Leu Ile Ile Tyr 295	Asp Glu Val 300
His Leu Leu Pro Ala Pro Val 305	Phe Arg Met Thr Ser 310	Asp Leu Gln Ser 315
Arg Arg Arg Leu Gly Leu Thr 325	Ala Thr Leu Val Arg Glu 330	Asp Gly Arg 335
Glu Gly Asp Val Phe Ser Leu 340	Ile Gly Pro Lys Arg Tyr 345	Asp Ala Pro 350
Trp Lys Asp Leu Glu Ser Gln 355	Gly Phe Ile Ala Thr Ala 360	Asp Cys Val 365
Glu Ile Arg Ser Thr Met Thr 370	Asp Ala Glu Arg Met Val 375	Tyr Ala Thr 380
Ala Glu Ser Ala Asp Arg Tyr 385	Arg Leu Ala Ala Thr Ala 390	His Thr Lys 395
Val Ala Val Val Arg Lys Leu 405	Leu Leu Glu Glu His Ala 410	Gly Lys Pro Thr 415
Leu Ile Ile Gly Ala Tyr Leu 420	Asp Gln Leu Glu Glu Leu 425	Gly Ala Glu 430

Phe Asn Ala Pro Val Ile Asp Gly Lys Thr Pro Asn Lys Lys Arg Glu  
435 440 445

Ala Leu Phe Asp Gln Phe Arg Ser Gly Ser Leu Ser Val Leu Val Val  
450 455 460

Ser Lys Val Ala Asn Phe Ser Ile Asp Leu Pro Glu Ala Ser Val Ala  
465 470 475 480

Ile Gln Val Ser Gly Thr Phe Gly Ser Arg Gln Glu Glu Ala Gln Arg  
485 490 495

Leu Gly Arg Leu Leu Arg Pro Lys His Asp Gly Ser Glu Ala His Phe  
500 505 510

Tyr Ser Ile Val Ser Arg Asp Thr Leu Asp Thr Glu Tyr Ala Ala His  
515 520 525

Arg Gln Arg Phe Leu Ala Glu Gln Gly Tyr Ala Tyr Arg Ile Leu Asp  
530 535 540

Ala Asp Asp Ile Leu Phe Pro Leu Pro Lys Lys Glu Leu  
545 550 555

<210> 253

<211> 849

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(826)

<223> RXN01066

<400> 253

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tttgaaccgc ctgggcttct agctttaagg gggtgagttc atg cgt agg gac agt 115  
Met Arg Arg Asp Ser 5

ttt cgg gac cgc gcg cta gta gtc aaa act tat gat ttt ggc gaa gcc 163  
Phe Arg Asp Arg Ala Leu Val Val Lys Thr Tyr Asp Phe Gly Glu Ala 20  
10 15

gac cgc att att gtg ctg ctc acc cga gac cac ggc atc gtg cgc gga 211  
Asp Arg Ile Ile Val Leu Leu Thr Arg Asp His Gly Ile Val Arg Gly 35  
25 30

gtt gcc aaa gga gta cgc cga tcc aaa tcc cgg ttt ggg tca agg ctg 259  
Val Ala Lys Gly Val Arg Arg Ser Lys Ser Arg Phe Gly Ser Arg Leu 50  
40 45

cag ctt ttt gtg gaa ctc gac gtg cag ctc tac cca ggt aga aaa ctg 307  
Gln Leu Phe Val Glu Leu Asp Val Gln Leu Tyr Pro Gly Arg Lys Leu 65  
55 60

tcc acc atc tct ggc gcg gac acc gtc ggc tac tac gca tca ggc atc 355  
Ser Thr Ile Ser Gly Ala Asp Thr Val Gly Tyr Tyr Ala Ser Gly Ile

70	75	80	85	
atc gag gac ttc act cgg tat tcc tgt gcg tcc gcc atc ctg gaa atc				403
Ile Glu Asp Phe Thr Arg Tyr Ser Cys Ala Ser Ala Ile Leu Glu Ile	90	95	100	
gcc acc cac atc gca gga ctg gaa aac gat ccg cac ctg ttt gaa gaa				451
Ala Thr His Ile Ala Gly Leu Glu Asn Asp Pro His Leu Phe Glu Glu	105	110	115	
acc acc cgg gcg ttg aaa aac att cag gac tcc cca gaa ccc atc ctc				499
Thr Thr Arg Ala Leu Lys Asn Ile Gln Asp Ser Pro Glu Pro Ile Leu	120	125	130	
aac cta gac gag ttc atg ctc cgc gcc atg aac cac gcc ggc tgg gca				547
Asn Leu Asp Glu Phe Met Leu Arg Ala Met Asn His Ala Gly Trp Ala	135	140	145	
cca agc ctt ttc gac tgc gca gcc tgc ggc cga cca gga cct cac aac				595
Pro Ser Leu Phe Asp Cys Ala Ala Cys Gly Arg Pro Gly Pro His Asn	150	155	160	165
gca ttc cac cca ggc gtc ggc ggg gca gtg tgc ctg tac tgc cga ccg				643
Ala Phe His Pro Gly Val Gly Gly Ala Val Cys Leu Tyr Cys Arg Pro	170	175	180	
ccg gga agc gcc gaa gtc cca cca gaa gca cta cac atg atg tgg ttg				691
Pro Gly Ser Ala Glu Val Pro Pro Glu Ala Leu His Met Trp Leu	185	190	195	
gtc gcc aac ggc caa gca gcc cgc att ccc cgg gaa cac cca gag cag				739
Val Ala Asn Gly Gln Ala Ala Arg Ile Pro Arg Glu His Pro Glu Gln	200	205	210	
caa acc acc att cac caa ctg aca acc gcg cat ctg cag tgg cat att				787
Gln Thr Thr Ile His Gln Leu Thr Thr Ala His Leu Gln Trp His Ile	215	220	225	
gaa aga aag ctg ccc acg ctg gcg gtg ctg gat cag gcc tagtgcttag				836
Glu Arg Lys Leu Pro Thr Leu Ala Val Leu Asn Ala	230	235	240	
gcttaggcgt ccg				849
<210> 254				
<211> 242				
<212> PRT				
<213> Corynebacterium glutamicum				
<400> 254				
Met Arg Arg Asp Ser Phe Arg Asp Arg Ala Leu Val Val Lys Thr Tyr	1	5	10	15
Asp Phe Gly Glu Ala Asp Arg Ile Ile Val Leu Leu Thr Arg Asp His	20	25	30	
Gly Ile Val Arg Gly Val Ala Lys Gly Val Arg Arg Ser Lys Ser Arg	35	40	45	
Phe Gly Ser Arg Leu Gln Leu Phe Val Glu Leu Asp Val Gln Leu Tyr				

50                      55                      60  
 Pro Gly Arg Lys Leu Ser Thr Ile Ser Gly Ala Asp Thr Val Gly Tyr  
 65                      70                      75                      80  
 Tyr Ala Ser Gly Ile Ile Glu Asp Phe Thr Arg Tyr Ser Cys Ala Ser  
 85                      90                      95  
 Ala Ile Leu Glu Ile Ala Thr His Ile Ala Gly Leu Glu Asn Asp Pro  
 100                      105                      110  
 His Leu Phe Glu Glu Thr Thr Arg Ala Leu Lys Asn Ile Gln Asp Ser  
 115                      120                      125  
 Pro Glu Pro Ile Leu Asn Leu Asp Glu Phe Met Leu Arg Ala Met Asn  
 130                      135                      140  
 His Ala Gly Trp Ala Pro Ser Leu Phe Asp Cys Ala Ala Cys Gly Arg  
 145                      150                      155                      160  
 Pro Gly Pro His Asn Ala Phe His Pro Gly Val Gly Gly Ala Val Cys  
 165                      170                      175  
 Leu Tyr Cys Arg Pro Pro Gly Ser Ala Glu Val Pro Pro Glu Ala Leu  
 180                      185                      190  
 His Met Met Trp Leu Val Ala Asn Gly Gln Ala Ala Arg Ile Pro Arg  
 195                      200                      205  
 Glu His Pro Glu Gln Gln Thr Thr Ile His Gln Leu Thr Thr Ala His  
 210                      215                      220  
 Leu Gln Trp His Ile Glu Arg Lys Leu Pro Thr Leu Ala Val Leu Asp  
 225                      230                      235                      240  
 Gln Ala

<210> 255  
 <211> 707  
 <212> DNA  
 <213> *Corynebacterium glutamicum*

<220>  
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 <222> (1)..(684)  
 <223> RXN01389

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 Gln Asp Gly Asp Lys Leu Ala Gly Arg His Gly Asn Lys Gly Val Val  
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 ggt aaa att ttg cct cag aaa gat atg cca ttc ctt cca gac ggc act 96  
 Gly Lys Ile Leu Pro Gln Lys Asp Met Pro Phe Leu Pro Asp Gly Thr  
 20                      25                      30  
 cct gtt gac atc atc ttg aac acc cac ggt gtt cca cgt cgt atg aac 144  
 Pro Val Asp Ile Ile Leu Asn Thr His Gly Val Pro Arg Arg Met Asn  
 35                      40                      45

att ggt cag gtt ctt gag acc cac ctt ggc tgg ctg gca tct gct ggt 192  
 ile Gly Gln Val Leu Glu Thr His Leu Gly Trp Leu Ala Ser Ala Gly  
 50 55 60

tgg tcc gtg gat cct gaa gat cct gag aac gct gag ctg gtc aag act 240  
 Trp Ser Val Asp Pro Glu Asp Pro Glu Asn Ala Glu Leu Val Lys Thr  
 65 70 75 80

ctg cct gca gac ctc ctc gag gtt cct gct ggt tcc ttg act gca act 288  
 Leu Pro Ala Asp Leu Leu Glu Val Pro Ala Gly Ser Leu Thr Ala Thr  
 85 90 95

cct gtg ttc gac ggt gcg tca aac gaa gag ctg gca ggc ctg etc gct 336  
 Pro Val Phe Asp Gly Ala Ser Asn Glu Glu Leu Ala Gly Leu Leu Ala  
 100 105 110

aat tca cgt cca aac cgc gac ggc gac gtc atg gtt aac gcg gat ggt 384  
 Asn Ser Arg Pro Asn Arg Asp Gly Asp Val Met Val Asn Ala Asp Gly  
 115 120 125

aaa gca acg ctt atc gac ggt cgc tcc ggt gag cct tac ccg tac ccg 432  
 Lys Ala Thr Leu Ile Asp Gly Arg Ser Gly Glu Pro Tyr Pro Tyr Pro  
 130 135 140

gtt tcc atc ggc tac atg tac atg ctg aag ctg cac cac ctc gtt gac 480  
 Val Ser Ile Gly Tyr Met Tyr Met Leu Lys Leu His His Leu Val Asp  
 145 150 155 160

gag aag atc cac gca cgt tcc act ggt cct tac tcc atg att acc cag 528  
 Glu Lys Ile His Ala Arg Ser Thr Gly Pro Tyr Ser Met Ile Thr Gln  
 165 170 175

cag cca ctg ggt ggt aaa gca cag ttc ggt gga cag cgt ttc ggc gaa 576  
 Gln Pro Leu Gly Gly Lys Ala Gln Phe Gly Gly Gln Arg Phe Gly Glu  
 180 185 190

atg gag gtg tgg gca atg cag gca tac ggc gct gcc tac aca ctt cag 624  
 Met Glu Val Trp Ala Met Gln Ala Tyr Gly Ala Ala Tyr Thr Leu Gln  
 195 200 205

gag ctg ctg mcc ann nnn nnn nnn nnn nnn nnn nnn nnt nnn 672  
 Glu Leu Leu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
 210 215 220

nnn nnn nnn nnn naannnnnnnn tgcattccggg atc 707  
 Xaa Xaa Xaa Xaa  
 225

<210> 256  
 <211> 228  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 256  
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 Gly Lys Ile Leu Pro Gln Lys Asp Met Pro Phe Leu Pro Asp Gly Thr  
 20 25 30

Pro Val Asp Ile Ile Leu Asn Thr His Gly Val Pro Arg Arg Met Asn  
35 40 45

Ile Gly Gln Val Leu Glu Thr His Leu Gly Trp Leu Ala Ser Ala Gly  
50 55 60

Trp Ser Val Asp Pro Glu Asp Pro Glu Asn Ala Glu Leu Val Lys Thr  
65 70 75 80

Leu Pro Ala Asp Leu Leu Glu Val Pro Ala Gly Ser Leu Thr Ala Thr  
85 90 95

Pro Val Phe Asp Gly Ala Ser Asn Glu Leu Ala Gly Leu Leu Ala  
100 105 110

Asn Ser Arg Pro Asn Arg Asp Gly Asp Val Met Val Asn Ala Asp Gly  
115 120 125

Lys Ala Thr Leu Ile Asp Gly Arg Ser Gly Glu Pro Tyr Pro Tyr Pro  
130 135 140

Val Ser Ile Gly Tyr Met Tyr Met Leu Lys Leu His His Leu Val Asp  
145 150 155 160

Glu Lys Ile His Ala Arg Ser Thr Gly Pro Tyr Ser Met Ile Thr Gln  
165 170 175

Gln Pro Leu Gly Gly Lys Ala Gln Phe Gly Gly Gln Arg Phe Gly Glu  
180 185 190

Met Glu Val Trp Ala Met Gln Ala Tyr Gly Ala Ala Tyr Thr Leu Gln  
195 200 205

Glu Leu Leu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
210 215 220

Xaa Xaa Xaa Xaa  
225

<210> 257  
<211> 1245  
<212> DNA  
<213> Corynebacterium glutamicum

<220>  
<221> CDS  
<222> (101)..(1222)  
<223> RXN02070

<400> 257  
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tttagggagt atcaaaactt gggactacta tcgatacgtg atg act caa gta acc 115  
Met Thr Gln Val Thr  
1 5  
gaa tcc gct gtc cgc agc gcg cta tcc cgc gta gag gat cca gag atc 163  
Glu Ser Ala Val Arg Ser Ala Leu Ser Arg Val Glu Asp Pro Glu Ile  
10 15 20

ggt aag ccc atc aca gag ctc ggc atg gtc aaa tca gtg tcc atc gac 211  
 Gly Lys Pro Ile Thr Glu Leu Gly Met Val Lys Ser Val Ser Ile Asp  
                   25                                  30                                  35

ggc tct gat gtc cag gtg gag gtc tac ctg acg atc gcg gct tgc ccg 259  
 Gly Ser Asp Val Gln Val Glu Val Tyr Leu Thr Ile Ala Ala Cys Pro  
                   40                                  45                                  50

atg aaa acc acc att gtc acc aac act gaa gca gct ctc aaa gac atc 307  
 Met Lys Thr Thr Ile Val Thr Asn Thr Glu Ala Ala Leu Lys Asp Ile  
                   55                                  60                                  65

gac ggg gtt ggc caa gtt cat gtc acc acc gat gtc atg agt gat gaa 355  
 Asp Gly Val Gly Gln Val His Val Thr Thr Asp Val Met Ser Asp Glu  
                   70                                  75                                  80                                  85

cag cgc cgt gcg ctc cgc gtc tcc ctg cgc ggt gaa act tct gag cca 403  
 Gln Arg Arg Ala Leu Arg Val Ser Leu Arg Gly Glu Thr Ser Glu Pro  
                                   90                                  95                                  100

gtg att cca ttc gct cag cct ggt tcc act acc cgc gtt tac gct gtt 451  
 Val Ile Pro Phe Ala Gln Pro Gly Ser Thr Thr Arg Val Tyr Ala Val  
                                   105                                  110                                  115

gct tcc ggc aaa ggt ggc gta gga aaa tcc tcc atg acg gtg aac ttg 499  
 Ala Ser Gly Lys Gly Gly Val Gly Lys Ser Ser Met Thr Val Asn Leu  
                                   120                                  125                                  130

gct gca gcc cta gcc aag cgc ggg ctg tct gtg gga att ttg gat gcc 547  
 Ala Ala Ala Leu Ala Lys Arg Gly Leu Ser Val Gly Ile Leu Asp Ala  
                                   135                                  140                                  145

gat att tac gga cac tca gtg ccc gga atg ctc ggc tcg gac caa cgc 595  
 Asp Ile Tyr Gly His Ser Val Pro Gly Met Leu Gly Ser Asp Gln Arg  
                                   150                                  155                                  160                                  165

cca cac cag gtc gat gac atg atc atg cct ccc cag gcg cac ggc gtg 643  
 Pro His Gln Val Asp Asp Met Ile Met Pro Pro Gln Ala His Gly Val  
                                   170                                  175                                  180

aag atg ata tcc att gct cac ttc acc gaa gga aat gct cct gtg gtg 691  
 Lys Met Ile Ser Ile Ala His Phe Thr Glu Gly Asn Ala Pro Val Val  
                                   185                                  190                                  195

tgg cgt gga cca atg ctg cac cgt gcc atc cag caa ttc ctc act gac 739  
 Trp Arg Gly Pro Met Leu His Arg Ala Ile Gln Gln Phe Leu Thr Asp  
                                   200                                  205                                  210

gtg ttc tgg ggc gac ctg gat att ttg ctg ctg gat ctt cct cca gga 787  
 Val Phe Trp Gly Asp Leu Asp Ile Leu Leu Leu Asp Leu Pro Pro Gly  
                                   215                                  220                                  225

act ggt gac atc gcc atc acc gtt gcc caa ttg atc ccg aat gct gag 835  
 Thr Gly Asp Ile Ala Ile Thr Val Ala Gln Leu Ile Pro Asn Ala Glu  
                                   230                                  235                                  240                                  245

ttg ctc att gtg acc act cct cag gct gcc gca gct gag gtt gcc gag 883  
 Leu Leu Ile Val Thr Thr Pro Gln Ala Ala Ala Ala Glu Val Ala Glu  
                                   250                                  255                                  260

cga gca gga acg atc tct gtg cag acc aac cag aag gtt gct ggc gtg 931  
 Arg Ala Gly Thr Ile Ser Val Gln Thr Asn Gln Lys Val Ala Gly Val  
 265 270 275

att gaa aac atg tct gcc atg gtg ctt cct gat ggc acc acc atg gat 979  
 Ile Glu Asn Met Ser Ala Met Val Leu Pro Asp Gly Thr Thr Met Asp  
 280 285 290

gtt ttc ggc acc ggc ggc ggt caa aag att gct gat cgt ctt acc gct 1027  
 Val Phe Gly Thr Gly Gly Gln Lys Ile Ala Asp Arg Leu Thr Ala  
 295 300 305

gtg aca ggt gaa gag gtc aag gtt atc gga tct gtt cca ttg gat ccg 1075  
 Val Thr Gly Glu Glu Val Lys Val Ile Gly Ser Val Pro Leu Asp Pro  
 310 315 320 325

aac ctg cgt atc ggt ggc gat gtg gga aat cct att gcg att tct gaa 1123  
 Asn Leu Arg Ile Gly Gly Asp Val Gly Asn Pro Ile Ala Ile Ser Glu  
 330 335 340

cca cac tcc cca acc gct gca gcg atc aat gag atc gct gaa cac cta 1171  
 Pro His Ser Pro Thr Ala Ala Ile Asn Glu Ile Ala Glu His Leu  
 345 350 355

gct cac cgc aag gta tcg ctg gtg ggt aaa acg ctt ggg ctt ggc gtt 1219  
 Ala His Arg Lys Val Ser Leu Val Gly Lys Thr Leu Gly Leu Gly Val  
 360 365 370

aaa taaaagctaa ataatatcgg tcc 1245  
 Lys

<210> 258  
 <211> 374  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 258  
 Met Thr Gln Val Thr Glu Ser Ala Val Arg Ser Ala Leu Ser Arg Val  
 1 5 10 15

Glu Asp Pro Glu Ile Gly Lys Pro Ile Thr Glu Leu Gly Met Val Lys  
 20 25 30

Ser Val Ser Ile Asp Gly Ser Asp Val Gln Val Glu Val Tyr Leu Thr  
 35 40 45

Ile Ala Ala Cys Pro Met Lys Thr Thr Ile Val Thr Asn Thr Glu Ala  
 50 55 60

Ala Leu Lys Asp Ile Asp Gly Val Gly Gln Val His Val Thr Thr Asp  
 65 70 75 80

Val Met Ser Asp Glu Gln Arg Arg Ala Leu Arg Val Ser Leu Arg Gly  
 85 90 95

Glu Thr Ser Glu Pro Val Ile Pro Phe Ala Gln Pro Gly Ser Thr Thr  
 100 105 110

Arg Val Tyr Ala Val Ala Ser Gly Lys Gly Gly Val Gly Lys Ser Ser



115                      120                      125

Met Thr Val Asn Leu Ala Ala Leu Ala Lys Arg Gly Leu Ser Val  
130                      135                      140

Gly Ile Leu Asp Ala Asp Ile Tyr Gly His Ser Val Pro Gly Met Leu  
145                      150                      155                      160

Gly Ser Asp Gln Arg Pro His Gln Val Asp Asp Met Ile Met Pro Pro  
165                      170                      175

Gln Ala His Gly Val Lys Met Ile Ser Ile Ala His Phe Thr Glu Gly  
180                      185                      190

Asn Ala Pro Val Val Trp Arg Gly Pro Met Leu His Arg Ala Ile Gln  
195                      200                      205

Gln Phe Leu Thr Asp Val Phe Trp Gly Asp Leu Asp Ile Leu Leu Leu  
210                      215                      220

Asp Leu Pro Pro Gly Thr Gly Asp Ile Ala Ile Thr Val Ala Gln Leu  
225                      230                      235                      240

Ile Pro Asn Ala Glu Leu Leu Ile Val Thr Thr Pro Gln Ala Ala Ala  
245                      250                      255

Ala Glu Val Ala Glu Arg Ala Gly Thr Ile Ser Val Gln Thr Asn Gln  
260                      265                      270

Lys Val Ala Gly Val Ile Glu Asn Met Ser Ala Met Val Leu Pro Asp  
275                      280                      285

Gly Thr Thr Met Asp Val Phe Gly Thr Gly Gly Gly Gln Lys Ile Ala  
290                      295                      300

Asp Arg Leu Thr Ala Val Thr Gly Glu Glu Val Lys Val Ile Gly Ser  
305                      310                      315                      320

Val Pro Leu Asp Pro Asn Leu Arg Ile Gly Gly Asp Val Gly Asn Pro  
325                      330                      335

Ile Ala Ile Ser Glu Pro His Ser Pro Thr Ala Ala Ala Ile Asn Glu  
340                      345                      350

Ile Ala Glu His Leu Ala His Arg Lys Val Ser Leu Val Gly Lys Thr  
355                      360                      365

Leu Gly Leu Gly Val Lys  
370

&lt;210&gt; 259

&lt;211&gt; 3010

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(3010)

&lt;223&gt; RXN02082

gctcgatcgc	gaaccaggt	catgtggaca	cagttattga	gcaatgggcc	gaqccgcgtg	60
acgttgaagg	ctttgtggag	cgctagacct	taaccccgtt	atg tat ttg aaa tcg		115
				Met Tyr Leu Lys Ser	5	
				1		
ttg acg ctc aag ggg	ttt aag tct ttc gcg tct gcg acg acc ctg aaa					163
Leu Thr Leu Lys Gly	Phe Lys Ser Phe Ala Ser Ala Thr Thr Leu Lys					
	10		15		20	
ttt gag cca ggc att	tgt gcc gtg gtg ggt ccg aat ggt tca ggc aaa					211
Phe Glu Pro Gln Ile	Cys Ala Val Val Gly Pro Asn Gly Ser Gly Lys					
	25		30		35	
tcc aat gtg gtt gat	gcg ctg gcc tgg gtg atg ggt gaa ggt tct gcg					259
Ser Asn Val Val Asp	Ala Leu Ala Trp Val Met Gly Glu Gly Ser Ala					
	40		45		50	
aag acc ttg cgt ggc	ggc aaa atg gaa gat gtc att ttt gct ggc gcg					307
Lys Thr Leu Arg Gly	Gly Lys Met Glu Asp Val Ile Phe Ala Gly Ala					
	55		60		65	
ggc gat cgt aaa ccg	ttg ggt cgc gca gaa gtc acg ctg acc att gat					355
Gly Asp Arg Lys Pro	Leu Gly Arg Ala Glu Val Thr Leu Thr Ile Asp					
	70		75		80	85
aac tct gat ggc gca	ctg ccc att gag tac acc gaa gtg tcg gtg acc					403
Asn Ser Asp Gly Ala	Leu Pro Ile Glu Tyr Thr Val Ser Val Thr					
	90		95		100	
aga cgg atg ttc cgt	gat ggt gca agt gaa tat gag atc aat ggg gcg					451
Arg Arg Met Phe Arg	Asp Gly Ala Ser Glu Tyr Glu Ile Asn Gly Ala					
	105		110		115	
aaa gct cga ttg atg	gat atc cag gag ctg ttg tcg gat acc ggt att					499
Lys Ala Arg Leu Met	Asp Ile Gln Glu Leu Leu Ser Asp Thr Gly Ile					
	120		125		130	
ggc cgt gaa atg cac	atc atg gtg ggg cag gga aag ctc gca gag att					547
Gly Arg Glu Met His	Ile Met Val Gly Gln Gly Lys Leu Ala Glu Ile					
	135		140		145	
ttg gag tcc cgc ccc	gaa gag cgc cga gcg tat atc gaa gaa gct gcg					595
Leu Glu Ser Arg Pro	Glu Glu Arg Arg Ala Tyr Ile Glu Glu Ala Ala					
	150		155		160	165
ggc gtg ctc aag cac	cgg cgc agg aaa gaa aag gcg cag cgc aaa ctt					643
Gly Val Leu Lys His	Arg Arg Arg Lys Glu Lys Ala Gln Arg Lys Leu					
	170		175		180	
cag ggc atg cag gtc	aat ctt gat cgt ttg cag gat ctg acc cat gag					691
Gln Gly Met Gln Val	Asn Leu Asp Arg Leu Gln Asp Leu Thr His Glu					
	185		190		195	
ttg gcc aag cag ctc	aag ccg ttg gct agg cag gcg gaa gca gcg cag					739
Leu Ala Lys Gln Leu	Lys Pro Leu Ala Arg Gln Ala Glu Ala Ala Gln					
	200		205		210	
cgt gcg gcg acg gtg	cag gct gat ttg cgt gat gcg cgt ttc cag att					787
Arg Ala Ala Thr Val	Gln Ala Asp Leu Arg Asp Ala Arg Phe Gln Ile					

215	220	225	
gct ggc ttt gag atc gtg aag ctc tcg gaa aag ctg gaa acc tct act			835
Ala Gly Phe Glu Ile Val Lys Leu Ser Glu Lys Leu Glu Thr Ser Thr			
230	235	240	245
gag cgc gag aaa atg att cgt gag cag gcg gaa gca gca caa gag cag			883
Glu Arg Glu Lys Met Ile Arg Glu Gln Ala Glu Ala Ala Gln Glu Gln			
250	255	260	
ctg gaa gaa gcc acc aca act cag atg gaa gtg gag atg gag ttg gcg			931
Leu Glu Glu Ala Thr Thr Thr Gln Met Glu Val Glu Met Glu Leu Ala			
265	270	275	
gag atc act cgc cag gct gaa gct gcg caa cag ttg tgg ttt gat ttg			979
Glu Ile Thr Pro Gln Ala Glu Ala Ala Gln Gln Leu Trp Phe Asp Leu			
280	285	290	
tct tcg ctg gct gag cgg gtg tcg gca acg atg cgt att gct gca gac			1027
Ser Ser Leu Ala Glu Arg Val Ser Ala Thr Met Arg Ile Ala Ala Asp			
295	300	305	
cgt gcg agt tca ggt gcc gcg gat gtg ccg tat gcg ggc cag gat cct			1075
Arg Ala Ser Ser Gly Ala Ala Asp Val Pro Tyr Ala Gly Gln Asp Pro			
310	315	320	325
gat gag ttg ctt ggt cgg gcc gaa act gct gac aaa gaa tta gaa gaa			1123
Asp Glu Leu Leu Gly Arg Ala Glu Thr Ala Asp Lys Glu Leu Glu Glu			
330	335	340	
ctc gag atg gcc gtg gaa atg acc acc gag cgt ttg acc tcc att caa			1171
Leu Glu Met Ala Val Glu Met Thr Thr Glu Arg Leu Thr Ser Ile Gln			
345	350	355	
gag gaa gcc gag gat aag gcc gcg cag gct cgt gag gct gag cgt gaa			1219
Glu Glu Ala Glu Asp Lys Ala Ala Gln Ala Arg Glu Ala Glu Arg Glu			
360	365	370	
cac ttg gcg cag gtc agg gcg att tct gat cgt cgt gaa ggt gtt gtg			1267
His Leu Ala Gln Val Arg Ala Ile Ser Asp Arg Arg Glu Gly Val Val			
375	380	385	
cgc ctg ctt gca tct gag gaa tct ttg gcg acc cag cac acg tca gca			1315
Arg Leu Leu Ala Ser Glu Glu Ser Leu Arg Thr Gln His Thr Ser Ala			
390	395	400	405
gag gag gaa gct gag cga ctc agt gag cag ctt gag gag ttc atc ggc			1363
Glu Glu Glu Ala Glu Arg Leu Ser Glu Gln Leu Glu Glu Phe Ile Gly			
410	415	420	
cgc att ttg gat gtg gaa cgt gaa cgt gcg ctc acc gat gag cgt aaa			1411
Arg Ile Leu Asp Val Glu Arg Glu Arg Arg Leu Thr Asp Glu Arg Lys			
425	430	435	
cag ggc gtt gac acg gat cgt gcg ccc ttg gaa gaa gcc ctc aaa cag			1459
Gln Gly Val Asp Thr Asp Arg Ala Pro Leu Glu Glu Ala Leu Lys Gln			
440	445	450	
gca aaa cat gaa gcc gaa gca gca gag act cgt ctt gag gag ctt cgt			1507
Ala Lys His Glu Ala Glu Ala Ala Glu Thr Arg Leu Glu Glu Leu Arg			
455	460	465	

act aag cgc agc gat ctg gaa aaa gaa gta tcc agg ttg cag tcg cgc 1555  
 Thr Lys Arg Ser Asp Leu Glu Lys Glu Val Ser Arg Leu Gln Ser Arg 485  
 470 475 480

att gag acg ctt aac caa aat agg cca cgt tcc gat gct gct gat gtg 1603  
 Ile Glu Thr Leu Asn Gln Asn Arg Pro Arg Ser Asp Ala Ala Asp Val 500  
 490 495 500

gtg gat tac ccg cag ctg gcc acg ttg att cga ccg caa cga aac gtc 1651  
 Val Asp Tyr Pro Gln Leu Ala Thr Leu Ile Arg Pro Gln Arg Asn Val 515  
 505 510 515

gat aag gct ctc gct gcc gcc ctg ggt gcg cat gcc gag gcg ctg gct 1699  
 Asp Lys Ala Leu Ala Ala Leu Gly Ala His Ala Glu Ala Leu Ala 530  
 520 525 530

ggc gag gct gcg gaa ggg ctc gtc gag aag ctt atc gac gcc ggc gtt 1747  
 Gly Glu Ala Ala Glu Gly Leu Val Glu Lys Leu Ile Asp Ala Gly Val 545  
 535 540 545

gca cgc acc atc atc gtt gat ggc acg cag gct ggc ggc gca tgg cgc 1795  
 Ala Arg Thr Ile Ile Val Asp Gly Thr Gln Ala Gly Gly Ala Trp Arg 565  
 550 555 560

ctg gac gcg aac att ccg gcc ggg gcg agc tgg ctg ctc gac cat gtt 1843  
 Leu Asp Ala Asn Ile Pro Ala Gly Ala Ser Trp Leu Leu Asp His Val 580  
 570 575 580

gat ctg gat ccg gcg att gcc gcc ccg gta aac ccg ctg ctt gcc gac 1891  
 Asp Leu Asp Pro Ala Ile Ala Gly Pro Val Asn Arg Leu Leu Ala Asp 595  
 585 590 595

gtt gtg ctt gtc gac gac ccc tcc ctc ggc cgc caa gca atc gag gat 1939  
 Val Val Leu Val Asp Asp Pro Ser Leu Gly Arg Gln Ala Ile Glu Asp 610  
 600 605 610

gat ccc cgt ctg cgt gcc gtt gac cgc aat ggt gtg ctc atc ggc gct 1987  
 Asp Pro Arg Leu Arg Ala Val Asp Arg Asn Gly Val Leu Ile Gly Ala 625  
 615 620 625

ggg tgg att cag gtc ggc acc gaa acc tog act gtg gaa atc aca gct 2035  
 Gly Trp Ile Gln Val Gly Thr Glu Thr Ser Thr Val Glu Ile Thr Ala 645  
 630 635 640 645

cat att gag gaa gca gaa gct caa ctt gct gcg gcc tct gcc gcc ttg 2083  
 His Ile Glu Glu Ala Glu Ala Gln Leu Ala Ala Ser Ala Ala Leu 660  
 650 655 660

gac gac att gcc ggc act ttt gat ggc gcc ctc cac gct gcc gac aac 2131  
 Asp Asp Ile Ala Gly Thr Phe Asp Gly Ala Leu His Ala Ala Asp Asn 675  
 665 670 675

act cgc gtc gag gtg gct gcc cgc acc gca gcc ctg cgc gaa ctc gac 2179  
 Thr Arg Val Glu Val Ala Ala Arg Thr Ala Ala Leu Arg Glu Leu Asp 690  
 680 685 690

atg acc agg gat tcc atc acc cgc gat ctc gcg cgc ttg gac aaa caa 2227  
 Met Thr Arg Asp Ser Ile Thr Arg Asp Leu Ala Arg Leu Asp Lys Gln 705  
 695 700 705

cat gag gcc gcc gaa tcc gag cgc gtc cgc cat gtt gga cgc ctg cat 2275  
His Glu Ala Ala Glu Ser Glu Arg Val Arg His Val Gly Arg Leu His  
710 715 720 725

gct gcg gaa aca cgc cgt gaa gag ctg cgc gaa cag tta gaa gac atc 2323  
Ala Ala Glu Thr Arg Arg Glu Glu Leu Arg Glu Gln Leu Glu Asp Ile  
730 735 740

gtc gat cga ctc tcc cgc gtg gaa gac gaa gaa gac gct gac gaa ccc 2371  
Val Asp Arg Leu Ser Arg Val Glu Asp Glu Glu Asp Ala Asp Glu Pro  
745 750 755

tca acc acc gcc cgc gac caa gca aat gcc gag ctg caa caa atc cgc 2419  
Ser Thr Thr Ala Arg Asp Gln Ala Asn Ala Glu Leu Gln Gln Ile Arg  
760 765 770

gcc atg gaa atg gaa gca cgc ctt gcc caa cgc acc gcc gaa gag cgc 2467  
Ala Met Glu Met Glu Ala Arg Leu Ala Gln Arg Thr Ala Glu Glu Arg  
775 780 785

gcc ggg cag cag cgg gcc aag gcc gat agt ctg cga cgc cag gcc gag 2515  
Ala Gly Gln Gln Arg Gly Lys Gly Asp Ser Leu Arg Arg Gln Ala Glu  
790 795 800 805

cat gag cgc caa gcc aaa atc cgg cat gaa caa gcc atg gaa gcc cgt 2563  
His Glu Arg Gln Ala Lys Ile Arg His Glu Gln Ala Met Glu Ala Arg  
810 815 820

cgc agg cgc acc caa ttg gct gca gcc gtg cat aat gcc gca cgc gat 2611  
Arg Arg Arg Thr Gln Leu Ala Ala Val His Asn Gly Ala Arg Asp  
825 830 835

gtg gcc gag cgt gtc tca agt gtc ctt gcc caa gca gcc atc gaa aga 2659  
Val Ala Glu Arg Val Ser Ser Val Leu Ala Gln Ala Ala Ile Glu Arg  
840 845 850

gat cag cac aac cgc gac aaa gcg ctg ctg acc tca cac tta gcg cgc 2707  
Asp Gln His Asn Arg Asp Lys Ala Leu Leu Thr Ser His Leu Ala Arg  
855 860 865

gcc aaa gat gct gtg agt gct gca cgc cag cac ctc aat cga ctc agc 2755  
Ala Lys Asp Ala Val Ser Ala Ala Arg Gln His Leu Asn Arg Leu Ser  
870 875 880 885

gac aac gcc cac tcc atg gaa ctt gcg cgc agc caa gct caa gtg cgc 2803  
Asp Asn Ala His Ser Met Glu Leu Ala Arg Ser Gln Ala Gln Val Arg  
890 895 900

atg gag gaa gcc gtt gcc aaa atc acc gag caa ctt gcc att cgg gtc 2851  
Met Glu Glu Ala Val Ala Lys Ile Thr Glu Gln Leu Gly Ile Pro Val  
905 910 915

gca gaa ttg ctg cgc gat tac acc cca gat gaa aac ttt gat gaa aag 2899  
Ala Glu Leu Leu Arg Asp Tyr Thr Pro Asp Glu Asn Phe Asp Glu Lys  
920 925 930

ttc caa cgg gca cgc ctc aaa caa gcc gaa aaa gac ctc gcc gca cta 2947  
Phe Gln Arg Ala Arg Leu Lys Gln Ala Glu Lys Asp Leu Ala Ala Leu  
935 940 945

ggc aaa gtc aac ccc ctg gcc ttg gaa gaa ttc aaa gcc ctt gga aga 2995

Gly Lys Val Asn Pro Leu Ala Leu Glu Glu Phe Lys Ala Leu Gly Arg  
 950 955 960 965

gcg cta cga gtt cct  
 Ala Leu Arg Val Pro  
 970

3010

&lt;210&gt; 260

&lt;211&gt; 970

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 260

Met Tyr Leu Lys Ser Leu Thr Leu Lys Gly Phe Lys Ser Phe Ala Ser  
 1 5 10 15

Ala Thr Thr Leu Lys Phe Glu Pro Gly Ile Cys Ala Val Val Gly Pro  
 20 25 30

Asn Gly Ser Gly Lys Ser Asn Val Val Asp Ala Leu Ala Trp Val Met  
 35 40 45

Gly Glu Gly Ser Ala Lys Thr Leu Arg Gly Gly Lys Met Glu Asp Val  
 50 55 60

Ile Phe Ala Gly Ala Gly Asp Arg Lys Pro Leu Gly Arg Ala Glu Val  
 65 70 75 80

Thr Leu Thr Ile Asp Asn Ser Asp Gly Ala Leu Pro Ile Glu Tyr Thr  
 85 90 95

Glu Val Ser Val Thr Arg Arg Met Phe Arg Asp Gly Ala Ser Glu Tyr  
 100 105 110

Glu Ile Asn Gly Ala Lys Ala Arg Leu Met Asp Ile Gln Glu Leu Leu  
 115 120 125

Ser Asp Thr Gly Ile Gly Arg Glu Met His Ile Met Val Gly Gln Gly  
 130 135 140

Lys Leu Ala Glu Ile Leu Glu Ser Arg Pro Glu Glu Arg Arg Ala Tyr  
 145 150 155 160

Ile Glu Glu Ala Ala Gly Val Leu Lys His Arg Arg Arg Lys Glu Lys  
 165 170 175

Ala Gln Arg Lys Leu Gln Gly Met Gln Val Asn Leu Asp Arg Leu Gln  
 180 185 190

Asp Leu Thr His Glu Leu Ala Lys Gln Leu Lys Pro Leu Ala Arg Gln  
 195 200 205

Ala Glu Ala Ala Gln Arg Ala Ala Thr Val Gln Ala Asp Leu Arg Asp  
 210 215 220

Ala Arg Phe Gln Ile Ala Gly Phe Glu Ile Val Lys Leu Ser Glu Lys  
 225 230 235 240

Leu Glu Thr Ser Thr Glu Arg Glu Lys Met Ile Arg Glu Gln Ala Glu  
 245 250 255

Ala Ala Gln Glu Gln Leu Glu Glu Ala Thr Thr Thr Gln Met Glu Val  
 260 265 270  
 Glu Met Glu Leu Ala Glu Ile Thr Pro Gln Ala Glu Ala Ala Gln Gln  
 275 280 285  
 Leu Trp Phe Asp Leu Ser Ser Leu Ala Glu Arg Val Ser Ala Thr Met  
 290 295 300  
 Arg Ile Ala Ala Asp Arg Ala Ser Ser Gly Ala Ala Asp Val Pro Tyr  
 305 310 315 320  
 Ala Gly Gln Asp Pro Asp Glu Leu Leu Gly Arg Ala Glu Thr Ala Asp  
 325 330 335  
 Lys Glu Leu Glu Glu Leu Glu Met Ala Val Glu Met Thr Thr Glu Arg  
 340 345 350  
 Leu Thr Ser Ile Gln Glu Glu Ala Glu Asp Lys Ala Ala Gln Ala Arg  
 355 360 365  
 Glu Ala Glu Arg Glu His Leu Ala Gln Val Arg Ala Ile Ser Asp Arg  
 370 375 380  
 Arg Glu Gly Val Val Arg Leu Leu Ala Ser Glu Glu Ser Leu Arg Thr  
 385 390 395 400  
 Gln His Thr Ser Ala Glu Glu Glu Ala Glu Arg Leu Ser Glu Gln Leu  
 405 410 415  
 Glu Glu Phe Ile Gly Arg Ile Leu Asp Val Glu Arg Glu Arg Arg Leu  
 420 425 430  
 Thr Asp Glu Arg Lys Gln Gly Val Asp Thr Asp Arg Ala Pro Leu Glu  
 435 440 445  
 Glu Ala Leu Lys Gln Ala Lys His Glu Ala Glu Ala Ala Glu Thr Arg  
 450 455 460  
 Leu Glu Glu Leu Arg Thr Lys Arg Ser Asp Leu Glu Lys Glu Val Ser  
 465 470 475 480  
 Arg Leu Gln Ser Arg Ile Glu Thr Leu Asn Gln Asn Arg Pro Arg Ser  
 485 490 495  
 Asp Ala Ala Asp Val Val Asp Tyr Pro Gln Leu Ala Thr Leu Ile Arg  
 500 505 510  
 Pro Gln Arg Asn Val Asp Lys Ala Leu Ala Ala Ala Leu Gly Ala His  
 515 520 525  
 Ala Glu Ala Leu Ala Gly Glu Ala Ala Glu Gly Leu Val Glu Lys Leu  
 530 535 540  
 Ile Asp Ala Gly Val Ala Arg Thr Ile Ile Val Asp Gly Thr Gln Ala  
 545 550 555 560  
 Gly Gly Ala Trp Arg Leu Asp Ala Asn Ile Pro Ala Gly Ala Ser Trp  
 565 570 575

Leu Leu Asp His Val Asp Leu Asp Pro Ala Ile Ala Gly Pro Val Asn  
 580 585 590  
 Arg Leu Leu Ala Asp Val Val Leu Val Asp Asp Pro Ser Leu Gly Arg  
 595 600 605  
 Gln Ala Ile Glu Asp Asp Pro Arg Leu Arg Ala Val Asp Arg Asn Gly  
 610 615 620  
 Val Leu Ile Gly Ala Gly Trp Ile Gln Val Gly Thr Glu Thr Ser Thr  
 625 630 635 640  
 Val Glu Ile Thr Ala His Ile Glu Glu Ala Glu Ala Gln Leu Ala Ala  
 645 650 655  
 Ala Ser Ala Ala Leu Asp Asp Ile Ala Gly Thr Phe Asp Gly Ala Leu  
 660 665 670  
 His Ala Ala Asp Asn Thr Arg Val Glu Val Ala Ala Arg Thr Ala Ala  
 675 680 685  
 Leu Arg Glu Leu Asp Met Thr Arg Asp Ser Ile Thr Arg Asp Leu Ala  
 690 695 700  
 Arg Leu Asp Lys Gln His Glu Ala Ala Glu Ser Glu Arg Val Arg His  
 705 710 715 720  
 Val Gly Arg Leu His Ala Ala Glu Thr Arg Arg Glu Glu Leu Arg Glu  
 725 730 735  
 Gln Leu Glu Asp Ile Val Asp Arg Leu Ser Arg Val Glu Asp Glu Glu  
 740 745 750  
 Asp Ala Asp Glu Pro Ser Thr Thr Ala Arg Asp Gln Ala Asn Ala Glu  
 755 760 765  
 Leu Gln Gln Ile Arg Ala Met Glu Met Glu Ala Arg Leu Ala Gln Arg  
 770 775 780  
 Thr Ala Glu Glu Arg Ala Gly Gln Gln Arg Gly Lys Gly Asp Ser Leu  
 785 790 795 800  
 Arg Arg Gln Ala Glu His Glu Arg Gln Ala Lys Ile Arg His Glu Gln  
 805 810 815  
 Ala Met Glu Ala Arg Arg Arg Arg Thr Gln Leu Ala Ala Val His  
 820 825 830  
 Asn Gly Ala Arg Asp Val Ala Glu Arg Val Ser Ser Val Leu Ala Gln  
 835 840 845  
 Ala Ala Ile Glu Arg Asp Gln His Asn Arg Asp Lys Ala Leu Leu Thr  
 850 855 860  
 Ser His Leu Ala Arg Ala Lys Asp Ala Val Ser Ala Ala Arg Gln His  
 865 870 875 880  
 Leu Asn Arg Leu Ser Asp Asn Ala His Ser Met Glu Leu Ala Arg Ser  
 885 890 895  
 Gln Ala Gln Val Arg Met Glu Glu Ala Val Ala Lys Ile Thr Glu Gln



900 905 910  
 Leu Gly Ile Pro Val Ala Glu Leu Leu Arg Asp Tyr Thr Pro Asp Glu  
 915 920 925  
 Asn Phe Asp Glu Lys Phe Gln Arg Ala Arg Leu Lys Gln Ala Glu Lys  
 930 935 940  
 Asp Leu Ala Ala Leu Gly Lys Val Asn Pro Leu Ala Leu Glu Glu Phe  
 945 950 955 960  
 Lys Ala Leu Gly Arg Ala Leu Arg Val Pro  
 965 970  
  
 <210> 261  
 <211> 570  
 <212> DNA  
 <213> Corynebacterium glutamicum  
  
 <220>  
 <221> CDS  
 <222> (101)..(547)  
 <223> RXA01495  
  
 <400> 261  
 taggaatagc agggtagata aacttatttaa aatttttcca attcagggta gaattccaaa 60  
 agaattattt cgactctgtg aagatgagga gtgggtccacc atg gct gac aac gcc 115  
 Met Ala Asp Asn Ala  
 1 5  
 cgc gcg gct cgt atg gca aag cgc att caa act atc gtg gcc agc gcc 163  
 Arg Ala Ala Arg Met Ala Lys Arg Ile Gln Thr Ile Val Ala Ser Ala  
 10 15 20  
 att gaa cgc gat atc aag gac cgc cga ctt gag ttc gtc aca att act 211  
 Ile Glu Arg Asp Ile Lys Asp Arg Arg Leu Glu Phe Val Thr Ile Thr  
 25 30 35  
 gat gtg acc atg acc ggt gac ctg cac gat gca aag gtg ttt tac acc 259  
 Asp Val Thr Met Thr Gly Asp Leu His Asp Ala Lys Val Phe Tyr Thr  
 40 45 50  
 gtt cgt gga gct tcc att gaa gaa gaa cca gat ctt gag gca gca gca 307  
 Val Arg Gly Ala Ser Ile Glu Glu Glu Pro Asp Leu Glu Ala Ala Ala  
 55 60 65  
 gag gct ctt cac cga gca cgc ggc cag ctg agg aag atc gtt ggc cag 355  
 Glu Ala Leu His Arg Ala Arg Gly Gln Leu Arg Lys Ile Val Gly Gln  
 70 75 80 85  
 cag ctg ggt gtt cgg ttt acc ccg acc ctg act tac agc atc gat acc 403  
 Gln Leu Gly Val Arg Phe Thr Pro Thr Leu Thr Tyr Ser Ile Asp Thr  
 90 95 100  
 gtc cca gag gca tcc gca cac atg gaa gct ttg ttg gat cgt gct cgc 451  
 Val Pro Glu Ala Ser Ala His Met Glu Ala Leu Leu Asp Arg Ala Arg  
 105 110 115  
 aag cgc gat gag gag ctg gct aaa ttg cgc gaa ggt gca gcg cct gca 499

Lys Arg Asp Glu Glu Leu Ala Lys Leu Arg Glu Gly Ala Ala Pro Ala  
 120 125 130

ggt gat gca gat cct tac aag act tca tcc aag tct gaa tct gag gaa 547  
 Gly Asp Ala Asp Pro Tyr Lys Thr Ser Ser Lys Ser Glu Ser Glu Glu  
 135 140 145

taacaccagt gacggataat agt

570

<210> 262

<211> 149

<212> PRT

<213> Corynebacterium glutamicum

<400> 262

Met Ala Asp Asn Ala Arg Ala Ala Arg Met Ala Lys Arg Ile Gln Thr  
 1 5 10 15

Ile Val Ala Ser Ala Ile Glu Arg Asp Ile Lys Asp Arg Arg Leu Glu  
 20 25 30

Phe Val Thr Ile Thr Asp Val Thr Met Thr Gly Asp Leu His Asp Ala  
 35 40 45

Lys Val Phe Tyr Thr Val Arg Gly Ala Ser Ile Glu Glu Glu Pro Asp  
 50 55 60

Leu Glu Ala Ala Ala Glu Ala Leu His Arg Ala Arg Gly Gln Leu Arg  
 65 70 75 80

Lys Ile Val Gly Gln Gln Leu Gly Val Arg Phe Thr Pro Thr Leu Thr  
 85 90 95

Tyr Ser Ile Asp Thr Val Pro Glu Ala Ser Ala His Met Glu Ala Leu  
 100 105 110

Leu Asp Arg Ala Arg Lys Arg Asp Glu Glu Leu Ala Lys Leu Arg Glu  
 115 120 125

Gly Ala Ala Pro Ala Gly Asp Ala Asp Pro Tyr Lys Thr Ser Ser Lys  
 130 135 140

Ser Glu Ser Glu Glu  
 145

<210> 263

<211> 678

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(655)

<223> RXA01893

<400> 263

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atcagaatcc acgctgtag aaaaacacag gaggtaataa atg att gat gaa att 115

Met Ile Asp Glu Ile  
1 5

ctg ttc gaa gcg gaa gag cgc atg acc gca acg gtc gag cac acc cgc 163  
Leu Phe Glu Ala Glu Glu Arg Met Thr Ala Thr Val Glu His Thr Arg  
10 15 20

gaa gac ttg acc acc att cgt acc ggt cgc gca aac ccg gct atg ttc 211  
Glu Asp Leu Thr Thr Ile Arg Thr Gly Arg Ala Asn Pro Ala Met Phe  
25 30 35

aac ggt gtc atg gct gaa tac tac ggc gtg cct act cct att act cag 259  
Asn Gly Val Met Ala Glu Tyr Tyr Gly Val Pro Thr Pro Ile Thr Gln  
40 45 50

atg tca ggc atc act gtt cca gag cct cgc atg ctg ctg atc aag cct 307  
Met Ser Gly Ile Thr Val Pro Glu Pro Arg Met Leu Leu Ile Lys Pro  
55 60 65

tat gag atg tct tcc atg cag gtc att gag aat gct atc cgt aac tct 355  
Tyr Glu Met Ser Ser Met Gln Val Ile Glu Asn Ala Ile Arg Asn Ser  
70 75 80 85

gac ctt ggt gtt aac ccc acc aac gat ggc cag gtg ctg cgt gtg acc 403  
Asp Leu Gly Val Asn Pro Thr Asn Asp Gly Gln Val Leu Arg Val Thr  
90 95 100

atc cca cag ctt act gaa gag cgt cgt aag gac atg gtc aag ctt gct 451  
Ile Pro Gln Leu Thr Glu Glu Arg Arg Lys Asp Met Val Lys Leu Ala  
105 110 115

aag ggt aag ggc gaa gac ggc aag att gcc att cgt aac atc cgc cgc 499  
Lys Gly Lys Gly Glu Asp Gly Lys Ile Ala Ile Arg Asn Ile Arg Arg  
120 125 130

aag ggc atg gac cag cta aag aag ctg caa aaa gat ggc gac gct ggc 547  
Lys Gly Met Asp Gln Leu Lys Lys Leu Gln Lys Asp Gly Asp Ala Gly  
135 140 145

gaa gat gaa gta cag gca gca gaa aaa gaa cta gat aaa gtc acc gct 595  
Glu Asp Glu Val Gln Ala Ala Glu Lys Glu Leu Asp Lys Val Thr Ala  
150 155 160 165

ggt ttt gtt gcg cag gtc gat gaa gtc gtt gct cgc aag gaa aag gaa 643  
Gly Phe Val Ala Gln Val Asp Glu Val Val Ala Arg Lys Glu Lys Glu  
170 175 180

ctg atg gag gtc tagaagacct ttatcgcaat ggc 678  
Leu Met Glu Val  
185

<210> 264  
<211> 185  
<212> PRT  
<213> *Corynebacterium glutamicum*

<400> 264  
Met Ile Asp Glu Ile Leu Phe Glu Ala Glu Glu Arg Met Thr Ala Thr  
1 5 10 15

Val Glu His Thr Arg Glu Asp Leu Thr Thr Ile Arg Thr Gly Arg Ala  
20 25 30

Asn Pro Ala Met Phe Asn Gly Val Met Ala Glu Tyr Tyr Gly Val Pro  
35 40 45

Thr Pro Ile Thr Gln Met Ser Gly Ile Thr Val Pro Glu Pro Arg Met  
50 55 60

Leu Leu Ile Lys Pro Tyr Glu Met Ser Ser Met Gln Val Ile Glu Asn  
65 70 75 80

Ala Ile Arg Asn Ser Asp Leu Gly Val Asn Pro Thr Asn Asp Gly Gln  
85 90 95

Val Leu Arg Val Thr Ile Pro Gln Leu Thr Glu Glu Arg Arg Lys Asp  
100 105 110

Met Val Lys Leu Ala Lys Gly Lys Gly Glu Asp Gly Lys Ile Ala Ile  
115 120 125

Arg Asn Ile Arg Arg Lys Gly Met Asp Gln Leu Lys Lys Leu Gln Lys  
130 135 140

Asp Gly Asp Ala Gly Glu Asp Glu Val Gln Ala Ala Glu Lys Glu Leu  
145 150 155 160

Asp Lys Val Thr Ala Gly Phe Val Ala Gln Val Asp Glu Val Val Ala  
165 170 175

Arg Lys Glu Lys Glu Leu Met Glu Val  
180 185

&lt;210&gt; 265

&lt;211&gt; 458

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(435)

&lt;223&gt; RXA01568

&lt;400&gt; 265

tgg gat aac atc acc tat ttg atg cgc gct gcg cga aaa ggc acc gtg 48  
Trp Asp Asn Ile Thr Tyr Leu Met Arg Ala Ala Arg Lys Gly Thr Val  
1 5 10 15

gtt ccc atg gtc atc gag ttg gat ggc cgg ttc gtg ggg cag ttg act 96  
Val Pro Met Val Ile Glu Leu Asp Gly Arg Phe Val Gly Gln Leu Thr  
20 25 30

atc ggc aac atc cag cac ggc ggc atc tcc gat gcc tgg att ggc tat 144  
Ile Gly Asn Ile Gln His Gly Gly Ile Ser Asp Ala Trp Ile Gly Tyr  
35 40 45

tgg gtt tcc agc gcg gtg acg ggg cgc ggt atc gct acg gcc gcc tgc 192  
Trp Val Ser Ser Ala Val Thr Gly Arg Gly Ile Ala Thr Ala Ala Cys  
50 55 60

gcg ctc ggc gtg gat cat gct ttt cga cgc ata ggt ctg cat cgc ctc 240  
 Ala Leu Gly Val Asp His Ala Phe Arg Arg Ile Gly Leu His Arg Leu  
 65 70 75 80

acc gcc acc tat cta ccc agc aac cca gca tcc ggg aag gtg ctc gga 288  
 Thr Ala Thr Tyr Leu Pro Ser Asn Pro Ala Ser Gly Lys Val Leu Gly  
 85 90 95

cac agc ggt ttc cgc cca gaa ggc tat ctc att aga aat ctg cat att 336  
 His Ser Gly Phe Arg Pro Glu Gly Tyr Leu Ile Arg Asn Leu His Ile  
 100 105 110

gat gga caa tgg atg gat cac cat ttt gtg gca ttg ctg gcg gat gag 384  
 Asp Gly Gln Trp Met Asp His His Phe Val Ala Leu Leu Ala Asp Glu  
 115 120 125

tat tca ata acc gcg gtg gaa cgt ctc act aga gag gga cga ttg cgc 432  
 Tyr Ser Ile Thr Ala Val Glu Arg Leu Thr Arg Glu Gly Arg Leu Arg  
 130 135 140

cga tgattactaa tgcgaagaaa ttt 458  
 Arg  
 145

<210> 266  
 <211> 145  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 266  
 Trp Asp Asn Ile Thr Tyr Leu Met Arg Ala Ala Arg Lys Gly Thr Val  
 1 5 10 15

Val Pro Met Val Ile Glu Leu Asp Gly Arg Phe Val Gly Gln Leu Thr  
 20 25 30

Ile Gly Asn Ile Gln His Gly Gly Ile Ser Asp Ala Trp Ile Gly Tyr  
 35 40 45

Trp Val Ser Ser Ala Val Thr Gly Arg Gly Ile Ala Thr Ala Ala Cys  
 50 55 60

Ala Leu Gly Val Asp His Ala Phe Arg Arg Ile Gly Leu His Arg Leu  
 65 70 75 80

Thr Ala Thr Tyr Leu Pro Ser Asn Pro Ala Ser Gly Lys Val Leu Gly  
 85 90 95

His Ser Gly Phe Arg Pro Glu Gly Tyr Leu Ile Arg Asn Leu His Ile  
 100 105 110

Asp Gly Gln Trp Met Asp His His Phe Val Ala Leu Leu Ala Asp Glu  
 115 120 125

Tyr Ser Ile Thr Ala Val Glu Arg Leu Thr Arg Glu Gly Arg Leu Arg  
 130 135 140

Arg  
 145

<210> 267  
 <211> 789  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(766)  
 <223> RXA01661

<400> 267  
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 gaaggccttc cttaccgcag cttgctggga ctttctgac ttg gac tca act aac 115  
 Leu Asp Ser Thr Asn  
 1 5  
 acc ccc ggc ccc acg gag tgg ggc gag tcc cgc gtg ggc aaa ggt cca 163  
 Thr Pro Gly Pro Thr Glu Trp Gly Glu Ser Arg Val Gly Lys Gly Pro  
 10 15 20  
 tgg gaa gag gaa aac ccc ggc gta cct cgg cct aca agc cgc ctt ttc 211  
 Trp Glu Glu Glu Asn Pro Gly Val Pro Arg Pro Thr Ser Pro Leu Phe  
 25 30 35  
 gac gtc acc ctc ctc aac gag ggc gat cgc cgc aac gtt gtt gac gcc 259  
 Asp Val Thr Leu Leu Asn Glu Gly Asp Arg Arg Asn Val Val Asp Ala  
 40 45 50  
 tat cgt tat tgg acc cgt gag gcg att gtt gaa gat atc gac acc cgc 307  
 Tyr Arg Tyr Trp Thr Arg Glu Ala Ile Val Glu Asp Ile Asp Thr Arg  
 55 60 65  
 cgc cac agc ctc cac gta gcg atc gaa aac ttt gaa aac gac gcc aac 355  
 Arg His Ser Leu His Val Ala Ile Glu Asn Phe Glu Asn Asp Ala Asn  
 70 75 80 85  
 atc ggc acc gtc gtg cgc acc gcc aac gcc ttt gcc gtg aac aca gtc 403  
 Ile Gly Thr Val Val Arg Thr Ala Asn Ala Phe Ala Val Asn Thr Val  
 90 95 100  
 cac att gtg ggc agg cgt cgg tgg aac cgc agg gga gcc atg gtg act 451  
 His Ile Val Gly Arg Arg Arg Trp Asn Arg Arg Gly Ala Met Val Thr  
 105 110 115  
 gac cgt tac cag cac ctc atg cac cac gaa gac gtt gat tcg ctg ctt 499  
 Asp Arg Tyr Gln His Leu Met His His Glu Asp Val Asp Ser Leu Leu  
 120 125 130  
 gcg tgg gca atc gcg gag cgg ctt acc atc gtc gcg atc gat aac acc 547  
 Ala Trp Ala Ile Ala Glu Arg Leu Thr Ile Val Ala Ile Asp Asn Thr  
 135 140 145  
 cca ggt tcc gtg cct ttg gaa acc gct gag ttg ccg aag aac tgc ctg 595  
 Pro Gly Ser Val Pro Leu Glu Thr Ala Glu Leu Pro Lys Asn Cys Leu  
 150 155 160 165  
 ttg ctg ttt ggt cag gaa ggc cca ggt gtc acc gaa gct gcg cgt gca 643  
 Leu Leu Phe Gly Gln Glu Gly Pro Gly Val Thr Glu Ala Ala Arg Ala  
 170 175 180

ggt gcg tta atg acc tgt tgc att gcc caa ttt ggt tcc act cga tcc 691  
 Gly Ala Leu Met Thr Cys Ser Ile Ala Gln Phe Gly Ser Thr Arg Ser  
                   185                                  190                                  195

atc aac gcg ggt gta gct gct ggt att gca atg cat gca tgg att cgt 739  
 Ile Asn Ala Gly Val Ala Ala Gly Ile Ala Met His Ala Trp Ile Arg  
                   200                                  205                                  210

caa cat gcc gac tta tgc caa gcc tgg taattttata ccctagatcg 786  
 Gln His Ala Asp Leu Ser Gln Ala Trp  
                   215                                  220

tta 789

<210> 268

<211> 222

<212> PRT

<213> Corynebacterium glutamicum

<400> 268

Leu Asp Ser Thr Asn Thr Pro Gly Pro Thr Glu Trp Gly Glu Ser Arg  
                   1                                  5                                  10                                  15

Val Gly Lys Gly Pro Trp Glu Glu Glu Asn Pro Gly Val Pro Arg Pro  
                   20                                  25                                  30

Thr Ser Pro Leu Phe Asp Val Thr Leu Leu Asn Glu Gly Asp Arg Arg  
                   35                                  40                                  45

Asn Val Val Asp Ala Tyr Arg Tyr Trp Thr Arg Glu Ala Ile Val Glu  
                   50                                  55                                  60

Asp Ile Asp Thr Arg Arg His Ser Leu His Val Ala Ile Glu Asn Phe  
                   65                  70                                  75                                  80

Glu Asn Asp Ala Asn Ile Gly Thr Val Val Arg Thr Ala Asn Ala Phe  
                   85                                  90                                  95

Ala Val Asn Thr Val His Ile Val Gly Arg Arg Arg Trp Asn Arg Arg  
                   100                                  105                                  110

Gly Ala Met Val Thr Asp Arg Tyr Gln His Leu Met His His Glu Asp  
                   115                                  120                                  125

Val Asp Ser Leu Leu Ala Trp Ala Ile Ala Glu Arg Leu Thr Ile Val  
                   130                                  135                                  140

Ala Ile Asp Asn Thr Pro Gly Ser Val Pro Leu Glu Thr Ala Glu Leu  
                   145                                  150                                  155                                  160

Pro Lys Asn Cys Leu Leu Leu Phe Gly Gln Glu Gly Pro Gly Val Thr  
                   165                                  170                                  175

Glu Ala Ala Arg Ala Gly Ala Leu Met Thr Cys Ser Ile Ala Gln Phe  
                   180                                  185                                  190

Gly Ser Thr Arg Ser Ile Asn Ala Gly Val Ala Ala Gly Ile Ala Met  
                   195                                  200                                  205

gct ggt gaa tca gta gat cca ctt ggc gca aaa gct gtg cgc tcc tca 595  
Ala Gly Glu Ser Val Asp Pro Leu Gly Ala Lys Ala Val Arg Ser Ser  
150 155 160 165

[illegible]



gcg gga tcg ctg ttt cac att cca gtg gca cgc aac aac aac atc gca 643  
Ala Gly Ser Leu Phe His Ile Pro Val Ala Arg Asn Asn Asn Ile Ala  
170 175 180

gat gtc ttg ggg cag ctt cgt tcc aag ggt ctg cag atc ctt gcg acc 691  
Asp Val Leu Gly Gln Leu Arg Ser Lys Gly Leu Gln Ile Leu Ala Thr  
185 190 195

tca gcc gat ggg gaa gta gac ctc gat gac gcc gat gag ctg cta gcc 739  
Ser Ala Asp Gly Glu Val Asp Leu Asp Asp Ala Asp Glu Leu Leu Ala  
200 205 210

aag cca acc gca tgg ctt ttt ggt aat gaa gct cac gga ctt gat gag 787  
Lys Pro Thr Ala Trp Leu Phe Gly Asn Glu Ala His Gly Leu Asp Glu  
215 220 225

agc ctg ctt gct cag gct gat cac cgc gtg cgt att ccg atc cgc ggc 835  
Ser Leu Leu Ala Gln Ala Asp His Arg Val Arg Ile Pro Ile Arg Gly  
230 235 240 245

cgc gca gaa tca ctc aat ttg gcc aca gca cgc tca att tgt ctg tac 883  
Arg Ala Glu Ser Leu Asn Leu Ala Thr Ala Ala Ser Ile Cys Leu Tyr  
250 255 260

gaa tcc tcc aag gca cta ttc gcc ggt gag taaaccccaa ttcattgccca 933  
Glu Ser Ser Lys Ala Leu Phe Ala Gly Glu  
265 270

gcg 936

<210> 270  
<211> 271  
<212> PRT  
<213> Corynebacterium glutamicum

<400> 270  
Met Ala Leu Asp Phe Asn Glu Ala Phe Thr Glu Arg Thr Pro Arg Ile  
1 5 10 15

Val Asn Ala Ala Lys Leu His Arg Ala Ala Gln Arg Lys Lys Asp Lys  
20 25 30

Arg Phe Leu Val Glu Gly Glu Asn Ser Val Glu Ala Ala Val Ala Thr  
35 40 45

Gly Ala Ala Thr Asp Leu Phe Val Thr Glu Ser Ala Ala Glu Arg Phe  
50 55 60

Glu Glu Ile Val Arg Thr Ala Gly Tyr Met Asn Val Tyr Thr His Ala  
65 70 75 80

Ile Thr Asp Lys Ala Ala Lys His Leu Ser Asp Thr Val Thr Thr Thr  
85 90 95

Gly Ile Phe Ala Leu Cys Asp Asp Val Leu Trp Ser Val Gly Lys Ala  
100 105 110

Ile Thr Gly Gln Pro Arg Leu Val Ser Val Pro Val Glu Thr Arg Glu  
115 120 125

Pro Gly Asn Ala Gly Thr Leu Ile Arg Val Ser Asp Ala Val Gly Ala  
130 135 140

Asp Ala Val Val Phe Ala Gly Glu Ser Val Asp Pro Leu Gly Ala Lys  
145 150 155 160

Ala Val Arg Ser Ser Ala Gly Ser Leu Phe His Ile Pro Val Ala Arg  
165 170 175

Asn Asn Asn Ile Ala Asp Val Leu Gly Gln Leu Arg Ser Lys Gly Leu  
180 185 190

Gln Ile Leu Ala Thr Ser Ala Asp Gly Glu Val Asp Leu Asp Asp Ala  
195 200 205

Asp Glu Leu Leu Ala Lys Pro Thr Ala Trp Leu Phe Gly Asn Glu Ala  
210 215 220

His Gly Leu Asp Glu Ser Leu Leu Ala Gln Ala Asp His Arg Val Arg  
225 230 235 240

Ile Pro Ile Arg Gly Arg Ala Glu Ser Leu Asn Leu Ala Thr Ala Ala  
245 250 255

Ser Ile Cys Leu Tyr Glu Ser Ser Lys Ala Leu Phe Ala Gly Glu  
260 265 270

<210> 271

<211> 1062

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1039)

<223> RXA00313

<400> 271

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ttgcagtaat tacagacact ttttaaggaga taatttaaac atg gca gga aat gac 115  
Met Ala Gly Asn Asp  
1 5

agt cgt cga ggc ggc tta cgc aag acc aat aaa aaa ggt gca acc aag 163  
Ser Arg Arg Gly Gly Leu Arg Lys Thr Asn Lys Lys Gly Ala Thr Lys  
10 15 20

ggc agt ggc gga cag gtt cgt cgc ggt ctg aaa ggt aag ggg cct acc 211  
Gly Ser Gly Gly Gln Val Arg Arg Gly Leu Lys Gly Lys Gly Pro Thr  
25 30 35

cct aaa gct gag gat cgc acc tat cac gca gct cac aag cgc aag gtg 259  
Pro Lys Ala Glu Asp Arg Thr Tyr His Ala Ala His Lys Arg Lys Val  
40 45 50

gag cgt gat cgt cgt gat cgt gga cgc cac cag cgt gaa atg cca gag 307  
Glu Arg Asp Arg Arg Asp Arg Gly Arg His Gln Arg Glu Met Pro Glu  
55 60 65

ttg gtt gtg ggc cgt aac cca gtg ctg gaa tgt ctg cat gca cgc gtt 355  
 Leu Val Val Gly Arg Asn Pro Val Leu Glu Cys Leu His Ala Arg Val  
 70 75 80 85

cca gcg act gct ttg tat gtt gca gag ggt gcg gcg aac gat gag cgt 403  
 Pro Ala Thr Ala Leu Tyr Val Ala Glu Gly Ala Ala Asn Asp Glu Arg  
 90 95 100

ctg agc gag gca gtg cac act gcg gct ggc cga aat ctt cca gtg ctg 451  
 Leu Ser Glu Ala Val His Thr Ala Ala Gly Arg Asn Leu Pro Val Leu  
 105 110 115

gag gtt aac aag ctg gag ctg gat cgt atg acc ggc aac ggc atg cac 499  
 Glu Val Asn Lys Leu Glu Leu Asp Arg Met Thr Gly Asn Gly Met His  
 120 125 130

cag ggc atc ggc ctg gcg atc cct cct tac gag tac gca gat gtt cat 547  
 Gln Gly Ile Gly Leu Ala Ile Pro Pro Tyr Glu Tyr Ala Asp Val His  
 135 140 145

gat ctg atc gcc aat gct gcg gct tct aag aag cca ggc atg ttc gtg 595  
 Asp Leu Ile Ala Asn Ala Ala Ala Ser Lys Lys Pro Gly Met Phe Val  
 150 155 160 165

att ctg gat aac atc acc gac cca cgt aac ttg ggt gct gtg att cgt 643  
 Ile Leu Asp Asn Ile Thr Asp Pro Arg Asn Leu Gly Ala Val Ile Arg  
 170 175 180

tcc gtc ggt gct ttc ggc ggc aac ggt gtc atc att ccg gag cgt cgt 691  
 Ser Val Gly Ala Phe Gly Gly Asn Glu Val Ile Pro Glu Arg Arg  
 185 190 195

tca gca tct gtg acc gct gtt gca tgg cgt act tct gct ggt acc gca 739  
 Ser Ala Ser Val Thr Ala Val Ala Trp Arg Thr Ser Ala Gly Thr Ala  
 200 205 210

gcg cgt gtg cca gtg gcg aag gaa acc aac atg act cgt gtc gtg aag 787  
 Ala Arg Val Pro Val Ala Lys Glu Thr Asn Met Thr Arg Val Val Lys  
 215 220 225

gaa ttc cag caa aac ggt tac cag gtc gtc ggc ctt gac gct ggc ggc 835  
 Glu Phe Gln Gln Asn Gly Tyr Gln Val Val Gly Leu Asp Ala Gly Gly  
 230 235 240 245

gac cac act ttg gac acc tac gac ggc acc gac aac gtt gtc atc gtc 883  
 Asp His Thr Leu Asp Thr Tyr Asp Gly Thr Asp Asn Val Val Ile Val  
 250 255 260

gtc ggt tct gag ggc aag gga att tcc cgt ctc gtt cgc gaa aac tgc 931  
 Val Gly Ser Glu Gly Lys Gly Ile Ser Arg Leu Val Arg Glu Asn Cys  
 265 270 275

gac acc atc atg tcc ata ccc acc gag ggc tgg gtt gaa tgc ctg aac 979  
 Asp Thr Ile Met Ser Ile Pro Thr Glu Gly Trp Val Glu Ser Leu Asn  
 280 285 290

gct tgc gtt gct gcc ggc gtc gtg ctg tgc gag ttc tgc cgc cag cgt 1027  
 Ala Ser Val Ala Ala Gly Val Val Leu Ser Glu Phe Ser Arg Gln Arg  
 295 300 305

cgc att aag ggt taagccggag gttggcgtcg aaa 1062

Arg Ile Lys Gly  
310

<210> 272  
<211> 313  
<212> PRT  
<213> *Corynebacterium glutamicum*

<400> 272  
Met Ala Gly Asn Asp Ser Arg Arg Gly Gly Leu Arg Lys Thr Asn Lys  
1 5 10 15  
Lys Gly Ala Thr Lys Gly Ser Gly Gly Gln Val Arg Arg Gly Leu Lys  
20 25 30  
Gly Lys Gly Pro Thr Pro Lys Ala Glu Asp Arg Thr Tyr His Ala Ala  
35 40 45  
His Lys Arg Lys Val Glu Arg Asp Arg Arg Asp Arg Gly Arg His Gln  
50 55 60  
Arg Glu Met Pro Glu Leu Val Val Gly Arg Asn Pro Val Leu Glu Cys  
65 70 75 80  
Leu His Ala Arg Val Pro Ala Thr Ala Leu Tyr Val Ala Glu Gly Ala  
85 90 95  
Ala Asn Asp Glu Arg Leu Ser Glu Ala Val His Thr Ala Ala Gly Arg  
100 105 110  
Asn Leu Pro Val Leu Glu Val Asn Lys Leu Glu Leu Asp Arg Met Thr  
115 120 125  
Gly Asn Gly Met His Gln Gly Ile Gly Leu Ala Ile Pro Pro Tyr Glu  
130 135 140  
Tyr Ala Asp Val His Asp Leu Ile Ala Asn Ala Ala Ser Lys Lys  
145 150 155 160  
Pro Gly Met Phe Val Ile Leu Asp Asn Ile Thr Asp Pro Arg Asn Leu  
165 170 175  
Gly Ala Val Ile Arg Ser Val Gly Ala Phe Gly Gly Asn Gly Val Ile  
180 185 190  
Ile Pro Glu Arg Arg Ser Ala Ser Val Thr Ala Val Ala Trp Arg Thr  
195 200 205  
Ser Ala Gly Thr Ala Ala Arg Val Pro Val Ala Lys Glu Thr Asn Met  
210 215 220  
Thr Arg Val Val Lys Glu Phe Gln Gln Asn Gly Tyr Gln Val Val Gly  
225 230 235 240  
Leu Asp Ala Gly Gly Asp His Thr Leu Asp Thr Tyr Asp Gly Thr Asp  
245 250 255  
Asn Val Val Ile Val Val Gly Ser Glu Gly Lys Gly Ile Ser Arg Leu  
260 265 270

Val Arg Glu Asn Cys Asp Thr Ile Met Ser Ile Pro Thr Glu Gly Trp  
 275 280 285

Val Glu Ser Leu Asn Ala Ser Val Ala Ala Gly Val Val Leu Ser Glu  
 290 295 300

Phe Ser Arg Gln Arg Arg Ile Lys Gly  
 305 310

<210> 273

<211> 594

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(571)

<223> RXN00460

<400> 273

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 Met Pro Glu His Pro  
 1 5

ctt cac gtt atc ttc gac aat cct gtc atc cct ccc aac acc gga aac 163  
 Leu His Val Ile Phe Asp Asn Pro Val Ile Pro Pro Asn Thr Glu Asn  
 10 15 20

gcc atc cga atg tgt gca gga aca ggc gct cac ctg cac ctt gtt gaa 211  
 Ala Ile Arg Met Cys Ala Gly Thr Gly Ala His Leu His Leu Val Glu  
 25 30 35

cct tta ggc ttt gag ctg aca gaa aag cac ctt cgc cga gca ggc ctt 259  
 Pro Leu Gly Phe Glu Leu Thr Glu Lys His Leu Arg Arg Ala Gly Leu  
 40 45 50

gac tac cac gac tta gcc gat gtc aca gtg cat gca acc ttc gat gaa 307  
 Asp Tyr His Asp Leu Ala Asp Val Thr Val His Ala Thr Phe Asp Glu  
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gcc atg gct gca gtc cct ggt cgc gta ttt gcc ttc acc aca acg gcc 355  
 Ala Met Ala Ala Val Pro Gly Arg Val Phe Ala Phe Thr Thr Thr Ala  
 70 75 80 85

aat acc cgc ttc acc gat atc get ttt gaa cct ggc gat gca ctc ctt 403  
 Asn Thr Arg Phe Thr Asp Ile Ala Phe Glu Pro Gly Asp Ala Leu Leu  
 90 95 100

ttt gga act gaa cca aca gga ctc cct caa gaa cat gtt gag cat tcc 451  
 Phe Gly Thr Glu Pro Thr Gly Leu Pro Gln Glu His Val Glu His Ser  
 105 110 115

cga atc acc agt gag ctt cgg atc ccc atg ctt ccc ggt agg cgt tcc 499  
 Arg Ile Thr Ser Glu Leu Arg Ile Pro Met Leu Pro Gly Arg Arg Ser  
 120 125 130

atg aac ctt tca aat tcc gcg gcg gta gcg acc tat gaa gca tgg cgt 547  
 Met Asn Leu Ser Asn Ser Ala Ala Val Ala Thr Tyr Glu Ala Trp Arg

135

140

145

caa ctc gga ttt gtg ggt ggg gtt tagttttttg ctgggcttct ggg  
 Gln Leu Gly Phe Val Gly Gly Val  
 150 155

594

&lt;210&gt; 274

&lt;211&gt; 157

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 274

Met Pro Glu His Pro Leu His Val Ile Phe Asp Asn Pro Val Ile Pro  
 1 5 10 15

Pro Asn Thr Gly Asn Ala Ile Arg Met Cys Ala Gly Thr Gly Ala His  
 20 25 30

Leu His Leu Val Glu Pro Leu Gly Phe Glu Leu Thr Glu Lys His Leu  
 35 40 45

Arg Arg Ala Gly Leu Asp Tyr His Asp Leu Ala Asp Val Thr Val His  
 50 55 60

Ala Thr Phe Asp Glu Ala Met Ala Ala Val Pro Gly Arg Val Phe Ala  
 65 70 75 80

Phe Thr Thr Thr Ala Asn Thr Arg Phe Thr Asp Ile Ala Phe Glu Pro  
 85 90 95

Gly Asp Ala Leu Leu Phe Gly Thr Glu Pro Thr Gly Leu Pro Gln Glu  
 100 105 110

His Val Glu His Ser Arg Ile Thr Ser Glu Leu Arg Ile Pro Met Leu  
 115 120 125

Pro Gly Arg Arg Ser Met Asn Leu Ser Asn Ser Ala Ala Val Ala Thr  
 130 135 140

Tyr Glu Ala Trp Arg Gln Leu Gly Phe Val Gly Gly Val  
 145 150 155

&lt;210&gt; 275

&lt;211&gt; 478

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(478)

&lt;223&gt; FRXA00460

&lt;400&gt; 275

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ctattattcc acccttttcc aaggccttac aatcaaacac atg ccg gaa cac cca 115  
 Met Pro Glu His Pro  
 1 5

ctt cac gtt atc ttc gac aat cct gtc atc cct ccc aac acc gga aac 163  
 Leu His Val Ile Phe Asp Asn Pro Val Ile Pro Pro Asn Thr Gly Asn  
 10 15 20

gcc atc cga atg tgt gca gga aca ggc gct cac ctg cac ctt gtt gaa 211  
 Ala Ile Arg Met Cys Ala Gly Thr Gly Ala His Leu His Leu Val Glu  
 25 30 35

cct tta ggc ttt gag ctg aca gaa aag cac ctt cgc cga gca ggc ctt 259  
 Pro Leu Gly Phe Glu Leu Thr Glu Lys His Leu Arg Arg Ala Gly Leu  
 40 45 50

gac tac cac gac tta gcc gat gtc aca gtg cat gca acc ttc gat gaa 307  
 Asp Tyr His Asp Leu Ala Asp Val Thr Val His Ala Thr Phe Asp Glu  
 55 60 65

gcc atg gct gca gtc cct ggt cgc gta ttt gcc ttc acc aca acg gcc 355  
 Ala Met Ala Ala Val Pro Gly Arg Val Phe Ala Phe Thr Thr Thr Ala  
 70 75 80 85

aat acc cgc ttc acc gat atc gct ttt gaa cct ggc gat gca ctc ctt 403  
 Asn Thr Arg Phe Thr Asp Ile Ala Phe Glu Pro Gly Asp Ala Leu Leu  
 90 95 100

ttt gga act gaa cca aca gga ctc cct caa gaa cat gtt gag cat tcc 451  
 Phe Gly Thr Glu Pro Thr Gly Leu Pro Gln Glu His Val Glu His Ser  
 105 110 115

cga atc acc agt gag ctt cgg atc cta 478  
 Arg Ile Thr Ser Glu Leu Arg Ile Leu  
 120 125

<210> 276  
 <211> 126  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 276  
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Pro Asn Thr Gly Asn Ala Ile Arg Met Cys Ala Gly Thr Gly Ala His  
 20 25 30

Leu His Leu Val Glu Pro Leu Gly Phe Glu Leu Thr Glu Lys His Leu  
 35 40 45

Arg Arg Ala Gly Leu Asp Tyr His Asp Leu Ala Asp Val Thr Val His  
 50 55 60

Ala Thr Phe Asp Glu Ala Met Ala Ala Val Pro Gly Arg Val Phe Ala  
 65 70 75 80

Phe Thr Thr Thr Ala Asn Thr Arg Phe Thr Asp Ile Ala Phe Glu Pro  
 85 90 95

Gly Asp Ala Leu Leu Phe Gly Thr Glu Pro Thr Gly Leu Pro Gln Glu  
 100 105 110

His Val Glu His Ser Arg Ile Thr Ser Glu Leu Arg Ile Leu





Val Arg Val Ser Met Gly His Val Leu Arg Leu Pro Phe Ala His Leu  
 170 175 180

gaa ggc acc tac acc acg tgg cag cgc agc tta gag cag ctc aaa gaa 691  
 Glu Gly Thr Tyr Thr Thr Trp Gln Arg Ser Leu Glu Gln Lys Glu  
 185 190 195

gcc gga ttc cac ctc gtt tca ctc acc cca gat cca gag gcg gaa cac 739  
 Ala Gly Phe His Leu Val Ser Leu Thr Pro Asp Pro Glu Ala Glu His  
 200 205 210

ctc gaa gat gcg ctc gca ggc aaa gac aaa gtg gct cta ctc gtg ggc 787  
 Leu Glu Asp Ala Leu Ala Gly Lys Asp Lys Val Ala Leu Leu Val Gly  
 215 220 225

gct gaa ggc cca ggc ctg acc gag cat gcg atg cgc gcc acc gat gtc 835  
 Ala Glu Gly Pro Gly Leu Thr Glu His Ala Met Arg Ala Thr Asp Val  
 230 235 240 245

cgc gcc cgc atc ccg atg gcg ccg ggt acc gat agc ttg aac ctg gct 883  
 Arg Ala Arg Ile Pro Met Ala Pro Gly Thr Asp Ser Leu Asn Leu Ala  
 250 255 260

acc tcg gcg gcg att gcg ttt tat gaa cgg gat cgc tca cag cgt 928  
 Thr Ser Ala Ala Ile Ala Phe Tyr Glu Arg Asp Arg Ser Gln Arg  
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taagtaacag cgctaagtag tag 951

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 <212> PRT  
 <213> Corynebacterium glutamicum

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 35 40 45

Leu Glu Ser Arg Tyr Pro Val Arg Ala Ile Val Gly Phe Lys Asn Lys  
 50 55 60

Leu Asp Ser Phe Leu Asp Ser Ile Asp Ala Ser Leu Val Glu Gly Ile  
 65 70 75 80

Pro Val Tyr Glu Val Ser Arg Glu Leu Leu Ala Glu Val Ala Gly Phe  
 85 90 95

Asp Met His Arg Gly Leu Leu Ala Thr Ala Asp Arg Thr Glu Glu Ala  
 100 105 110

Ser Val Ala Gln Val Leu Glu Asn Ala Arg Thr Val Val Val Leu Glu  
 115 120 125

Gly Val Gly Asp His Glu Asn Ile Gly Ser Met Phe Arg Asn Ala Ala

130 135 140

Gly Met Gly Val Asp Ala Ile Leu Phe Gly Asn Gly Cys Ala Asp Pro  
145 150 155 160

Leu Tyr Arg Arg Val Val Arg Val Ser Met Gly His Val Leu Arg Leu  
165 170 175

Pro Phe Ala His Leu Glu Gly Thr Tyr Thr Thr Trp Gln Arg Ser Leu  
180 185 190

Glu Gln Leu Lys Glu Ala Gly Phe His Leu Val Ser Leu Thr Pro Asp  
195 200 205

Pro Glu Ala Glu His Leu Glu Asp Ala Leu Ala Gly Lys Asp Lys Val  
210 215 220

Ala Leu Leu Val Gly Ala Glu Gly Pro Gly Leu Thr Glu His Ala Met  
225 230 235 240

Arg Ala Thr Asp Val Arg Ala Arg Ile Pro Met Ala Pro Gly Thr Asp  
245 250 255

Ser Leu Asn Leu Ala Thr Ser Ala Ala Ile Ala Phe Tyr Glu Arg Asp  
260 265 270

Arg Ser Gln Arg  
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<210> 279  
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<223> RXA02522

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Met Trp Ala Arg Asp  
1 5

ata aac ttt cta tac atg agt aca gag cag gaa ctg caa atc gga aaa 163  
Ile Asn Phe Leu Tyr Met Ser Thr Glu Gln Glu Leu Gln Ile Gly Lys  
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gtt gta aaa tcc cac ggc att cgg ggt gaa gtc gtg gta gaa ttg agc 211  
Val Val Lys Ser His Gly Ile Arg Gly Glu Val Val Val Glu Leu Ser  
25 30 35

acc gat gat cca gac att cgc ttc gcc att ggg gaa gtt ctc aac ggc 259  
Thr Asp Asp Pro Asp Ile Arg Phe Ala Ile Gly Glu Val Leu Asn Gly  
40 45 50

aag cag gca ggc aag gag cat tca ctg acc atc gat gca gcg cgc atg 307  
Lys Gln Ala Gly Lys Glu His Ser Leu Thr Ile Asp Ala Ala Arg Met

55 60 65

cac caa ggt cga ctc ttg gtg aag ttc gca gag gtc cca gat cgt acc 355  
 His Gln Gly Arg Leu Leu Val Lys Phe Ala Glu Val Pro Asp Arg Thr  
 70 75 80 85

gct gct gat tct ttg cgt gga act cga ttc ttt gcg gca cct ctt gag 403  
 Ala Ala Asp Ser Leu Arg Gly Thr Arg Phe Phe Ala Ala Pro Leu Glu  
 90 95 100

gat gaa gac gat gag gat ggc ttc tac gac cat gag ttg gaa ggt ctg 451  
 Asp Glu Asp Asp Glu Asp Gly Phe Tyr Asp His Glu Leu Glu Gly Leu  
 105 110 115

cgc gtc att cac gag ggc gag gat atc ggt gaa gtc acc ggc gtg atg 499  
 Arg Val Ile His Glu Gly Glu Asp Ile Gly Glu Val Thr Gly Val Met  
 120 125 130

cat ggc cca gcc ggt gag atc ctg gaa gtc cgc ctg acc tca ggc aag 547  
 His Gly Pro Ala Gly Glu Ile Leu Glu Val Arg Leu Thr Ser Gly Lys  
 135 140 145

gaa aca ctg att cct ttt gtg cac gcc att gtt cct gag gtg gat ctg 595  
 Glu Thr Leu Ile Pro Phe Val His Ala Ile Val Pro Glu Val Asp Leu  
 150 155 160 165

gaa gaa gga acc gca acg atc acc cct cca gag ggc ttg tta gat ctt 643  
 Glu Glu Gly Thr Ala Thr Ile Thr Pro Pro Glu Gly Leu Leu Asp Leu  
 170 175 180

taggctccga cagatttaat agt 666

<210> 280  
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 <212> PRT  
 <213> Corynebacterium glutamicum

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Leu Gln Ile Gly Lys Val Val Lys Ser His Gly Ile Arg Gly Glu Val  
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Val Val Glu Leu Ser Thr Asp Asp Pro Asp Ile Arg Phe Ala Ile Gly  
 35 40 45

Glu Val Leu Asn Gly Lys Gln Ala Gly Lys Glu His Ser Leu Thr Ile  
 50 55 60

Asp Ala Ala Arg Met His Gln Gly Arg Leu Leu Val Lys Phe Ala Glu  
 65 70 75 80

Val Pro Asp Arg Thr Ala Ala Asp Ser Leu Arg Gly Thr Arg Phe Phe  
 85 90 95

Ala Ala Pro Leu Glu Asp Glu Asp Asp Glu Asp Gly Phe Tyr Asp His  
 100 105 110

Glu Leu Glu Gly Leu Arg Val Ile His Glu Gly Glu Asp Ile Gly Glu

115 120 125

Val Thr Gly Val Met His Gly Pro Ala Gly Glu Ile Leu Glu Val Arg  
130 135 140

Leu Thr Ser Gly Lys Glu Thr Leu Ile Pro Phe Val His Ala Ile Val  
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Pro Glu Val Asp Leu Glu Glu Gly Thr Ala Thr Ile Thr Pro Pro Glu  
165 170 175

Gly Leu Leu Asp Leu  
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Val Thr Pro Pro Ala  
1 5  
cgc cga gat ggc aca ccg gac aag aag cag agc aat cgc tct ggc gga 163  
Arg Arg Asp Gly Thr Pro Asp Lys Lys Gln Ser Asn Arg Ser Gly Gly  
10 15 20  
tac cgg tct tca gtt cgt ggc tac aag cca gga tca tcc cgc cca aac 211  
Tyr Arg Ser Ser Val Arg Gly Tyr Lys Pro Gly Ser Ser Arg Pro Asn  
25 30 35  
aca cgc cag cag cct cag aag aag gat gag att ctt ctc tcc aac gct 259  
Thr Arg Gln Gln Pro Gln Lys Lys Asp Glu Ile Leu Leu Ser Asn Ala  
40 45 50  
aag cct gcc aag aag caa aac gta aaa tcc gac gac gat tgg tcg atg 307  
Lys Pro Ala Lys Lys Gln Asn Val Lys Ser Asp Asp Asp Trp Ser Met  
55 60 65  
ggc ttc tta aac cgc aat gac tct gac gga gtt cgc ctg cag aag gtg 355  
Gly Phe Leu Asn Arg Asn Asp Ser Asp Gly Val Arg Leu Gln Lys Val  
70 75 80 85  
ctt gcc caa gca ggt gtg gca tca cgt cga cac gca gaa atc ctg att 403  
Leu Ala Gln Ala Gly Val Ala Ser Arg Arg His Ala Glu Ile Leu Ile  
90 95 100  
gat cag ggc cgt gtg gag gtc aac gat cgt atc gtg acc acc cag ggc 451  
Asp Gln Gly Arg Val Glu Val Asn Asp Arg Ile Val Thr Thr Gln Gly  
105 110 115  
gtg cgc gtg gat cca aac aac gat gtc atc cgt gtt gac ggc gtc cgc 499

Val Arg Val Asp Pro Asn Asn Asp Val Ile Arg Val Asp Gly Val Arg  
 120 125 130

atc cac atc aac gag gac ctc gag tac ttc gtg ctc aac aag cct cgt 547  
 Ile His Ile Asn Glu Asp Leu Glu Tyr Phe Val Leu Asn Lys Pro Arg  
 135 140 145

ggc atg cac tcc acc atg agc gat gaa ctt ggt cgc cca tgc gtg ggt 595  
 Gly Met His Ser Thr Met Ser Asp Glu Leu Gly Arg Pro Cys Val Gly  
 150 155 160 165

gat ctg gtc agt gag aag act gca tct gga cag cgt ctg ttc cac gtc 643  
 Asp Leu Val Ser Glu Lys Thr Ala Ser Gly Gln Arg Leu Phe His Val  
 170 175 180

ggt cgc ctc gac gcg gac acc gaa ggt ttg ctg ctg ctc acc aac gat 691  
 Gly Arg Leu Asp Ala Asp Thr Glu Gly Leu Leu Leu Thr Asn Asp  
 185 190 195

ggt gag ttg gct aac cgc ctc atg cac cct aag tac gaa gtg tcc aag 739  
 Gly Glu Leu Ala Asn Arg Leu Met His Pro Lys Tyr Glu Val Ser Lys  
 200 205 210

act tac ctt gct acc gtt cgc ggt gaa gca acc aat aag cta gtc agc 787  
 Thr Tyr Leu Ala Thr Val Arg Gly Glu Ala Thr Asn Lys Leu Val Ser  
 215 220 225

gct ctt cgt gat ggc gtg gag ttg gaa gat ggc cct gcc aag gct gac 835  
 Ala Leu Arg Asp Gly Val Glu Leu Glu Asp Gly Pro Ala Lys Ala Asp  
 230 235 240 245

ttt gcg cag att atc gac gta ttc cag ggc aag tcc ttg ttg cgc atc 883  
 Phe Ala Gln Ile Ile Asp Val Phe Gln Gly Lys Ser Leu Leu Arg Ile  
 250 255 260

gaa atc cac gaa ggc cgc aag cac att gtg cga cgc ctc ttc gat gag 931  
 Glu Ile His Glu Gly Arg Lys His Ile Val Arg Arg Leu Phe Asp Glu  
 265 270 275

ctc ggt ttc cca gtc gag cgc ctc gtg cgc acc aag ctg cac acc gtt 979  
 Leu Gly Phe Pro Val Glu Arg Leu Val Arg Thr Lys Leu His Thr Val  
 280 285 290

cag ctt ggt gat cag aag cca ggt tcc ctt cgt gca ctg aac tcc tct 1027  
 Gln Leu Gly Asp Gln Lys Pro Gly Ser Leu Arg Ala Leu Asn Ser Ser  
 295 300 305

gag ctg acc agc tta tac aag gtg gtc caa ctg tgacggaat ttccaacatg 1080  
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 310 315 320

cct 1083

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 <212> PRT  
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Ser Ser Arg Pro Asn Thr Arg Gln Gln Pro Gln Lys Lys Asp Glu Ile			
35	40		45
Leu Leu Ser Asn Ala Lys Pro Ala Lys Lys Gln Asn Val Lys Ser Asp			
50	55		60
Asp Asp Trp Ser Met Gly Phe Leu Asn Arg Asn Asp Ser Asp Gly Val			
65	70	75	80
Arg Leu Gln Lys Val Leu Ala Gln Ala Gly Val Ala Ser Arg Arg His			
	85	90	95
Ala Glu Ile Leu Ile Asp Gln Gly Arg Val Glu Val Asn Asp Arg Ile			
	100	105	110
Val Thr Thr Gln Gly Val Arg Val Asp Pro Asn Asn Asp Val Ile Arg			
	115	120	125
Val Asp Gly Val Arg Ile His Ile Asn Glu Asp Leu Glu Tyr Phe Val			
	130	135	140
Leu Asn Lys Pro Arg Gly Met His Ser Thr Met Ser Asp Glu Leu Gly			
	145	150	155
Arg Pro Cys Val Gly Asp Leu Val Ser Glu Lys Thr Ala Ser Gly Gln			
	165	170	175
Arg Leu Phe His Val Gly Arg Leu Asp Ala Asp Thr Glu Gly Leu Leu			
	180	185	190
Leu Leu Thr Asn Asp Gly Glu Leu Ala Asn Arg Leu Met His Pro Lys			
	195	200	205
Tyr Glu Val Ser Lys Thr Tyr Leu Ala Thr Val Arg Gly Glu Ala Thr			
	210	215	220
Asn Lys Leu Val Ser Ala Leu Arg Asp Gly Val Glu Leu Glu Asp Gly			
	225	230	235
Pro Ala Lys Ala Asp Phe Ala Gln Ile Ile Asp Val Phe Gln Gly Lys			
	245	250	255
Ser Leu Leu Arg Ile Glu Ile His Glu Gly Arg Lys His Ile Val Arg			
	260	265	270
Arg Leu Phe Asp Glu Leu Gly Phe Pro Val Glu Arg Leu Val Arg Thr			
	275	280	285
Lys Leu His Thr Val Gln Leu Gly Asp Gln Lys Pro Gly Ser Leu Arg			
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Ala Leu Asn Ser Ser Glu Leu Thr Ser Leu Tyr Lys Val Val Gln Leu			
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<223> RXA02615
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	Met Gln Phe Ala Gln 1               5
aac ccg cgt ctg acg aac gac gcg gtg atc tta gaa cca ctg tca cat	163
Asn Pro Arg Leu Thr Asn Asp Ala Val Ile Leu Glu Pro Leu Ser His	
	10              15              20
cag tgg act cag gat ctc cag gaa gct gtc gcc tca caa gaa ttg tgg	211
Gln Trp Thr Gln Asp Leu Gln Glu Ala Val Ala Ser Gln Glu Leu Trp	
	25              30              35
cgc cat tgg ttc gtc gct cta ccc acc cca gag ggc atg gcg gag gaa	259
Arg His Trp Phe Val Ala Leu Pro Thr Pro Glu Gly Met Ala Glu Glu	
	40              45              50
att gac cgc cgc cta gcc gaa cat gca gac gga ctg tgt gcg cct tgg	307
Ile Asp Arg Arg Leu Ala Glu His Ala Asp Gly Leu Cys Ala Pro Trp	
	55              60              65
gca atc att tcc gct gca aca ggc cgt gcc gtt ggc atg acc tca ttt	355
Ala Ile Ile Ser Ala Ala Thr Gly Arg Ala Val Gly Met Thr Ser Phe	
	70              75              80              85
cat acc ctt gac cac gcg aat aaa cgg ctg gaa att gga cgc aca tgg	403
His Thr Leu Asp His Ala Asn Lys Arg Leu Glu Ile Gly Arg Thr Trp	
	90              95              100
atg gct gcc cat gtc caa gga acc ggc atc aac ccc tcg gtg aaa ttc	451
Met Ala Ala His Val Gln Gly Thr Gly Ile Asn Pro Ser Val Lys Phe	
	105             110             115
ctg cag ttg cag cgc gct ttt gaa gac ctc ggt gtc aat gcc gtg gaa	499
Leu Gln Leu Gln Arg Ala Phe Glu Asp Leu Gly Val Asn Ala Val Glu	
	120             125             130
ttc cga acg aac tgg cac aac cac cgc tcc cgc gcc gca atc gaa cga	547
Phe Arg Thr Asn Trp His Asn His Arg Ser Arg Ala Ala Ile Glu Arg	
	135             140             145
ctc gga gca aaa caa gac ggc gta cta cgc aaa cat cgc atc cac cct	595
Leu Gly Ala Lys Gln Asp Gly Val Leu Arg Lys His Arg Ile His Pro	
	150             155             160             165
gac ggc acc gtc cgc gac acc gtc atc tat tcc atc acc aac gat gaa	643
Asp Gly Thr Val Arg Asp Thr Val Ile Tyr Ser Ile Thr Asn Asp Glu	

170	175	180	
tgg cct gcc gtc aaa ctg acg ctc atg gag cga ctg tac cgt cac atg			691
Trp Pro Ala Val Lys Leu Thr Leu Met Glu Arg Leu Tyr Arg His Met			
185	190	195	
cag gtt ccc atc att ccc aac gag gca tgg ett ttc gac gcc agc			736
Gln Val Pro Ile Ile Pro Asn Glu Ala Ser Leu Phe Asp Ala Ser			
200	205	210	
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Ser Gln Glu Leu Trp Arg His Trp Phe Val Ala Leu Pro Thr Pro Glu			
35	40	45	
Gly Met Ala Glu Glu Ile Asp Arg Arg Leu Ala Glu His Ala Asp Gly			
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Leu Cys Ala Pro Trp Ala Ile Ile Ser Ala Ala Thr Gly Arg Ala Val			
65	70	75	80
Gly Met Thr Ser Phe His Thr Leu Asp His Ala Asn Lys Arg Leu Glu			
85	90	95	
Ile Gly Arg Thr Trp Met Ala Ala His Val Gln Gly Thr Gly Ile Asn			
100	105	110	
Pro Ser Val Lys Phe Leu Gln Leu Gln Arg Ala Phe Glu Asp Leu Gly			
115	120	125	
Val Asn Ala Val Glu Phe Arg Thr Asn Trp His Asn His Arg Ser Arg			
130	135	140	
Ala Ala Ile Glu Arg Leu Gly Ala Lys Gln Asp Gly Val Leu Arg Lys			
145	150	155	160
His Arg Ile His Pro Asp Gly Thr Val Arg Asp Thr Val Ile Tyr Ser			
165	170	175	
Ile Thr Asn Asp Glu Trp Pro Ala Val Lys Leu Thr Leu Met Glu Arg			
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Leu Tyr Arg His Met Gln Val Pro Ile Ile Pro Asn Glu Ala Ser Leu			
195	200	205	
Phe Asp Ala Ser			
210			



<210> 285  
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 <212> DNA  
 <213> *Corynebacterium glutamicum*

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 <222> (101)..(808)  
 <223> RXN01343

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 Met Ser Lys Asn Ser  
 1 5  
 aag gcg tac cgc gag gcc gct gag aag atc gac gct ggt cgc atc tac 163  
 Lys Ala Tyr Arg Glu Ala Ala Glu Lys Ile Asp Ala Gly Arg Ile Tyr  
 10 15 20  
 tcc cca ctg gag gct gca aac ctg gtc aag gag acc tcc tcc aag aac 211  
 Ser Pro Leu Glu Ala Ala Asn Leu Val Lys Glu Thr Ser Ser Lys Asn  
 25 30 35  
 tac gac gct tcc atc gac gta gct atc cgc ctg ggc gtt gac cca cgt 259  
 Tyr Asp Ala Ser Ile Asp Val Ala Ile Arg Leu Gly Val Asp Pro Arg  
 40 45 50  
 aag gct gat cag ctt gtt cgt ggc acc gtc tcc ctg cct aac ggc acc 307  
 Lys Ala Asp Gln Leu Val Arg Gly Thr Val Ser Leu Pro Asn Gly Thr  
 55 60 65  
 ggt aag acc gtt cgc gtt gct gtg ttc gca cag ggc gag aag gct act 355  
 Gly Lys Thr Val Arg Val Ala Val Phe Ala Gln Gly Glu Lys Ala Thr  
 70 75 80 85  
 gag gct gag gct gct ggc gct gac ttc gtt ggc acc gac gag ctg gtt 403  
 Glu Ala Glu Ala Ala Gly Ala Asp Phe Val Gly Thr Asp Glu Leu Val  
 90 95 100  
 gag aag atc cag ggt ggc tgg acc gac ttc gac gtt gct att gca acc 451  
 Glu Lys Ile Gln Gly Gly Trp Thr Asp Phe Asp Val Ala Ile Ala Thr  
 105 110 115  
 cct gat cag atg gct aag atc ggc cgt atc gct cgt gtc ttg ggc cca 499  
 Pro Asp Gln Met Ala Lys Ile Gly Arg Ile Ala Arg Val Leu Gly Pro  
 120 125 130  
 cgt ggt ctg atg cct aac cct aag acc ggc acc gtc acc aac gat gtc 547  
 Arg Gly Leu Met Pro Asn Pro Lys Thr Gly Thr Val Thr Asn Asp Val  
 135 140 145  
 gct aag gct atc gaa gag gtc aag ggc ggc aag att tcc ttc cgc gtt 595  
 Ala Lys Ala Ile Glu Glu Val Lys Gly Gly Lys Ile Ser Phe Arg Val  
 150 155 160 165  
 gac aag gct tcc aac ctg cac gct gca att ggt aag gct tcc ttc gat 643  
 Asp Lys Ala Ser Asn Leu His Ala Ala Ile Gly Lys Ala Ser Phe Asp  
 170 175 180

gcg aag aag ctg gct gag aac tac ggc gct ctc ctc gac gag atc atc 691  
 Ala Lys Lys Leu Ala Glu Asn Tyr Gly Ala Leu Leu Asp Glu Ile Ile  
 185 190 195

cgt atc aag cct tct tcc gct aag ggc atc tac gtc aag cgc gtg acc 739  
 Arg Ile Lys Pro Ser Ser Ala Lys Gly Ile Tyr Val Lys Arg Val Thr  
 200 205 210

ctg tct tcc acc acc ggt cct ggt gtt gag gtt gac act cac gtc acc 787  
 Leu Ser Ser Thr Thr Gly Pro Gly Val Glu Val Asp Thr His Val Thr  
 215 220 225

aag aac tac gca gaa gag gca taagccttcc cagcgtaac tct 831  
 Lys Asn Tyr Ala Glu Glu Ala  
 230 235

<210> 286

<211> 236

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 286

Met Ser Lys Asn Ser Lys Ala Tyr Arg Glu Ala Ala Glu Lys Ile Asp  
 1 5 10 15

Ala Gly Arg Ile Tyr Ser Pro Leu Glu Ala Ala Asn Leu Val Lys Glu  
 20 25 30

Thr Ser Ser Lys Asn Tyr Asp Ala Ser Ile Asp Val Ala Ile Arg Leu  
 35 40 45

Gly Val Asp Pro Arg Lys Ala Asp Gln Leu Val Arg Gly Thr Val Ser  
 50 55 60

Leu Pro Asn Gly Thr Gly Lys Thr Val Arg Val Ala Val Phe Ala Gln  
 65 70 75 80

Gly Glu Lys Ala Thr Glu Ala Glu Ala Ala Gly Ala Asp Phe Val Gly  
 85 90 95

Thr Asp Glu Leu Val Glu Lys Ile Gln Gly Gly Trp Thr Asp Phe Asp  
 100 105 110

Val Ala Ile Ala Thr Pro Asp Gln Met Ala Lys Ile Gly Arg Ile Ala  
 115 120 125

Arg Val Leu Gly Pro Arg Gly Leu Met Pro Asn Pro Lys Thr Gly Thr  
 130 135 140

Val Thr Asn Asp Val Ala Lys Lys Ala Ile Glu Glu Val Lys Gly Gly Lys  
 145 150 155 160

Ile Ser Phe Arg Val Asp Lys Ala Ser Asn Leu His Ala Ala Ile Gly  
 165 170 175

Lys Ala Ser Phe Asp Ala Lys Lys Leu Ala Glu Asn Tyr Gly Ala Leu  
 180 185 190

Leu Asp Glu Ile Ile Arg Ile Lys Pro Ser Ser Ala Lys Gly Ile Tyr

205

4400> 287	atc tac tcc cca ctc gag gct gca aac ctg gtc aag gag acc tcc tcc	48
	Ile Tyr Ser Pro Leu Glu Ala Ala Asn Leu Val Lys Glu Thr Ser Ser	
	1 5 10 15	
aag aac tac gac gct tcc atc gac gta gct atc cgc ctg ggc gtt gac	96	
Lys Asn Tyr Asp Ala Ser Ile Asp Val Ala Ile Arg Leu Gly Val Asp		
	20 25 30	
cca cgt aag gct gat cag ctt gtt cgt ggc acc gtc tcc ctg cct aac	144	
Pro Arg Lys Ala Asp Gln Leu Val Arg Gly Thr Val Ser Leu Pro Asn		
	35 40 45	
ggc acc ggt aag acc gtt cgc gtt gct gtg ttc gca cag ggc gag aag	192	
Gly Thr Gly Lys Thr Val Arg Val Ala Val Phe Ala Gln Gly Glu Lys		
	50 55 60	
gct act gag gct gag gct gct ggc gct gac ttc gtt ggc acc gac gag	240	
Ala Thr Glu Ala Glu Ala Ala Gly Ala Asp Phe Val Gly Thr Asp Glu		
	65 70 75 80	
ctc gtt gag aag atc cag ggt ggc tgg acc gac ttc gac gtt gct att	288	
Leu Val Glu Lys Ile Gln Gly Gly Trp Thr Asp Phe Asp Val Ala Ile		
	85 90 95	
gca acc cct gat cag atg gct aag atc ggc cgt atc gct cgt gtc ttg	336	
Ala Thr Pro Asp Gln Met Ala Lys Ile Gly Arg Ile Ala Arg Val Leu		
	100 105 110	
ggc cca cgt ggt ctg atg cct aac cct aag acc ggc acc cct acc aac	384	
Gly Pro Arg Gly Leu Met Pro Asn Pro Lys Thr Gly Thr Val Thr Asn		
	115 120 125	
gat gtc gct aag gct atc gaa gag gtc aag ggc ggc aag att tcc ttc	432	
Asp Val Ala Lys Ala Ile Glu Glu Val Lys Gly Gly Lys Ile Ser Phe		
	130 135 140	
cgc gtt gac aag gct tcc aac ctg cac gct gca att ggt aag gct tcc	480	
Arg Val Asp Lys Ala Ser Asn Leu His Ala Ala Ile Gly Lys Ala Ser		
	145 150 155 160	
ttc gat gcg aag aag ctg gct gag aac tac ggc gct ctc ctc gac gag	528	

Phe Asp Ala Lys Lys Leu Ala Glu Asn Tyr Gly Ala Leu Leu Asp Glu  
 165 170 175

atc atc cgt atc aag cct tct tcc gct aag ggc atc tac gtc aag cgc 576  
 ile ile arg ile lys pro ser ser ala lys gly ile tyr val lys arg  
 180 185 190

gtg acc ctg tct tcc acc acc ggt cct ggt gtt gag gtt gac act cac 624  
 val thr leu ser ser thr thr gly pro gly val glu val asp thr his  
 195 200 205

gtc acc aag aac tac gca gaa gag gca taagccttcc cagcgtaac 671  
 val thr lys asn tyr ala glu glu ala  
 210 215

tct 674

<210> 288  
 <211> 217  
 <212> PRT  
 <213> *Corynebacterium glutamicum*

<400> 288  
 ile tyr ser pro leu glu ala ala asn leu val lys glu thr ser ser  
 1 5 10 15

lys asn tyr asp ala ser ile asp val ala ile arg leu gly val asp  
 20 25 30

pro arg lys ala asp gln leu val arg gly thr val ser leu pro asn  
 35 40 45

gly thr gly lys thr val arg val ala val phe ala gln gly glu lys  
 50 55 60

ala thr glu ala glu ala ala gly ala asp phe val gly thr asp glu  
 65 70 75 80

leu val glu lys ile gln gly gly trp thr asp phe asp val ala ile  
 85 90 95

ala thr pro asp gln met ala lys ile gly arg ile ala arg val leu  
 100 105 110

gly pro arg gly leu met pro asn pro lys thr gly thr val thr asn  
 115 120 125

asp val ala lys ala ile glu glu val lys gly gly lys ile ser phe  
 130 135 140

arg val asp lys ala ser asn leu his ala ala ile gly lys ala ser  
 145 150 155 160

phe asp ala lys lys leu ala glu asn tyr gly ala leu leu asp glu  
 165 170 175

ile ile arg ile lys pro ser ser ala lys gly ile tyr val lys arg  
 180 185 190

val thr leu ser ser thr thr gly pro gly val glu val asp thr his

195

200

205

Val Thr Lys Asn Tyr Ala Glu Glu Ala  
210 215

&lt;210&gt; 289

&lt;211&gt; 684

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(661)

&lt;223&gt; RXA01951

&lt;400&gt; 289

cgctaccgcg tcactcgactt ccgtcgtaac gacaaggatg gcgtattggc aaaggtcgct 60

cacatcgagt acgacccaaa ccgtaccgct aacattgcac ttg ctt cac tac ttc 115  
Leu Leu His Tyr Phe  
1 5

gat ggc gag aag cgt tac atc ctc gca ccg aag ggc ctg acc cag ggc 163  
Asp Gly Glu Lys Arg Tyr Ile Leu Ala Pro Lys Gly Leu Thr Gln Gly  
10 15 20

acc gtt atc gag tcc ggc gct gca gcc gac atc aag gtt ggt aac aac 211  
Thr Val Ile Glu Ser Gly Ala Ala Ala Asp Ile Lys Val Gly Asn Asn  
25 30 35

ctg cca ctg cgt aac atc ccg act ggt acc acc atc cac aac gtg gag 259  
Leu Pro Leu Arg Asn Ile Pro Thr Gly Thr Thr Ile His Asn Val Glu  
40 45 50

ttg aag cca ggc gca ggt gca aag ctg gca cgt tcc gct gga gct tcc 307  
Leu Lys Pro Gly Ala Gly Ala Lys Leu Ala Arg Ser Ala Gly Ala Ser  
55 60 65

atc cag ctt ctt ggt aag gaa ggc tcc tac gca gtt ctg cgt atg cca 355  
Ile Gln Leu Leu Gly Lys Glu Gly Ser Tyr Ala Val Leu Arg Met Pro  
70 75 80 85

tcc tcc gag atc cga cgc gta aac atc cgc tgc cgc gcg act gtt ggt 403  
Ser Ser Glu Ile Arg Arg Val Asn Ile Arg Cys Arg Ala Thr Val Gly  
90 95 100

gag gtc ggc aac gcc gag cag atc aac att cgt tgg ggt aaa gct ggt 451  
Glu Val Gly Asn Ala Glu Gln Ile Asn Ile Arg Trp Gly Lys Ala Gly  
105 110 115

cgt atg cgt tgg aag ggc tgg cgc cca acc gtc cgt ggt gtc gtt atg 499  
Arg Met Arg Trp Lys Gly Trp Arg Pro Thr Val Arg Gly Val Val Met  
120 125 130

aac ccg gtc gac cac cca cac ggt ggt ggt gaa ggt aag act tct ggt 547  
Asn Pro Val Asp His Pro His Gly Gly Gly Glu Gly Lys Thr Ser Gly  
135 140 145

ggt cgc cac cca gtc tcc cca tgg gga cag aag gaa ggc cgc acc cgc 595  
Gly Arg His Pro Val Ser Pro Trp Gly Gln Lys Glu Gly Arg Thr Arg

150                      155                      160                      165  
aag cct aag cgt tac agc gat gac atg atc gtt cgt cgc cgt cgt gct 643  
Lys Pro Lys Arg Tyr Ser Asp Asp Met Ile Val Arg Arg Arg Ala  
                         170                      175                      180  
aac aag aac aag aag cgt taagaggagg taacggtgaa tgt 684  
Asn Lys Asn Lys Lys Arg  
                         185

&lt;210&gt; 290

&lt;211&gt; 187

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 290

Leu Leu His Tyr Phe Asp Gly Glu Lys Arg Tyr Ile Leu Ala Pro Lys  
                         1                      5                      10                      15

Gly Leu Thr Gln Gly Thr Val Ile Glu Ser Gly Ala Ala Ala Asp Ile  
                         20                      25                      30

Lys Val Gly Asn Asn Leu Pro Leu Arg Asn Ile Pro Thr Gly Thr Thr  
                         35                      40                      45

Ile His Asn Val Glu Leu Lys Pro Gly Ala Gly Ala Lys Leu Ala Arg  
                         50                      55                      60

Ser Ala Gly Ala Ser Ile Gln Leu Leu Gly Lys Glu Gly Ser Tyr Ala  
                         65                      70                      75                      80

Val Leu Arg Met Pro Ser Ser Glu Ile Arg Arg Val Asn Ile Arg Cys  
                         85                      90                      95

Arg Ala Thr Val Gly Glu Val Gly Asn Ala Glu Gln Ile Asn Ile Arg  
                         100                      105                      110

Trp Gly Lys Ala Gly Arg Met Arg Trp Lys Gly Trp Arg Pro Thr Val  
                         115                      120                      125

Arg Gly Val Val Met Asn Pro Val Asp His Pro His Gly Gly Gly Glu  
                         130                      135                      140

Gly Lys Thr Ser Gly Gly Arg His Pro Val Ser Pro Trp Gly Gln Lys  
                         145                      150                      155                      160

Glu Gly Arg Thr Arg Lys Pro Lys Arg Tyr Ser Asp Asp Met Ile Val  
                         165                      170                      175

Arg Arg Arg Arg Ala Asn Lys Asn Lys Lys Arg  
                         180                      185

&lt;210&gt; 291

&lt;211&gt; 507

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101) .. (484)

&lt;223&gt; FRXA01950

&lt;400&gt; 291

ggctaccaag cgcgccttatg tgactcttcg cgaaggcagc gactccatcg acatcttcag 60

cggctccgtc gcttaagacg tcgatagaaa aggacacatt atg gct att cgt aag 115  
 Met Ala Ile Arg Lys 5  
 1

tac aag ccg aca acc ccg ggt cgc cgc gca agc tcc gtt tcc atg ttc 163  
 Tyr Lys Pro Thr Thr Pro Gly Arg Arg Ala Ser Ser Val Ser Met Phe  
 10 15 20

acg gag atc acc cgt tcg acc cct gag aag tca ctt ctg cgc cca ctg 211  
 Thr Glu Ile Thr Arg Ser Thr Pro Glu Lys Ser Leu Leu Arg Pro Leu  
 25 30 35

agc aag acc ggc gga cgt aac tct cac ggc cac atc acc acc cgt cac 259  
 Ser Lys Thr Gly Gly Arg Asn Ser His Gly His Ile Thr Thr Arg His  
 40 45 50

cgc ggt ggt gga cac aag cgc cgc tac cgc gtc atc gac ttc cgt cgt 307  
 Arg Gly Gly Gly His Lys Arg Arg Tyr Arg Val Ile Asp Phe Arg Arg  
 55 60 65

aac gac aag gat ggc gta ttg gca aag gtc gct cac atc gag tac gac 355  
 Asn Asp Lys Asp Gly Val Leu Ala Lys Val Ala His Ile Glu Tyr Asp  
 70 75 80 85

cca aac cgt acc gct aac att gca ctt gct tca cta ctt cga tgg cga 403  
 Pro Asn Arg Thr Ala Asn Ile Ala Leu Ala Ser Leu Leu Arg Trp Arg  
 90 95 100

gaa cgc tta cat cct cgc acc gaa ggg cct gac cca ggg cac cgt tat 451  
 Glu Ala Leu His Pro Arg Thr Glu Gly Pro Asp Pro Gly His Arg Tyr  
 105 110 115

cga gtc cgg cgc tgc agc cga cat caa ggt tgg taacaacctg ccaatgcgta 504  
 Arg Val Arg Arg Cys Ser Arg His Gln Gly Trp  
 120 125

aca 507

&lt;210&gt; 292

&lt;211&gt; 128

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 292

Met Ala Ile Arg Lys Tyr Lys Pro Thr Thr Pro Gly Arg Arg Ala Ser  
 1 5 10 15

Ser Val Ser Met Phe Thr Glu Ile Thr Arg Ser Thr Pro Glu Lys Ser  
 20 25 30

Leu Leu Arg Pro Leu Ser Lys Thr Gly Gly Arg Asn Ser His Gly His  
 35 40 45

Ile Thr Thr Arg His Arg Gly Gly Gly His Lys Arg Arg Tyr Arg Val

50					55					60					
Ile	Asp	Phe	Arg	Arg	Asn	Asp	Lys	Asp	Gly	Val	Leu	Ala	Lys	Val	Ala
65					70					75					80
His	Ile	Glu	Tyr	Asp	Pro	Asn	Arg	Thr	Ala	Asn	Ile	Ala	Leu	Ala	Ser
				85					90					95	
Leu	Leu	Arg	Trp	Arg	Glu	Ala	Leu	His	Pro	Arg	Thr	Glu	Gly	Pro	Asp
			100					105					110		
Pro	Gly	His	Arg	Tyr	Arg	Val	Arg	Cys	Ser	Arg	His	Gln	Gly	Trp	
		115				120					125				

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<210> 293
<211> 777
<212> DNA
<213> Corynebacterium glutamicum
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<220>
<221> CDS
<222> (101)..(754)
<223> RXA01286
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[illegible]



105 110 115

acc aag ggt aag ggc tac gcc ggc gct atg aag cgc cat ggc ttc gct 499  
 Thr Lys Gly Lys Gly Tyr Ala Gly Ala Met Lys Arg His Gly Phe Ala  
 120 125 130

ggc cag ggt gcc ggc cac ggt aac cag gct gca cac cgc cgc gta ggt 547  
 Gly Gln Gly Ala Gly His Gly Asn Gln Ala Ala His Arg Arg Val Gly  
 135 140 145

ggc att ggt gca gct gct acc cca ggt cgc atc ttc aag ggc aag cgt 595  
 Gly Ile Gly Ala Ala Thr Pro Gly Arg Ile Phe Lys Gly Lys Arg  
 150 155 160 165

atg gct ggc cgc atg ggt aat gac cgc gtc acc acc cag aac ctc aag 643  
 Met Ala Gly Arg Met Gly Asn Asp Arg Val Thr Thr Gln Asn Leu Lys  
 170 175 180

gtt cag aag att gac gcc gat gcc aac atc atc ctt atc aag ggc gca 691  
 Val Gln Lys Ile Asp Ala Asp Ala Asn Ile Ile Leu Ile Lys Gly Ala  
 185 190 195

atc cct ggt aac cgt ggt ggc atc gtt acc gtt aag acc gca gtg aag 739  
 Ile Pro Gly Asn Arg Gly Gly Ile Val Thr Val Lys Thr Ala Val Lys  
 200 205 210

ggc ggt gca cac gca tgacgaatct gaagctgtat gtt 777  
 Gly Gly Ala His Ala  
 215

<210> 294  
 <211> 218  
 <212> PRT  
 <213> *Corynebacterium glutamicum*

<400> 294  
 Met Ser Glu Asn Glu Ile Lys Gly Ile Leu Gly Thr Lys Leu Gly Met  
 1 5 10 15  
 Thr Gln Ile Phe Asp Glu Glu Asn Arg Val Ile Pro Val Thr Val Val  
 20 25 30  
 Glu Ala Gly Pro Cys Val Val Ser Gln Ile Arg Thr Val Glu Thr Asp  
 35 40 45  
 Gly Tyr Asn Ala Ile Gln Ile Ala Tyr Gly Glu Ile Asp Pro Arg Lys  
 50 55 60  
 Val Asn Gln Pro Leu Thr Gly His Phe Lys Lys Ala Gly Val Thr Pro  
 65 70 75 80  
 Arg Arg His Val Thr Glu Ile Arg Met Asp Asp Val Ser Gly Tyr Glu  
 85 90 95  
 Val Gly Gln Asp Val Thr Val Glu Ile Phe Asn Asp Ile Lys Phe Val  
 100 105 110  
 Asp Val Thr Gly Thr Thr Lys Gly Lys Gly Tyr Ala Gly Ala Met Lys  
 115 120 125

Arg His Gly Phe Ala Gly Gln Gly Ala Gly His Gly Asn Gln Ala Ala  
 130 135 140

His Arg Arg Val Gly Gly Ile Gly Ala Ala Ala Thr Pro Gly Arg Ile  
 145 150 155 160

Phe Lys Gly Lys Arg Met Ala Gly Arg Met Gly Asn Asp Arg Val Thr  
 165 170 175

Thr Gln Asn Leu Lys Val Gln Lys Ile Asp Ala Asp Ala Asn Ile Ile  
 180 185 190

Leu Ile Lys Gly Ala Ile Pro Gly Asn Arg Gly Gly Ile Val Thr Val  
 195 200 205

Lys Thr Ala Val Lys Gly Gly Ala His Ala  
 210 215

<210> 295  
 <211> 626  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (1)..(603)  
 <223> RXA01948

<400> 295  
 tct gta gaa ctc cct gca gag att ttt gac cgt gag gtc tcc gtc gca 48  
 Ser Val Glu Leu Pro Ala Glu Ile Phe Asp Arg Glu Val Ser Val Ala  
 1 5 10 15

ctg ctg cac cag gtt gtc aac gca cag ctt gca gca gct cga cag ggc 96  
 Leu Leu His Gln Val Val Asn Ala Gln Leu Ala Ala Arg Gln Gly  
 20 25 30

acc cac tcc acc aag acc cgt ggc gaa gta cgt ggc ggt ggc cgt aag 144  
 Thr His Ser Thr Lys Thr Arg Gly Glu Val Arg Gly Gly Arg Lys  
 35 40 45

cca ttc cgt cag aag gga acc ggt cgc gct cgt cag ggc tcg atc cgc 192  
 Pro Phe Arg Gln Lys Gly Thr Gly Arg Ala Arg Gln Gly Ser Ile Arg  
 50 55 60

gca cct cac ttc acc ggt ggt ggc atc tcc cac ggc cct aag cca cgc 240  
 Ala Pro His Phe Thr Gly Gly Gly Ile Ser His Gly Pro Lys Pro Arg  
 65 70 75 80

gac tac tct cag cgc acc cct aag aag atg atc aag gct gca ctt tac 288  
 Asp Tyr Ser Gln Arg Thr Pro Lys Lys Met Ile Lys Ala Ala Leu Tyr  
 85 90 95

ggt gca ctg tct gat cgt gca cgc aat gca cgt atc cac gtc gtc tcc 336  
 Gly Ala Leu Ser Asp Arg Ala Arg Asn Ala Arg Ile His Val Val Ser  
 100 105 110

gaa ttg gtg cct ggc cag acc cct tcg acc aag tct gca aag gct ttc 384  
 Glu Leu Val Pro Gly Gln Thr Pro Ser Thr Lys Ser Ala Lys Ala Phe  
 115 120 125

atc gag cgt ctg acc gag cgt aag tcc gtg ctg ctc gta gtg agc cgt 432  
 ile glu arg leu thr glu arg lys ser val leu leu val val ser arg  
 130 135 140

gag gat atc aac gcc cag aag agt gct aac aac ctg cct ggc gtc cac 480  
 glu asp ile asn ala gln lys ser ala asn asn leu pro gly val his  
 145 150 155 160

atc ctg gcc gct gat cag ctg aac acc tac gac gtt ctc aag tct gac 528  
 ile leu ala ala asp gln leu asn thr tyr asp val leu lys ser asp  
 165 170 175

gac gtt gtg ttc tcc gtt gag gct ctc cac acc ttc atc aac cgc gct 576  
 asp val val phe ser val glu ala leu his thr phe ile asn arg ala  
 180 185 190

tcc ggt gcg gca cag gag gag cag aac taatggctac tatcgccaac 623  
 ser gly ala ala gln glu glu gln asn  
 195 200

cca 626

<210> 296  
 <211> 201  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 296  
 ser val glu leu pro ala glu ile phe asp arg glu val ser val ala  
 1 5 10 15

leu leu his gln val val asn ala gln leu ala ala arg gln gly  
 20 25 30

thr his ser thr lys thr arg gly glu val arg gly gly gly arg lys  
 35 40 45

pro phe arg gln lys gly thr gly arg ala arg gln gly ser ile arg  
 50 55 60

ala pro his phe thr gly gly ile ser his gly pro lys pro arg  
 65 70 75 80

asp tyr ser gln arg thr pro lys lys met ile lys ala ala leu tyr  
 85 90 95

gly ala leu ser asp arg ala arg asn ala arg ile his val val ser  
 100 105 110

glu leu val pro gly gln thr pro ser thr lys ser ala lys ala phe  
 115 120 125

ile glu arg leu thr glu arg lys ser val leu leu val val ser arg  
 130 135 140

glu asp ile asn ala gln lys ser ala asn asn leu pro gly val his  
 145 150 155 160

ile leu ala ala asp gln leu asn thr tyr asp val leu lys ser asp

165 170 175  
 Asp Val Val Phe Ser Val Glu Ala Leu His Thr Phe Ile Asn Arg Ala  
 180 185 190  
 Ser Gly Ala Ala Gln Glu Glu Gln Asn  
 195 200

&lt;210&gt; 297

&lt;211&gt; 696

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(673)

&lt;223&gt; RXN00706

&lt;400&gt; 297

tggtcatcga ctccgacgga aacccaactc gcgttggtcga ccggttcgat gaaaacggca 60

agaaggtccg cgtttctcgt cgcaatggga aggatatcta atg act gag aat tac 115  
 Met Thr Glu Asn Tyr  
 1 5

atc cct cgt ctg aag acc cgt tac cag gac gaa atc cgc acc aag ctt 163  
 Ile Pro Arg Leu Lys Thr Arg Tyr Gln Asp Glu Ile Arg Thr Lys Leu  
 10 15 20

cag ggc gag ttc gag ttc gaa aac gtc atg cag atc cca ggc gtc acc 211  
 Gln Gly Glu Phe Glu Phe Glu Asn Val Met Gln Ile Pro Gly Val Thr  
 25 30 35

aag att gtc gtc aac atg ggt gtc ggc gac gca gct cgt gac tcc aag 259  
 Lys Ile Val Val Asn Met Gly Val Gly Asp Ala Ala Arg Asp Ser Lys  
 40 45 50

ctc atc aac ggc gct atc gag gac ctc acc gca atc acc ggt cag aag 307  
 Leu Ile Asn Gly Ala Ile Glu Asp Leu Thr Ala Ile Thr Gly Gln Lys  
 55 60 65

cca cag ctt cgc cgt gcg aag aag tcc atc gct aac ttc aag ctc cgt 355  
 Pro Gln Leu Arg Arg Ala Lys Lys Ser Ile Ala Asn Phe Lys Leu Arg  
 70 75 80 85

gaa ggc atg cca atc ggc gca aag gtt acc ctg cgc ggc gac cgc atg 403  
 Glu Gly Met Pro Ile Gly Ala Lys Val Thr Leu Arg Gly Asp Arg Met  
 90 95 100

tgg gag ttc ctg gac cgt ctg ctg acc gtg gca ctg cca cgt atc cgc 451  
 Trp Glu Phe Leu Asp Arg Leu Leu Thr Val Ala Leu Pro Arg Ile Arg  
 105 110 115

gac ttc cgt gga ctt tcc gac cag cag ttc gac ggc cac ggt aac tac 499  
 Asp Phe Arg Gly Leu Ser Asp Gln Gln Phe Asp Gly His Gly Asn Tyr  
 120 125 130

acc ttc ggc ctc acc gag cag acc atg ttc tac gaa atc gac gtc gac 547  
 Thr Phe Gly Leu Thr Glu Gln Thr Met Phe Tyr Glu Ile Asp Val Asp  
 135 140 145

aag atc gac cgt cct cgt ggt atg gac atc acc gtt gtt acc acc gct 595  
 Lys Ile Asp Arg Pro Arg Gly Met Asp Ile Thr Val Val Thr Thr Ala  
 150 155 160 165

gta acc gac gat gaa ggt cgc tcc ctg ctc cgc gag ctc ggc ttc cca 643  
 Val Thr Asp Asp Glu Gly Arg Ser Leu Leu Arg Glu Leu Gly Phe Pro  
 170 175 180

ttc aag ggt gaa gac ggc aac cgc cag cag taaactgcat agttaaaagc 693  
 Phe Lys Gly Glu Asp Gly Asn Arg Gln Gln  
 185 190

act 696

<210> 298  
 <211> 191  
 <212> PRT  
 <213> *Corynebacterium glutamicum*

<400> 298  
 Met Thr Glu Asn Tyr Ile Pro Arg Leu Lys Thr Arg Tyr Gln Asp Glu  
 1 5 10 15

Ile Arg Thr Lys Leu Gln Gly Glu Phe Glu Phe Glu Asn Val Met Gln  
 20 25 30

Ile Pro Gly Val Thr Lys Ile Val Val Asn Met Gly Val Gly Asp Ala  
 35 40 45

Ala Arg Asp Ser Lys Leu Ile Asn Gly Ala Ile Glu Asp Leu Thr Ala  
 50 55 60

Ile Thr Gly Gln Lys Pro Gln Leu Arg Arg Ala Lys Lys Ser Ile Ala  
 65 70 75 80

Asn Phe Lys Leu Arg Glu Gly Met Pro Ile Gly Ala Lys Val Thr Leu  
 85 90 95

Arg Gly Asp Arg Met Trp Glu Phe Leu Asp Arg Leu Leu Thr Val Ala  
 100 105 110

Leu Pro Arg Ile Arg Asp Phe Arg Gly Leu Ser Asp Gln Gln Phe Asp  
 115 120 125

Gly His Gly Asn Tyr Thr Phe Gly Leu Thr Glu Gln Thr Met Phe Tyr  
 130 135 140

Glu Ile Asp Val Asp Lys Ile Asp Arg Pro Arg Gly Met Asp Ile Thr  
 145 150 155 160

Val Val Thr Thr Ala Val Thr Asp Asp Glu Gly Arg Ser Leu Leu Arg  
 165 170 175

Glu Leu Gly Phe Pro Phe Lys Gly Glu Asp Gly Asn Arg Gln Gln  
 180 185 190

<210> 299  
 <211> 256

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(256)

&lt;223&gt; FRXA00711

&lt;400&gt; 299

tggtcatcga ctccgacgga aacccaactc gcgttggtcga ccgtttcgat gaaaacggca 60

agaaggtccg cggtttctcgt cgcaatggga aggatatcta atg act gag aat tac 115  
Met Thr Glu Asn Tyr  
1 5

atc cct cgt ctg aag acc cgt tac cag gac gaa atc cgc acc aag ctt 163  
Ile Pro Arg Leu Lys Thr Arg Tyr Gln Asp Glu Ile Arg Thr Lys Leu  
10 15 20

cag ggc gag ttc gag ttc gaa aac gtc atg cag atc cca ggc gtc acc 211  
Gln Gly Glu Phe Glu Phe Glu Asn Val Met Gln Ile Pro Gly Val Thr  
25 30 35

aag att gtc gtc aac atg ggt gtc ggc gac gca gct cgt gac tcc 256  
Lys Ile Val Val Asn Met Gly Val Gly Asp Ala Ala Arg Asp Ser  
40 45 50

&lt;210&gt; 300

&lt;211&gt; 52

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 300

Met Thr Glu Asn Tyr Ile Pro Arg Leu Lys Thr Arg Tyr Gln Asp Glu  
1 5 10 15

Ile Arg Thr Lys Leu Gln Gly Glu Phe Glu Asn Val Met Gln  
20 25 30

Ile Pro Gly Val Thr Lys Ile Val Val Asn Met Gly Val Gly Asp Ala  
35 40 45

Ala Arg Asp Ser  
50

&lt;210&gt; 301

&lt;211&gt; 290

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(267)

&lt;223&gt; FRXA00706

&lt;400&gt; 301

gag ttc ctg gac cgt ctg ctg acc gtg gca ctg cca cgt atc cgc gac 48  
Glu Phe Leu Asp Arg Leu Leu Thr Val Ala Leu Pro Arg Ile Arg Asp  
1 5 10 15

ttc cgt gga ctt tcc gac cag cag ttc gac ggc cac ggt aac tac acc 96  
 Phe Arg Gly Leu Ser Asp Gln Gln Phe Asp Gly His Gly Asn Tyr Thr  
 20 25 30

ttc ggc ctc acc gag cag acc atg ttc tac gaa atc gac gtc gac aag 144  
 Phe Gly Leu Thr Glu Gln Thr Met Phe Tyr Glu Ile Asp Val Asp Lys  
 35 40 45

atc gac cgt cct cgt ggt atg gac atc acc gtt gtt acc acc get gta 192  
 Ile Asp Arg Pro Arg Gly Met Asp Ile Thr Val Val Thr Thr Ala Val  
 50 55 60

acc gac gat gaa ggt cgc tcc ctg ctc cgc gag ctc ggc ttc cca ttc 240  
 Thr Asp Asp Glu Gly Arg Ser Leu Leu Arg Glu Leu Gly Phe Pro Phe  
 65 70 75 80

aag ggt gaa gac ggc aac cgc cag cag taaactgcat agttaaagc 287  
 Lys Gly Glu Asp Gly Asn Arg Gln Gln  
 85

act 290

<210> 302  
 <211> 89  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 302  
 Glu Phe Leu Asp Arg Leu Leu Thr Val Ala Leu Pro Arg Ile Arg Asp  
 1 5 10 15

Phe Arg Gly Leu Ser Asp Gln Gln Phe Asp Gly His Gly Asn Tyr Thr  
 20 25 30

Phe Gly Leu Thr Glu Gln Thr Met Phe Tyr Glu Ile Asp Val Asp Lys  
 35 40 45

Ile Asp Arg Pro Arg Gly Met Asp Ile Thr Val Val Thr Thr Ala Val  
 50 55 60

Thr Asp Asp Glu Gly Arg Ser Leu Leu Arg Glu Leu Gly Phe Pro Phe  
 65 70 75 80

Lys Gly Glu Asp Gly Asn Arg Gln Gln  
 85

<210> 303  
 <211> 657  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(634)  
 <223> RXA00695

<400> 303  
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gtcctcgccct acgtctggta ataggaggagga ttgactaaat atg tca cgt atc gga 115  
Met Ser Arg Ile Gly  
1 5

aaa gaa ccg atc acc atc cca tcc ggt gtc gaa acc aag att gac gga 163  
Lys Glu Pro Ile Thr Ile Pro Ser Gly Val Glu Thr Lys Ile Asp Gly  
10 15 20

cag ctc gtt gag gtt aag ggt cct aag ggc acc ctg aac gtt aac gtt 211  
Gln Leu Val Glu Val Lys Gly Pro Lys Gly Thr Leu Asn Val Asn Val  
25 30 35

cca gag cca atc tcc gtt gca gtg gaa gac ggc aag att gtc gtc acc 259  
Pro Glu Pro Ile Ser Val Ala Val Glu Asp Gly Lys Ile Val Val Thr  
40 45 50

cgc ccg gat gat cac cgc act aac cgt tcc ctc cac ggt ctc tcc cgc 307  
Arg Pro Asp Asp His Arg Thr Asn Arg Ser Leu His Gly Leu Ser Arg  
55 60 65

tcc ctg gtt aac aac ctg gtt gtc ggc gtc acc gag ggc tac acc atc 355  
Ser Leu Val Asn Asn Leu Val Val Gly Val Thr Glu Gly Tyr Thr Ile  
70 75 80 85

aag atg gaa atc ttc ggt gtc ggt tac cgt gtc ggc ctg aag ggc aag 403  
Lys Met Glu Ile Phe Gly Val Gly Tyr Arg Val Ala Leu Lys Gly Lys  
90 95 100

gac ctt gag ttc tcc ctc ggc tac tca cac cca gtt ctg att gaa gct 451  
Asp Leu Glu Phe Ser Leu Gly Tyr Ser His Pro Val Leu Ile Glu Ala  
105 110 115

tct gaa ggc atc act ttc gca gtt gat ggc aac acc aag ctt tca gtt 499  
Ser Glu Gly Ile Thr Phe Ala Val Asp Gly Asn Thr Lys Leu Ser Val  
120 125 130

tct ggc atc gac aag cag aag gtt gga cag gtc gca gca gtg atc cgc 547  
Ser Gly Ile Asp Lys Gln Lys Val Gly Gln Val Ala Ala Val Ile Arg  
135 140 145

cgc ctg cgt aag gac gat cct tac aag ggt aag ggc atc cgc tac gag 595  
Arg Leu Arg Lys Asp Asp Pro Tyr Lys Gly Lys Gly Ile Arg Tyr Glu  
150 155 160 165

ggg gag cag atc cgc cgc aag gtc gga aag acg ggt aag taagcaatga 644  
Gly Glu Gln Ile Arg Arg Lys Val Gly Lys Thr Gly Lys  
170 175

gcaacactga aaa 657

<210> 304  
<211> 178  
<212> PRT  
<213> Corynebacterium glutamicum

<400> 304  
Met Ser Arg Ile Gly Lys Glu Pro Ile Thr Ile Pro Ser Gly Val Glu  
1 5 10 15



Thr Lys Ile Asp Gly Gln Leu Val Glu Val Lys Gly Pro Lys Gly Thr  
 20 25 30  
 Leu Asn Val Asn Val Pro Glu Pro Ile Ser Val Ala Val Glu Asp Gly  
 35 40 45  
 Lys Ile Val Val Thr Arg Pro Asp Asp His Arg Thr Asn Arg Ser Leu  
 50 55 60  
 His Gly Leu Ser Arg Ser Leu Val Asn Asn Leu Val Val Gly Val Thr  
 65 70 75 80  
 Glu Gly Tyr Thr Ile Lys Met Glu Ile Phe Gly Val Gly Tyr Arg Val  
 85 90 95  
 Ala Leu Lys Gly Lys Asp Leu Glu Phe Ser Leu Gly Tyr Ser His Pro  
 100 105 110  
 Val Leu Ile Glu Ala Ser Glu Gly Ile Thr Phe Ala Val Asp Gly Asn  
 115 120 125  
 Thr Lys Leu Ser Val Ser Gly Ile Asp Lys Gln Lys Val Gly Gln Val  
 130 135 140  
 Ala Ala Val Ile Arg Arg Leu Arg Lys Asp Asp Pro Tyr Lys Gly Lys  
 145 150 155 160  
 Gly Ile Arg Tyr Glu Gly Glu Gln Ile Arg Arg Lys Val Gly Lys Thr  
 165 170 175  
 Gly Lys

<210> 305  
 <211> 549  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(526)  
 <223> RXA00543

<400> 305  
 gctccggcgg gttccggcgc gcagacgatg gccaccggtt cttaagcttt tcttttctaa 60  
 aacattcaca aacactcaaa aaccacgaaa ggcagggtatc atg aag ctg atc ctc 115  
 Met Lys Leu Ile Leu  
 1 5  
 acc gcc gcc gtt gaa aac ctt ggt gtc gct gcc gac atc gta gag gtt 163  
 Thr Ala Ala Val Glu Asn Leu Gly Val Ala Gly Asp Ile Val Glu Val  
 10 15 20  
 aag aac gcc tac gga cgt aac ctg ctg ctc ccc cgt gcc ctg gca atc 211  
 Lys Asn Gly Tyr Gly Arg Asn Leu Leu Leu Pro Arg Gly Leu Ala Ile  
 25 30 35  
 gta gcc acc ccg ggt gct gag aag cag atc gag gcc atc aag cgt gcc 259  
 Val Ala Thr Pro Gly Ala Glu Lys Gln Ile Glu Gly Ile Lys Arg Ala

40 45 50

cag gag gct cgc gag att cgc gac ctc gac cac gct cgc gaa gtt aag 307  
 Gln Glu Ala Arg Glu Ile Arg Asp Leu Asp His Ala Arg Glu Val Lys  
 55 60 65

gta gca ctg gaa gca ctt gaa ggt gtt acc att gca gtc cgc acc tcc 355  
 Val Ala Leu Glu Ala Leu Glu Gly Val Thr Ile Ala Val Arg Thr Ser  
 70 75 80 85

gag agc gga aaa ctg ttc ggc tcc gtt aag act gac gac atc gtc gac 403  
 Glu Ser Gly Lys Leu Phe Gly Ser Val Lys Thr Asp Asp Ile Val Asp  
 90 95 100

gca gtc aag gca gcc ggc ggc ccg aac ctg gac aag cgt gcc att gtt 451  
 Ala Val Lys Ala Ala Gly Gly Pro Asn Leu Asp Lys Arg Ala Ile Val  
 105 110 115

ctc ccg aag aac ctg gtt aag acc acc ggt aag tac cag gta gaa gca 499  
 Leu Pro Lys Asn Leu Val Lys Thr Thr Gly Lys Tyr Gln Val Glu Ala  
 120 125 130

aag ctc acc gac gga att gtt tcc gcg tgaagttga ggctgcgca 546  
 Lys Leu Thr Asp Gly Ile Val Ser Ala  
 135 140

gcg 549

<210> 306  
 <211> 142  
 <212> PRT  
 <213> *Corynebacterium glutamicum*

<400> 306  
 Met Lys Leu Ile Leu Thr Ala Ala Val Glu Asn Leu Gly Val Ala Gly  
 1 5 10 15

Asp Ile Val Glu Val Lys Asn Gly Tyr Gly Arg Asn Leu Leu Leu Pro  
 20 25 30

Arg Gly Leu Ala Ile Val Ala Thr Pro Gly Ala Glu Lys Gln Ile Glu  
 35 40 45

Gly Ile Lys Arg Ala Gln Glu Ala Arg Glu Ile Arg Asp Leu Asp His  
 50 55 60

Ala Arg Glu Val Lys Val Ala Leu Glu Ala Leu Glu Gly Val Thr Ile  
 65 70 75 80

Ala Val Arg Thr Ser Glu Ser Gly Lys Leu Phe Gly Ser Val Lys Thr  
 85 90 95

Asp Asp Ile Val Asp Ala Val Lys Ala Ala Gly Gly Pro Asn Leu Asp  
 100 105 110

Lys Arg Ala Ile Val Leu Pro Lys Asn Leu Val Lys Thr Thr Gly Lys  
 115 120 125

Tyr Gln Val Glu Ala Lys Leu Thr Asp Gly Ile Val Ser Ala  
 130 135 140

&lt;210&gt; 307

&lt;211&gt; 636

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(613)

&lt;223&gt; RXA01335

&lt;400&gt; 307

gcgcctgtg ctcttgcaag gggcttttct cattgggtta ttgacctgt gaaagctcgg 60

cggatcagta gattacacat aagaggaagg aggcgaagta atg gca aac cca aga 115  
 Met Ala Asn Pro Arg  
 1 5

aac gaa gca gct ctg gca gag ctc aag gca cgt ttc gct gag acc gac 163  
 Asn Glu Ala Ala Leu Ala Glu Leu Lys Ala Arg Phe Ala Glu Thr Asp  
 10 15 20

acc gtc gtt ctc acc gag tac cgt ggc ctg acc gtg gct cag acc acc 211  
 Thr Val Val Leu Thr Glu Tyr Arg Gly Leu Thr Val Ala Gln Thr Thr  
 25 30 35

gaa ctg cgt aag gca ctg ggc ttc gat gtc cag tac tcc gtc gcc aag 259  
 Glu Leu Arg Lys Ala Leu Gly Phe Asp Val Gln Tyr Ser Val Ala Lys  
 40 45 50

aac acc ctt gtt aag atc gcc gct aac gaa gct ggc gtc gag gcc ctt 307  
 Asn Thr Leu Val Lys Ile Ala Ala Asn Glu Ala Gly Val Glu Gly Leu  
 55 60 65

gat gat ctc ctg acc ggt cca acc gct gtt gcc ttc atc aag gcc gaa 355  
 Asp Asp Leu Leu Thr Gly Pro Thr Ala Val Ala Phe Ile Lys Gly Glu  
 70 75 80 85

gca gtt gac acc gct aag gtg ctg aag aaa ttc ggc gaa gaa aac aag 403  
 Ala Val Asp Thr Ala Lys Val Leu Lys Lys Phe Gly Glu Glu Asn Lys  
 90 95 100

gca ttc gta gtc aag ggt ggc tac atg gat ggc aac gcg ctg acc gct 451  
 Ala Phe Val Val Lys Gly Gly Tyr Met Asp Gly Asn Ala Leu Thr Ala  
 105 110 115

gaa cag gtc aac gca atc gcc gag ctg gac aac cgt gag acc act ctc 499  
 Glu Gln Val Asn Ala Ile Ala Glu Leu Asp Asn Arg Glu Thr Thr Leu  
 120 125 130

gcg aag ctt gcc ggc gcc atg aag ggc agc ttg gca aag gcc gca ggc 547  
 Ala Lys Leu Ala Gly Ala Met Lys Gly Ser Leu Ala Lys Ala Ala Gly  
 135 140 145

ctg ttc aac gct cct gct tcc cag gtc gca cgc ctc gcc gtt gcg ctc 595  
 Leu Phe Asn Ala Pro Ala Ser Gln Val Ala Arg Leu Ala Val Ala Leu  
 150 155 160 165

cag gac aag aag gac gca taagtcgcca ccaggcgac cag 636  
 Gln Asp Lys Lys Asp Ala

170

<210> 308  
 <211> 171  
 <212> PRT  
 <213> *Corynebacterium glutamicum*

<400> 308  
 Met Ala Asn Pro Arg Asn Glu Ala Ala Leu Ala Glu Leu Lys Ala Arg  
 1 5 10 15

Phe Ala Glu Thr Asp Thr Val Val Leu Thr Glu Tyr Arg Gly Leu Thr  
 20 25 30

Val Ala Gln Thr Thr Glu Leu Arg Lys Ala Leu Gly Phe Asp Val Gln  
 35 40 45

Tyr Ser Val Ala Lys Asn Thr Leu Val Lys Ile Ala Ala Asn Glu Ala  
 50 55 60

Gly Val Glu Gly Leu Asp Asp Leu Leu Thr Gly Pro Thr Ala Val Ala  
 65 70 75 80

Phe Ile Lys Gly Glu Ala Val Asp Thr Ala Lys Val Leu Lys Lys Phe  
 85 90 95

Gly Glu Glu Asn Lys Ala Phe Val Val Lys Gly Gly Tyr Met Asp Gly  
 100 105 110

Asn Ala Leu Thr Ala Glu Gln Val Asn Ala Ile Ala Glu Leu Asp Asn  
 115 120 125

Arg Glu Thr Thr Leu Ala Lys Leu Ala Gly Ala Met Lys Gly Ser Leu  
 130 135 140

Ala Lys Ala Ala Gly Leu Phe Asn Ala Pro Ala Ser Gln Val Ala Arg  
 145 150 155 160

Leu Ala Val Ala Leu Gln Asp Lys Lys Asp Ala  
 165 170

<210> 309  
 <211> 558  
 <212> DNA  
 <213> *Corynebacterium glutamicum*

<220>  
 <221> CDS  
 <222> (101)..(535)  
 <223> RXN02826

<400> 309  
 agcgatcacc tgaagttgtg gcgggaccga gcatccggac gggttactagt ggggtttcat 60

cgtcccagtt gtggcccgta acaaggaagc aggtttaacg atg gct cct aag aag 115  
 Met Ala Pro Lys Lys  
 1 5

aag aag aag gtc act ggc etc atc aag etc cag atc cag gca gga cag 163

Lys Lys Lys Val Thr Gly Leu Ile Lys Leu Gln Ile Gln Ala Gly Gln  
                     10                    15                    20  
 gca aac cct gct cct cca gtt ggc cca gca ctt ggt gct cac ggc gtc 211  
 Ala Asn Pro Ala Pro Pro Val Gly Pro Ala Leu Gly Ala His Gly Val  
                     25                    30                    35  
 aac atc atg gaa ttc tgc aag gct tac aac gct gcg act gaa aac cag 259  
 Asn Ile Met Glu Phe Cys Lys Ala Tyr Asn Ala Ala Thr Glu Asn Gln  
                     40                    45                    50  
 cgc ggc aac gtt gtt cct gtt gag atc acc gtt tac gaa gac cgt tca 307  
 Arg Gly Asn Val Val Pro Val Glu Ile Thr Val Tyr Glu Asp Arg Ser  
                     55                    60                    65  
 ttc gac ttc aag ctg aag act cct cca gct gca aag ctt ctt ctg aag 355  
 Phe Asp Phe Lys Leu Lys Thr Pro Pro Ala Ala Lys Leu Leu Lys  
                     70                    75                    80                    85  
 gct gct ggc ctg cag aag ggc tcc ggc gtt cct cac acc cag aag gtc 403  
 Ala Ala Gly Leu Gln Lys Gly Ser Gly Val Pro His Thr Gln Lys Val  
                     90                    95                    100  
 ggc aag gtt tcc atg gct cag gtt cgt gag atc gct gag acc aag aag 451  
 Gly Lys Val Ser Met Ala Gln Val Arg Glu Ile Ala Glu Thr Lys Lys  
                     105                    110                    115  
 gaa gac ctg aac gct cgc gat atc gac gct gct gcg aag atc atc gct 499  
 Glu Asp Leu Asn Ala Arg Asp Ile Asp Ala Ala Ala Lys Ile Ile Ala  
                     120                    125                    130  
 ggt acc gct cgt tcc atg ggc atc acc gtc gaa ggc taaaagcttt 545  
 Gly Thr Ala Arg Ser Met Gly Ile Thr Val Glu Gly  
                     135                    140                    145  
 cacaccgggtt agt 558  
  
 <210> 310  
 <211> 145  
 <212> PRT  
 <213> Corynebacterium glutamicum  
  
 <400> 310  
 Met Ala Pro Lys Lys Lys Lys Lys Val Thr Gly Leu Ile Lys Leu Gln  
                     1                    5                    10                    15  
 Ile Gln Ala Gly Gln Ala Asn Pro Ala Pro Pro Val Gly Pro Ala Leu  
                     20                    25                    30  
 Gly Ala His Gly Val Asn Ile Met Glu Phe Cys Lys Ala Tyr Asn Ala  
                     35                    40                    45  
 Ala Thr Glu Asn Gln Arg Gly Asn Val Val Pro Val Glu Ile Thr Val  
                     50                    55                    60  
 Tyr Glu Asp Arg Ser Phe Asp Phe Lys Leu Lys Thr Pro Pro Ala Ala  
                     65                    70                    75                    80  
 Lys Leu Leu Leu Lys Ala Ala Gly Leu Gln Lys Gly Ser Gly Val Pro  
                     85                    90                    95

His Thr Gln Lys Val Gly Lys Val Ser Met Ala Gln Val Arg Glu Ile  
100 105 110

Ala Glu Thr Lys Lys Glu Asp Leu Asn Ala Arg Asp Ile Asp Ala Ala  
115 120 125

Ala Lys Ile Ile Ala Gly Thr Ala Arg Ser Met Gly Ile Thr Val Glu  
130 135 140

Gly  
145

<210> 311  
<211> 465  
<212> DNA  
<213> Corynebacterium glutamicum

<220>  
<221> CDS  
<222> (67) .. (465)  
<223> FRXA02826

<400> 311  
ccggacgggt tctagtgggg ttctatcgtc ccagttgtgg ccggtatacaa ggaagcaggt 60

ttaacgatg gct cct aag aag aag aag gtc act ggc ctc atc aag ctc 111  
Met Ala Pro Lys Lys Lys Lys Val Thr Gly Leu Ile Lys Leu  
1 5 10 15

cag atc cag gca gga cag gca aac cct gct cct cca gtt ggc cca gaa 159  
Gln Ile Gln Ala Gly Gln Ala Asn Pro Ala Pro Pro Val Gly Pro Glu  
20 25 30

ctt ggt gct cac ggc gtc aac atc atg gaa ttc tgc aag gct tac aac 207  
Leu Gly Ala His Gly Val Asn Ile Met Glu Phe Cys Lys Ala Tyr Asn  
35 40 45

gct gcg act gaa aac cag cgc ggg aac gtt gtt cct gtt gag atc acc 255  
Ala Ala Thr Glu Asn Gln Arg Gly Asn Val Val Pro Val Glu Ile Thr  
50 55 60

ggt tac gaa gac cgt tca ttc gac ttc aag ctg aag act cct cca gct 303  
Val Tyr Glu Asp Arg Ser Phe Asp Phe Lys Leu Lys Thr Pro Pro Ala  
65 70 75

gca aag ctt ctt ctg aaa gct gct ggc ctg cag aag ggc tcc ggc gtt 351  
Ala Lys Leu Leu Leu Lys Ala Ala Gly Leu Gln Lys Gly Ser Gly Val  
80 85 90 95

cct cac acc cag aag gtc ggc aag gtt tcc atg gct cag gtt cgt gag 399  
Pro His Thr Gln Lys Val Gly Lys Val Ser Met Ala Gln Val Arg Glu  
100 105 110

atc cct gcg acc aag aac gaa gac ctg acg ctc gcg ata tcg acg ctg 447  
Ile Pro Ala Thr Lys Asn Glu Asp Leu Thr Leu Ala Ile Ser Thr Leu  
115 120 125

ctg cga aga tca tcg ctg 465  
Leu Arg Arg Ser Ser Leu

130

&lt;210&gt; 312

&lt;211&gt; 133

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 312

Met Ala Pro Lys Lys Lys Lys Val Thr Gly Leu Ile Lys Leu Gln  
 1 5 10 15

Ile Gln Ala Gly Gln Ala Asn Pro Ala Pro Pro Val Gly Pro Glu Leu  
 20 25 30

Gly Ala His Gly Val Asn Ile Met Glu Phe Cys Lys Ala Tyr Asn Ala  
 35 40 45

Ala Thr Glu Asn Gln Arg Gly Asn Val Val Pro Val Glu Ile Thr Val  
 50 55 60

Tyr Glu Asp Arg Ser Phe Asp Phe Lys Leu Lys Thr Pro Pro Ala Ala  
 65 70 75 80

Lys Leu Leu Leu Lys Ala Ala Gly Leu Gln Lys Gly Ser Gly Val Pro  
 85 90 95

His Thr Gln Lys Val Gly Lys Val Ser Met Ala Gln Val Arg Glu Ile  
 100 105 110

Pro Ala Thr Lys Asn Glu Asp Leu Thr Leu Ala Ile Ser Thr Leu Leu  
 115 120 125

Arg Arg Ser Ser Leu  
 130

&lt;210&gt; 313

&lt;211&gt; 507

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(484)

&lt;223&gt; RXA01334

&lt;400&gt; 313

tccaggacaa gaaggacgca taagtcgcca ccaggcgac cagttttacc ccaaactttt 60

tcgagcgtgt taaacgctca acaacaggaa ggaatgccacc atg gct aag ctc acc 115  
 Met Ala Lys Leu Thr  
 1 5

aaa gac gag ctc atc gag gct ttc aag gaa atg acc ctc atc gag ctc 163  
 Lys Asp Glu Leu Ile Glu Ala Phe Lys Glu Met Thr Leu Ile Glu Leu  
 10 15 20

tcc gag ttc gtt aag gaa ttc gaa gag gtc ttc gac gta acc gca gct 211  
 Ser Glu Phe Val Lys Glu Phe Glu Glu Val Phe Asp Val Thr Ala Ala  
 25 30 35

gct cca gtt gca gtt gct gct gca ggc gct gca ggc ggc gaa gct gct 259  
Ala Pro Val Ala Val Ala Ala Ala Gly Ala Ala Gly Glu Ala Ala  
40 45 50

gct gca gaa gag aag gac gag ttc gac gtc gtt ctc gaa gac gca ggc 307  
Ala Ala Glu Glu Lys Asp Glu Phe Asp Val Val Leu Glu Asp Ala Gly  
55 60 65

gca aag aag atc ggc gtc atc aag gct gtc cgc gag ctc gtc tcc ggc 355  
Ala Lys Lys Ile Gly Val Ile Lys Ala Val Arg Glu Leu Val Ser Gly  
70 75 80 85

ctg ggc ctg aag gaa gca aag gag ctc gtt gag ggc gca cct aag gct 403  
Leu Gly Leu Lys Glu Ala Lys Glu Leu Val Glu Gly Ala Pro Lys Ala  
90 95 100

atc ctc gag ggc gca aac aag gac gac gct gag gct gca aag gct aag 451  
Ile Leu Glu Gly Ala Asn Lys Asp Asp Ala Glu Ala Ala Lys Ala Lys  
105 110 115

ctc gaa gag gct ggc gca aag gtc acc ctt aag taagaacttt cttacacctt 504  
Leu Glu Glu Ala Gly Ala Lys Val Thr Leu Lys  
120 125

ttc 507

<210> 314  
<211> 128  
<212> PRT  
<213> Corynebacterium glutamicum

<400> 314  
Met Ala Lys Leu Thr Lys Asp Glu Leu Ile Glu Ala Phe Lys Glu Met  
1 5 10 15  
Thr Leu Ile Glu Leu Ser Glu Phe Val Lys Glu Phe Glu Glu Val Phe  
20 25 30  
Asp Val Thr Ala Ala Ala Pro Val Ala Val Ala Ala Gly Ala Ala  
35 40 45  
Gly Gly Glu Ala Ala Ala Ala Glu Glu Lys Asp Glu Phe Asp Val Val  
50 55 60  
Leu Glu Asp Ala Gly Ala Lys Lys Ile Gly Val Ile Lys Ala Val Arg  
65 70 75 80  
Glu Leu Val Ser Gly Leu Gly Leu Lys Glu Ala Lys Glu Leu Val Glu  
85 90 95  
Gly Ala Pro Lys Ala Ile Leu Glu Gly Ala Asn Lys Asp Asp Ala Glu  
100 105 110  
Ala Ala Lys Ala Lys Leu Glu Glu Ala Gly Ala Lys Val Thr Leu Lys  
115 120 125



<210> 315  
 <211> 353  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (1)..(330)  
 <223> RXA02037

<400> 315  
 ggc aag ggc aag cct ttg tac gca cct aac gtt gac tgc ggc gac cac 48  
 Gly Lys Gly Lys Pro Leu Tyr Ala Pro Asn Val Asp Cys Gly Asp His  
 1 5 10 15  
 gta atc gtg atc aac gct gac aag gtt gca gtt acc tcc aac aag cgc 96  
 Val Ile Val Ile Asn Ala Asp Lys Val Ala Val Thr Ser Asn Lys Arg  
 20 25 30  
 gag cgc gaa atg cgt tac cgc cac tcc ggt tac cct ggt ggc ctg aag 144  
 Glu Arg Glu Met Arg Tyr Arg His Ser Gly Tyr Pro Gly Gly Leu Lys  
 35 40 45  
 tcc atg acc ctg ggt cgt tcc ctg gat ctg cac cca gag cgc acc atc 192  
 Ser Met Thr Leu Gly Arg Ser Leu Asp Leu His Pro Glu Arg Thr Ile  
 50 55 60  
 gag gat tcc atc gtc ggc atg atg cca cac aac aag ctg act gct gct 240  
 Glu Asp Ser Ile Val Gly Met Met Pro His Asn Lys Leu Thr Ala Ala  
 65 70 75 80  
 tcc gca aag aag ctg cac gtt ttc tcc ggc tcc gag cac cca tac gct 288  
 Ser Ala Lys Lys Leu His Val Phe Ser Gly Ser Glu His Pro Tyr Ala  
 85 90 95  
 gct cag aag cct gag gcc tac gag atc aag aag gtg gcc cag 330  
 Ala Gln Lys Pro Glu Ala Tyr Glu Ile Lys Lys Val Ala Gln  
 100 105 110  
 taatgtcaga gectatccag aac 353

<210> 316  
 <211> 110  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 316  
 Gly Lys Gly Lys Pro Leu Tyr Ala Pro Asn Val Asp Cys Gly Asp His  
 1 5 10 15  
 Val Ile Val Ile Asn Ala Asp Lys Val Ala Val Thr Ser Asn Lys Arg  
 20 25 30  
 Glu Arg Glu Met Arg Tyr Arg His Ser Gly Tyr Pro Gly Gly Leu Lys  
 35 40 45  
 Ser Met Thr Leu Gly Arg Ser Leu Asp Leu His Pro Glu Arg Thr Ile  
 50 55 60

Glu Asp Ser Ile Val Gly Met Met Pro His Asn Lys Leu Thr Ala Ala  
 65 70 75 80

Ser Ala Lys Lys Leu His Val Phe Ser Gly Ser Glu His Pro Tyr Ala  
 85 90 95

Ala Gln Lys Pro Glu Ala Tyr Glu Ile Lys Lys Val Ala Gln  
 100 105 110

<210> 317  
 <211> 567  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(544)  
 <223> RXA00699

<400> 317  
 ccacaccgtg atccgccccc ataccgccaga ggtacgtggc atgacccctgg cagttcgcca 60  
 cctgatcgtc gtcgaagaag tggcggggga gtaggtaaca atg agc gaa cca att 115  
 Met Ser Glu Pro Ile  
 1 5

aag etc cac gat ttg cgc cca gca gcg ggc tca aac aaa gct aag acc 163  
 Lys Leu His Asp Leu Arg Pro Ala Ala Gly Ser Asn Lys Ala Lys Thr  
 10 15 20

cgc gtt ggt cga ggc gaa gca tcc aag ggt aag act gca ggt cgc ggt 211  
 Arg Val Gly Arg Gly Glu Ala Ser Lys Gly Lys Thr Ala Gly Arg Gly  
 25 30 35

acc aag ggt acc aag gca cgc aag cag gtt tct gca gca ttc gaa ggt 259  
 Thr Lys Gly Thr Lys Ala Arg Lys Gln Val Ser Ala Ala Phe Glu Gly  
 40 45 50

ggc cag atg cca ctg cag atg cgt ctt cct aag ctg aag ggc ttc aag 307  
 Gly Gln Met Pro Leu Gln Met Arg Leu Pro Lys Leu Lys Gly Phe Lys  
 55 60 65

aac cct aac aag gtt gac tac cag gta gtt aac att gca gat ctc gca 355  
 Asn Pro Asn Lys Val Asp Tyr Gln Val Val Asn Ile Ala Asp Leu Ala  
 70 75 80 85

gag aag ttc cca cag ggc ggc gac gtc agc att gct gac atc gtt gca 403  
 Glu Lys Phe Pro Gln Gly Gly Asp Val Ser Ile Ala Asp Ile Val Ala  
 90 95 100

gca gga ctt gtc cgc aag aac gaa ctg gtt aag gtt ctt ggc aac ggc 451  
 Ala Gly Leu Val Arg Lys Asn Glu Leu Val Lys Val Leu Gly Asn Gly  
 105 110 115

gac atc agc gtc aag ctg aac gtc acc gct aac aag ttc tcc ggc tct 499  
 Asp Ile Ser Val Lys Leu Asn Val Thr Ala Asn Lys Phe Ser Gly Ser  
 120 125 130

gcc aag gaa aag atc gaa gcc gct ggc ggc tcc gca acc gtg gca 544  
 Ala Lys Glu Lys Ile Glu Ala Ala Gly Gly Ser Ala Thr Val Ala

135

140

145

taagttcacc agaactttaa aaa

567

&lt;210&gt; 318

&lt;211&gt; 148

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 318

Met Ser Glu Pro Ile Lys Leu His Asp Leu Arg Pro Ala Ala Gly Ser  
 1 5 10 15

Asn Lys Ala Lys Thr Arg Val Gly Arg Gly Glu Ala Ser Lys Gly Lys  
 20 25 30

Thr Ala Gly Arg Gly Thr Lys Gly Thr Lys Ala Arg Lys Gln Val Ser  
 35 40 45

Ala Ala Phe Glu Gly Gly Gln Met Pro Leu Gln Met Arg Leu Pro Lys  
 50 55 60

Leu Lys Gly Phe Lys Asn Pro Asn Lys Val Asp Tyr Gln Val Val Asn  
 65 70 75 80

Ile Ala Asp Leu Ala Glu Lys Phe Pro Gln Gly Gly Asp Val Ser Ile  
 85 90 95

Ala Asp Ile Val Ala Ala Gly Leu Val Arg Lys Asn Glu Leu Val Lys  
 100 105 110

Val Leu Gly Asn Gly Asp Ile Ser Val Lys Leu Asn Val Thr Ala Asn  
 115 120 125

Lys Phe Ser Gly Ser Ala Lys Glu Lys Ile Glu Ala Ala Gly Gly Ser  
 130 135 140

Ala Thr Val Ala  
 145

&lt;210&gt; 319

&lt;211&gt; 537

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(514)

&lt;223&gt; RXA02042

&lt;400&gt; 319

atgcacccgc agagcgctgc ggccgcggcg accgcaacgc acgtccgcgt cgtggtggcc 60

agcgtcgta cgtgctgag cagaagcagg agggctaaac atg ctt att cct aag 115  
 Met Leu Ile Pro Lys  
 1 5

cgc gtt aag tac cgt cgc cag cac cgt cct acc cgt agt ggt atc tcc 163  
 Arg Val Lys Tyr Arg Arg Gln His Arg Pro Thr Arg Ser Gly Ile Ser

10 15 20  
 aag ggc ggc aac cgc gtc act ttc ggt gag tac ggc atc cag gct ctc 211  
 Lys Gly Gly Ala Tyr 25 Phe Gly Glu Tyr Gly Ile Gln Ala Leu 35  
 gag cct gcc tac atc acc aac cgt cag att gaa tct gca cgt att gca 259  
 Glu Pro Ala Tyr 40 Ile Thr Asn Arg Gln Ile Glu Ser Ala Arg Ile Ala 50  
 atc aac cgc cac gtc agg cgt ggt ggc aag gtt tgg atc aac atc ttc 307  
 Ile Asn Arg His Val Arg Arg Gly Gly Lys Val Trp 60 Ile Asn Ile Phe 65  
 cca gac cgc cca ctg acc cag aag cca ctc ggc gtt cgt atg ggt tcc 355  
 Pro Asp Arg Pro Leu Thr Gln Lys Pro Leu Gly Val Arg Met Gly Ser 85  
 ggt aag ggc cct gtg gag aag tgg gtt gca aac atc aag ccg ggc cgt 403  
 Gly Lys Gly Pro Val Glu Lys Trp Val Ala Asn Ile Lys Pro Gly Arg 90 95 100  
 atc ctc ttc gag atg agc tac ccg gac gaa gct act gct ctc gag gct 451  
 Ile Leu Phe Glu Met Ser Tyr Pro Asp Glu Ala Thr Ala Leu Glu Ala 105 110 115  
 ctg cgc cgc gct ggc cag aag ctt cca tgc aag gtc cgt atc gtc aag 499  
 Leu Arg Arg Ala Gly Gln Lys Leu Pro Cys Lys Val Arg Ile Val Lys 120 125 130  
 agg gag gat cag ctc taatggctat cggtacccca gca 537  
 Arg Glu Asp Gln Leu 135  
 <210> 320  
 <211> 138  
 <212> PRT  
 <213> Corynebacterium glutamicum  
 <400> 320  
 Met Leu Ile Pro Lys Arg Val Lys Tyr Arg Arg Gln His Arg Pro Thr  
 1 5 10 15  
 Arg Ser Gly Ile Ser Lys Gly Gly Asn Arg Val Thr Phe Gly Glu Tyr  
 20 25 30  
 Gly Ile Gln Ala Leu Glu Pro Ala Tyr Ile Thr Asn Arg Gln Ile Glu  
 35 40 45  
 Ser Ala Arg Ile Ala Ile Asn Arg His Val Arg Arg Gly Gly Lys Val  
 50 55 60  
 Trp Ile Asn Ile Phe Pro Asp Arg Pro Leu Thr Gln Lys Pro Leu Gly  
 65 70 75 80  
 Val Arg Met Gly Ser Gly Lys Gly Pro Val Glu Lys Trp Val Ala Asn  
 85 90 95  
 Ile Lys Pro Gly Arg Ile Leu Phe Glu Met Ser Tyr Pro Asp Glu Ala  
 100 105 110

Thr Ala Leu Glu Ala Leu Arg Arg Ala Gly Gln Lys Leu Pro Cys Lys  
 115 120 125

Val Arg Ile Val Lys Arg Glu Asp Gln Leu  
 130 135

<210> 321

<211> 612

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(589)

<223> RXA00670

<400> 321

gaaactgggtg gctacatcga tgtcgaggcg gaagattccg agtaagtcgc atgggtccaat 60

tcattgggccc gcgtaaatca acgtacaagg agtacatcta atg cct acc cct aag 115  
 Met Pro Thr Pro Lys  
 1 5

aag ggc gcc cgc ctc ggc gga tcc gca agc cac cag aag aag atc ctc 163  
 Lys Gly Ala Arg Leu Gly Gly Ser Ala Ser His Gln Lys Lys Ile Leu  
 10 15 20

tct aac ctg gct gca tct ctg ttc gag cat ggc gca atc aag acc acc 211  
 Ser Asn Leu Ala Ala Ser Leu Phe Glu His Gly Ala Ile Lys Thr Thr  
 25 30 35

gat gct aag gca aag gct ctg cgt cca tac gct gag aag ctg atc acc 259  
 Asp Ala Lys Ala Lys Ala Leu Arg Pro Tyr Ala Glu Lys Leu Ile Thr  
 40 45 50

aag gct aag tcc ggt tcc gtt gca gat cgt cgt aac gtt ctc gca ctg 307  
 Lys Ala Lys Ser Gly Ser Val Ala Asp Arg Arg Asn Val Leu Ala Leu  
 55 60 65

gtt cct aac aag gaa atc gtg gct tac ctg ttc aac gaa ctt gct cct 355  
 Val Pro Asn Lys Glu Ile Val Ala Tyr Leu Phe Asn Glu Leu Ala Pro  
 70 75 80 85

aag ttc gag aac cgt cca ggt ggt tac acc cgc atc atc aag ctg gag 403  
 Lys Phe Glu Asn Arg Pro Gly Gly Tyr Thr Arg Ile Ile Lys Leu Glu  
 90 95 100

aac cgt aag ggc gac aac gct cct atg tcc cag atc tcc ctc gtt ctc 451  
 Asn Arg Lys Gly Asp Asn Ala Pro Met Ser Gln Ile Ser Leu Val Leu  
 105 110 115

gag gag acc gtc tcc gca gaa gca tcc cgc gca acc cgc gca tct gct 499  
 Glu Glu Thr Val Ser Ala Glu Ala Ser Arg Ala Thr Arg Ala Ser Ala  
 120 125 130

tcc aag aag gct gct gaa gag gct gag acc gaa gag gta gtc gag gct 547  
 Ser Lys Lys Ala Ala Glu Glu Ala Glu Thr Glu Glu Val Val Glu Ala  
 135 140 145

cca gct gag gag acc gca acc gaa gag gct gca gaa gag aag  
 Pro Ala Glu Glu Thr Ala Thr Glu Glu Ala Ala Glu Glu Lys  
 150 155 160

589

taaatttctc taactccgca tag

612

&lt;210&gt; 322

&lt;211&gt; 163

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 322

Met Pro Thr Pro Lys Lys Gly Ala Arg Leu Gly Gly Ser Ala Ser His  
 1 5 10 15

Gln Lys Lys Ile Leu Ser Asn Leu Ala Ala Ser Leu Phe Glu His Gly  
 20 25 30

Ala Ile Lys Thr Thr Asp Ala Lys Ala Lys Ala Leu Arg Pro Tyr Ala  
 35 40 45

Glu Lys Leu Ile Thr Lys Ala Lys Ser Gly Ser Val Ala Asp Arg Arg  
 50 55 60

Asn Val Leu Ala Leu Val Pro Asn Lys Glu Ile Val Ala Tyr Leu Phe  
 65 70 75 80

Asn Glu Leu Ala Pro Lys Phe Glu Asn Arg Pro Gly Gly Tyr Thr Arg  
 85 90 95

Ile Ile Lys Leu Glu Asn Arg Lys Gly Asp Asn Ala Pro Met Ser Gln  
 100 105 110

Ile Ser Leu Val Leu Glu Glu Thr Val Ser Ala Glu Ala Ser Arg Ala  
 115 120 125

Thr Arg Ala Ser Ala Ser Lys Lys Ala Ala Glu Glu Ala Glu Thr Glu  
 130 135 140

Glu Val Val Glu Ala Pro Ala Glu Glu Thr Ala Thr Glu Glu Ala Ala  
 145 150 155 160

Glu Glu Lys

&lt;210&gt; 323

&lt;211&gt; 525

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(502)

&lt;223&gt; RXA00696

&lt;400&gt; 323

gatccgccgc ctgcgtaagg acgatacctta caagggttaag ggcatccgct acgaggggtga 60

gcagatccgc cgcaaggtcg gaaagacggg taagtaagca atg agc aac act gaa 115

	Met	Ser	Asn	Thr	Glu	
	1				5	
aac aag cag aag cgc gtt tcc gtt ggc aag gac atc gcg act cgt cgt						163
Asn Lys Gln Lys Arg Val Ser Val Gly Lys Asp Ile Ala Thr Arg Arg						
			10		20	
cgc gtt gcc cgt gca cgc cgc cac ttc cgc atc cgc aag aac ctg cgt						211
Arg Val Ala Arg Ala Arg Arg His Phe Arg Ile Arg Lys Asn Leu Arg						
			25		35	
ggc acc cca gag gct cca cgt ttg gtt gtc cac cgc tct tct cgc cac						259
Gly Thr Pro Glu Ala Pro Arg Leu Val Val His Arg Ser Ser Arg His						
			40		50	
atg cac gtt cag atc atc gat gac gtt gca ggc cac acc ctg gct gca						307
Met His Val Gln Ile Ile Asp Asp Val Ala Gly His Thr Leu Ala Ala						
			55		65	
gct tct tcc atc gag gct gag gtt cgc gca act gag ggc gac aag aag						355
Ala Ser Ser Ile Glu Ala Glu Val Arg Ala Thr Glu Gly Asp Lys Lys						
			70		80	
gct aag ggc gca aag gtc ggt cag ctg atc gcc gag cgc gct aag gct						403
Ala Lys Gly Ala Lys Val Gly Gln Leu Ile Ala Glu Arg Ala Lys Ala						
			90		100	
gct ggt atc gag cag gtc gtc ttc gac cgc gct ggt tac aag tac cac						451
Ala Gly Ile Glu Gln Val Val Phe Asp Arg Ala Gly Tyr Lys Tyr His						
			105		115	
ggc cgc gtt gca gct ctc gct gac gcc gct cgt gaa ggt ggt ctg aaa						499
Gly Arg Val Ala Ala Leu Ala Asp Ala Arg Glu Gly Gly Leu Lys						
			120		130	
ttc taatgatgac catttctaag aac						525
Phe						

&lt;210&gt; 324

&lt;211&gt; 134

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 324

Met	Ser	Asn	Thr	Glu	Asn	Lys	Gln	Lys	Arg	Val	Ser	Val	Gly	Lys	Asp
1					5				10					15	

Ile	Ala	Thr	Arg	Arg	Val	Ala	Arg	Ala	Arg	Arg	His	Phe	Arg	Ile
			20				25					30		

Arg	Lys	Asn	Leu	Arg	Gly	Thr	Pro	Glu	Ala	Pro	Arg	Leu	Val	Val	His
	35					40						45			

Arg	Ser	Ser	Arg	His	Met	His	Val	Gln	Ile	Ile	Asp	Asp	Val	Ala	Gly
	50					55					60				

His	Thr	Leu	Ala	Ala	Ala	Ser	Ser	Ile	Glu	Ala	Glu	Val	Arg	Ala	Thr
	65					70				75				80	

Glu Gly Asp Lys Lys Ala Lys Gly Ala Lys Val Gly Gln Leu Ile Ala  
85 90 95

Glu Arg Ala Lys Ala Ala Gly Ile Glu Gln Val Val Phe Asp Arg Ala  
100 105 110

Gly Tyr Lys Tyr His Gly Arg Val Ala Ala Leu Ala Asp Ala Ala Arg  
115 120 125

Glu Gly Gly Leu Lys Phe  
130

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<210> 325
<211> 462
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (101)..(439)  
<223> RXA01353
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[illegible]



<210> 326  
 <211> 113  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 326  
 Met Asn Ile Leu Asp Lys Ile Asp Ala Ala Ser Leu Arg Asp Asp Val  
 1 5 10 15

Pro Ala Phe Arg Ala Gly Asp Thr Leu Asp Val His Val Lys Val Ile  
 20 25 30

Glu Gly Thr Thr Thr Arg Thr Gln Leu Phe Lys Gly Val Val Ile Arg  
 35 40 45

Arg Gln Gly Gly Gly Ile Arg Glu Thr Phe Thr Val Arg Lys Val Ser  
 50 55 60

Phe Gly Ile Gly Val Glu Arg Thr Phe Pro Val His Ser Pro Asn Ile  
 65 70 75 80

Glu Lys Ile Glu Val Ile Arg Arg Gly Asp Val Arg Arg Ala Lys Leu  
 85 90 95

Tyr Tyr Leu Arg Glu Leu Arg Gly Lys Ala Ala Arg Ile Lys Glu Lys  
 100 105 110

Arg

<210> 327  
 <211> 504  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(481)  
 <223> RXA02420

<400> 327  
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ccccccacc ttccaagaca agatttaagg aagtaccacc gtg gca cgt gtc aag 115  
 Val Ala Arg Val Lys  
 1 5

cgg tcc gtt aac gca aag aag aag cgt cgc gaa att ctg aag tcc gca 163  
 Arg Ser Val Asn Ala Lys Lys Lys Arg Arg Glu Ile Leu Lys Ser Ala  
 10 15 20

aag ggc tac cgc ggc cag cgc tca cgc ctt tac cgt aag gct aag gag 211  
 Lys Gly Tyr Arg Gly Gln Arg Ser Arg Leu Tyr Arg Lys Ala Lys Glu  
 25 30 35

cag tgg ctg cac tcc atg act tac tct tac cgc gat cgt cgc gcc cgt 259  
 Gln Trp Leu His Ser Met Thr Tyr Ser Tyr Arg Asp Arg Arg Ala Arg  
 40 45 50

aag agc gag ttc cgt aag ctg tgg atc cag cgt atc aac gct gct gca 307

Lys Ser Glu Phe Arg Lys Leu Trp Ile Gln Arg Ile Asn Ala Ala Ala  
 55 60 65 355  
 cgt atg aac ggc atc acc tac aac cgt ctc atc cag ggc ctt cgc ctt  
 Arg Met Asn Gly Ile Thr Tyr Asn Arg Leu Ile Gln Gly Leu Arg Leu  
 70 75 80 85  
 gct gag atc gag gtc gac cgc aag atc ctc gct gat ctc gca gtc aac 403  
 Ala Glu Ile Glu Val Asp Arg Lys Ile Leu Ala Asp Leu Ala Val Asn  
 90 95 100  
 gac ttt gca acc ttc tcc gca atc tgc gag gct gca aag gct gca ctt 451  
 Asp Phe Ala Thr Phe Ser Ala Ile Cys Glu Ala Ala Lys Ala Ala Leu  
 105 110 115  
 cct gag gac gtt aac gct cca aag gct gct taagcttaca aacgaattga 501  
 Pro Glu Asp Val Asn Ala Pro Lys Ala Ala  
 120 125  
 cct 504  
  
 <210> 328  
 <211> 127  
 <212> PRT  
 <213> Corynebacterium glutamicum  
  
 <400> 328  
 Val Ala Arg Val Lys Arg Ser Val Asn Ala Lys Lys Lys Arg Arg Glu  
 1 5 10 15  
 Ile Leu Lys Ser Ala Lys Gly Tyr Arg Gly Gln Arg Ser Arg Leu Tyr  
 20 25 30  
 Arg Lys Ala Lys Glu Gln Trp Leu His Ser Met Thr Tyr Ser Tyr Arg  
 35 40 45  
 Asp Arg Arg Ala Arg Lys Ser Glu Phe Arg Lys Leu Trp Ile Gln Arg  
 50 55 60  
 Ile Asn Ala Ala Ala Arg Met Asn Gly Ile Thr Tyr Asn Arg Leu Ile  
 65 70 75 80  
 Gln Gly Leu Arg Leu Ala Glu Ile Glu Val Asp Arg Lys Ile Leu Ala  
 85 90 95  
 Asp Leu Ala Val Asn Asp Phe Ala Thr Phe Ser Ala Ile Cys Glu Ala  
 100 105 110  
 Ala Lys Ala Ala Leu Pro Glu Asp Val Asn Ala Pro Lys Ala Ala  
 115 120 125  
  
 <210> 329  
 <211> 415  
 <212> DNA  
 <213> Corynebacterium glutamicum  
  
 <220>  
 <221> CDS  
 <222> (101)..(415)

&lt;223&gt; RXN02371

&lt;400&gt; 329

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cgagtacctg agccgagaat cagataaggg gtagccctct atg tac gcg atc gtc 115  
Met Tyr Ala Ile Val  
1 5

aag acc ggc gga aag cag tac aag gtt gcc gaa ggt gac ctc gtt aag 163  
Lys Thr Gly Gly Lys Lys Gln Tyr Lys Val Ala Glu Gly Asp Leu Val Lys  
10 15 20

gtc gag aag atc gag ggt gag ccg ggt gca tcc gtg gct ctc acc ccg 211  
Val Glu Lys Ile Glu Gly Glu Pro Gly Ala Ser Val Ala Leu Thr Pro  
25 30 35

gtt ctg ctc gtc gat ggc gcc gat gta acc acc gcc gct gac aag ctc 259  
Val Leu Leu Val Asp Gly Ala Asp Val Thr Thr Ala Ala Asp Lys Leu  
40 45 50

gct tct gtg agc gtc aac acc gag atc gtc gag cac acc aag ggc ccg 307  
Ala Ser Val Ser Val Asn Thr Glu Ile Val Glu His Thr Lys Gly Pro  
55 60 65

aag atc aag atc ctg aag tac aag aac aag acc gga tac aag aag cgc 355  
Lys Ile Lys Ile Leu Lys Tyr Lys Asn Lys Thr Gly Tyr Lys Lys Arg  
70 75 80 85

cag gga cac cgt cag ccc ctg acc gtt ctg aag gta acc gga aat caa 403  
Gln Gly His Arg Gln Pro Leu Thr Val Leu Lys Val Thr Gly Asn Gln  
90 95 100

gta agc cct cgg 415  
Val Ser Pro Arg  
105

&lt;210&gt; 330

&lt;211&gt; 105

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 330

Met Tyr Ala Ile Val Lys Thr Gly Gly Lys Gln Tyr Lys Val Ala Glu  
1 5 10 15

Gly Asp Leu Val Lys Val Glu Lys Ile Glu Gly Glu Pro Gly Ala Ser  
20 25 30

Val Ala Leu Thr Pro Val Leu Leu Val Asp Gly Ala Asp Val Thr Thr  
35 40 45

Ala Ala Asp Lys Leu Ala Ser Val Ser Val Asn Thr Glu Ile Val Glu  
50 55 60

His Thr Lys Gly Pro Lys Ile Lys Ile Leu Lys Tyr Lys Asn Lys Thr  
65 70 75 80

Gly Tyr Lys Lys Arg Gln Gly His Arg Gln Pro Leu Thr Val Leu Lys  
85 90 95

Val Thr Gly Asn Gln Val Ser Pro Arg  
100 105

<210> 331  
<211> 370  
<212> DNA  
<213> *Corynebacterium glutamicum*

<220>  
<221> CDS  
<222> (101)..(370)  
<223> FRXA02371

<400> 331  
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cgagtacctg agccgagaat cagataaggg gtagccctct atg tac gcg atc gtc 115  
Met Tyr Ala Ile Val  
1 5  
aag acc ggc gga aag cag tac aag gtt gcc gaa ggt gac etc gtt aag 163  
Lys Thr Gly Gly Lys Gln Tyr Lys Val Ala Glu Gly Asp Leu Val Lys  
10 15 20  
gtc gag aag atc gag ggt gag ccg ggt gca tcc gtg gct etc acc ccg 211  
Val Glu Lys Ile Glu Gly Glu Pro Gly Ala Ser Val Ala Leu Thr Pro  
25 30 35  
gtt ctg etc gtc gat ggc gcc gat gta acc acc gcc gct gac aag etc 259  
Val Leu Leu Val Asp Gly Ala Asp Val Thr Thr Ala Ala Asp Lys Leu  
40 45 50  
gct tct gtg agc gtc aac acc gag atc gtc gag cac acc aag ggc ccg 307  
Ala Ser Val Ser Val Asn Thr Glu Ile Val Glu His Thr Lys Gly Pro  
55 60 65  
aag atc aag atc ctg aag tac aag aac aag acc gga tac aag aag cgc 355  
Lys Ile Lys Ile Leu Lys Tyr Lys Asn Lys Thr Gly Tyr Lys Lys Arg  
70 75 80 85  
cag gga cac cgt cag 370  
Gln Gly His Arg Gln  
90

<210> 332  
<211> 90  
<212> PRT  
<213> *Corynebacterium glutamicum*

<400> 332  
Met Tyr Ala Ile Val Lys Thr Gly Gly Lys Gln Tyr Lys Val Ala Glu  
1 5 10 15  
Gly Asp Leu Val Lys Val Glu Lys Ile Glu Gly Glu Pro Gly Ala Ser  
20 25 30  
Val Ala Leu Thr Pro Val Leu Leu Val Asp Gly Ala Asp Val Thr Thr  
35 40 45

Ala Ala Asp Lys Leu Ala Ser Val Ser Val Asn Thr Glu Ile Val Glu  
50 55 60

His Thr Lys Gly Pro Lys Ile Lys Ile Leu Lys Tyr Lys Asn Lys Thr  
65 70 75 80

Gly Tyr Lys Lys Arg Gln Gly His Arg Gln  
85 90

<210> 333

<211> 426

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101) .. (403)

<223> RXA01949

<400> 333

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tcaaccgcgc ttccgggtgcg gcacaggagg agcagaacta atg gct act atc gcc 115  
Met Ala Thr Ile Ala  
1 5

aac cca cgc gac atc atc atc gca cgc gtc gtt tct gag aag tcc tac 163  
Asn Pro Arg Asp Ile Ile Ile Ala Pro Val Val Ser Glu Lys Ser Tyr  
10 15 20

ggc ctc atg gag cag aac gtt tac acg ttc ttc gtc tcc act gac gct 211  
Gly Leu Met Glu Gln Asn Val Tyr Thr Phe Phe Val Ser Thr Asp Ala  
25 30 35

aac aag act cag atc aag att gcc atc gaa gag atc ttc ggc gtc aag 259  
Asn Lys Thr Gln Ile Lys Ile Ala Ile Glu Glu Ile Phe Gly Val Lys  
40 45 50

gtt gca tct gtg aac acc gtt aac cgt gca ggt aag cgc aag cgc tcc 307  
Val Ala Ser Val Asn Thr Val Asn Arg Ala Gly Lys Arg Lys Arg Ser  
55 60 65

cgc acc ggc ttc ggt act cgc aag gct acc aag cgc gct tat gtg act 355  
Arg Thr Gly Phe Gly Thr Arg Lys Ala Thr Lys Arg Ala Tyr Val Thr  
70 75 80 85

ctt cgc gaa ggc agc gac tcc atc gac atc ttc agc ggc tcc gtc gct 403  
Leu Arg Glu Gly Ser Asp Ser Ile Asp Ile Phe Ser Gly Ser Val Ala  
90 95 100

taagacgtcg atagaaaagg aca 426

<210> 334

<211> 101

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 334

Met Ala Thr Ile Ala Asn Pro Arg Asp Ile Ile Ile Ala Pro Val Val  
 1 5 10 15  
 Ser Glu Lys Ser Tyr Gly Leu Met Glu Gln Asn Val Tyr Thr Phe Phe  
 20 25 30  
 Val Ser Thr Asp Ala Asn Lys Thr Gln Ile Lys Ile Ala Ile Glu Glu  
 35 40 45  
 Ile Phe Gly Val Lys Val Ala Ser Val Asn Thr Val Asn Arg Ala Gly  
 50 55 60  
 Lys Arg Lys Arg Ser Arg Thr Gly Phe Gly Thr Arg Lys Ala Thr Lys  
 65 70 75 80  
 Arg Ala Tyr Val Thr Leu Arg Glu Gly Ser Asp Ser Ile Asp Ile Phe  
 85 90 95  
 Ser Gly Ser Val Ala  
 100

<210> 335  
 <211> 489  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(466)  
 <223> RXN00709

<400> 335  
 ttgccacat tcgtggagta tgtagacatc tgtagtacaa agaccacgcg tgtttgggac 60  
 ggaaatccag cagcattaa tccaggtcag gagaccagta gtg att cag cag gaa 115  
 Val Ile Gln Gln Glu 5  
 1  
 tcg cgt ctg aag gtc gcc gac aac act ggt gca cgt gaa att ctg tgc 163  
 Ser Arg Leu Lys Val Ala Asp Asn Thr Gly Ala Arg Glu Ile Leu Cys 20  
 10 15  
 atc cgc gtt ctg ggt gga tcc acc cga cgt ttt gct ggc att ggt gac 211  
 Ile Arg Val Leu Gly Gly Ser Thr Arg Arg Phe Ala Gly Ile Gly Asp 35  
 25 30  
 gtc atc gtc gcc act gtc aag gaa gca acc cca ggc ggc aac gta aag 259  
 Val Ile Val Ala Thr Val Lys Glu Ala Thr Pro Gly Gly Asn Val Lys 50  
 40 45  
 tct ggc gaa atc gtc aag gct gtt atc gtt cgc acc aag aag gag acc 307  
 Ser Gly Glu Ile Val Lys Ala Val Ile Val Arg Thr Lys Lys Glu Thr 65  
 55 60  
 cgt cgt gca gac ggt tct tac atc tcc ttc gat gag aac gct gcc gtc 355  
 Arg Arg Ala Asp Gly Ser Tyr Ile Ser Phe Asp Glu Asn Ala Ala Val 85  
 70 75 80  
 atc atc aag aac gac aac gag cca cgt ggc acc cgt atc ttc gga cca 403  
 Ile Ile Lys Asn Asp Asn Glu Pro Arg Gly Thr Arg Ile Phe Gly Pro

	90	95	100	
gtt gct cgt gaa ctt cgt gag aag aag ttc atg aag atc gtt tct ctc				451
Val Ala Arg Glu Leu Arg Glu Lys Lys Phe Met Lys Ile Val Ser Leu				
	105	110	115	

gca ccg gag gtg att taagaatgaa ggtccacaag ggc		489
Ala Pro Glu Val Ile		
	120	

&lt;210&gt; 336

&lt;211&gt; 122

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 336

Val Ile Gln Gln Glu Ser Arg Leu Lys Val Ala Asp Asn Thr Gly Ala		
	1	15

Arg Glu Ile Leu Cys Ile Arg Val Leu Gly Gly Ser Thr Arg Arg Phe		
	20	30

Ala Gly Ile Gly Asp Val Ile Val Ala Thr Val Lys Glu Ala Thr Pro		
	35	45

Gly Gly Asn Val Lys Ser Gly Glu Ile Val Lys Ala Val Ile Val Arg		
	50	60

Thr Lys Lys Glu Thr Arg Arg Ala Asp Gly Ser Tyr Ile Ser Phe Asp		
	65	80

Glu Asn Ala Ala Val Ile Ile Lys Asn Asp Asn Glu Pro Arg Gly Thr		
	85	95

Arg Ile Phe Gly Pro Val Ala Arg Glu Leu Arg Glu Lys Lys Phe Met		
	100	110

Lys Ile Val Ser Leu Ala Pro Glu Val Ile	
	115 120

&lt;210&gt; 337

&lt;211&gt; 362

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(339)

&lt;223&gt; PRXA00709

&lt;400&gt; 337

gtc gcc gac aac act ggt gca cgt gaa att ctg tgc atc cgc gtt ctc		48
Val Ala Asp Asn Thr Gly Ala Arg Glu Ile Leu Cys Ile Arg Val Leu		
	1	15

ggg gga tcc acc cga cgt ttt gct ggc att ggt gac gtc atc gtc gcc		96
Gly Gly Ser Thr Arg Arg Phe Ala Gly Ile Gly Asp Val Ile Val Ala		
	20	30

act gtc aag gaa gca acc cca ggc ggc aac gta aag tct ggc gaa atc 144  
 Thr Val Lys Glu Ala Thr Pro Gly Gly Asn Val Lys Ser Gly Glu Ile  
           35                          40                          45

gtc aag gct gtt atc gtt cgc acc aag aag gag acc cgt cgt gca gac 192  
 Val Lys Ala Val Ile Val Arg Thr Lys Lys Glu Thr Arg Arg Ala Asp  
           50                          55                          60

ggt tct tac atc tcc ttc gat gag aac gct gcc gtc atc atc aag aac 240  
 Gly Ser Tyr Ile Ser Phe Asp Glu Asn Ala Ala Val Ile Ile Lys Asn  
           65                          70                          75                          80

gac aac gag cca cgt ggc acc cgt atc ttc gga cca gtt gct cgt gaa 288  
 Asp Asn Glu Pro Arg Gly Thr Arg Ile Phe Gly Pro Val Ala Arg Glu  
                           85                          90                          95

ctt cgt gag aag aag ttc atg aag atc gtt tct ctc gca ccg gag gtg 336  
 Leu Arg Glu Lys Lys Phe Met Lys Ile Val Ser Leu Ala Pro Glu Val  
                           100                          105                          110

att taagaatgaa ggtccacaag ggc 362  
 Ile

<210> 338  
 <211> 113  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 338  
 Val Ala Asp Asn Thr Gly Ala Arg Glu Ile Leu Cys Ile Arg Val Leu  
   1                          5                          10                          15

Gly Gly Ser Thr Arg Arg Phe Ala Gly Ile Gly Asp Val Ile Val Ala  
                           20                          25                          30

Thr Val Lys Glu Ala Thr Pro Gly Gly Asn Val Lys Ser Gly Glu Ile  
           35                          40                          45

Val Lys Ala Val Ile Val Arg Thr Lys Lys Glu Thr Arg Arg Ala Asp  
           50                          55                          60

Gly Ser Tyr Ile Ser Phe Asp Glu Asn Ala Ala Val Ile Ile Lys Asn  
           65                          70                          75                          80

Asp Asn Glu Pro Arg Gly Thr Arg Ile Phe Gly Pro Val Ala Arg Glu  
                           85                          90                          95

Leu Arg Glu Lys Lys Phe Met Lys Ile Val Ser Leu Ala Pro Glu Val  
                           100                          105                          110

Ile

<210> 339  
 <211> 435  
 <212> DNA  
 <213> Corynebacterium glutamicum



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<220>  
<221> CDS  
<222> (101)..(412)  
<223> RXA00710
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[illegible]

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<210> 340
<211> 104
<212> PRT
<213> Corynebacterium glutamicum
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400> 340
Met Lys Val His Lys Gly Asp Met Val Leu Val Ile Ser Gly Pro Asp
  1          5          10          15
Lys Gly Ala Lys Gly Gln Val Ile Ala Ala Phe Pro Lys Thr Glu Lys
      20          25          30
Val Leu Val Glu Gly Val Asn Arg Ile Lys Lys His Val Ala Asn Ser
      35          40          45
Ala Pro Glu Arg Gly Ala Glu Ser Gly Gly Ile Val Thr Gln Glu Ala
      50          55          60
Pro Ile His Val Ser Asn Val Met Val Ile Asp Ser Asp Gly Asn Pro
  65          70          75          80

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Thr Arg Val Gly Tyr Arg Phe Asp Glu Asn Gly Lys Lys Val Arg Val  
                     85                    90                    95

Ser Arg Arg Asn Gly Lys Asp Ile  
                     100

<210> 341  
 <211> 357  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(334)  
 <223> RXA02635

<400> 341  
 aaatattcgt tategccccc tcagctggca tgctcgcgcc cgggtcaccc ggtgcggcgc 60  
 gtcttctaac tgaatgtggg cggctaggag aaagtaagtt atg tcg gca cat tgc 115  
   Met Ser Ala His Cys  
   1                    5  
 cag gta acg gga cgc aag ccg agt ttc ggc aag tet gtc tca cac tcg 163  
 Gln Val Thr Gly Arg Lys Pro Ser Phe Gly Lys Ser Val Ser His Ser  
                             10                            15                            20  
 cac cga cgc act tcc cgc cgt tgg aac ccc aac gtg cag cgt cgc aag 211  
 His Arg Arg Thr Ser Arg Arg Trp Asn Pro Asn Val Gln Arg Arg Lys  
                             25                            30                            35  
 ttc tat gtc cct tcc gag gga cgc acc atc act ctg acc gtt tcc acc 259  
 Phe Tyr Val Pro Ser Glu Gly Arg Thr Ile Thr Leu Thr Val Ser Thr  
                             40                            45                            50  
 aag ggt ctg aag gtc att gac cgc gac ggc atc gaa gcc gtt gtt gct 307  
 Lys Gly Leu Lys Val Ile Asp Arg Asp Gly Ile Glu Ala Val Val Ala  
                             55                            60                            65  
 cag att cgc gca cgt ggg gag aag atc taaagatggc acgtaatgat 354  
 Gln Ile Arg Ala Arg Gly Glu Lys Ile  
                             70                            75  
 atc 357

<210> 342  
 <211> 78  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 342  
 Met Ser Ala His Cys Gln Val Thr Gly Arg Lys Pro Ser Phe Gly Lys  
                     1                    5                    10                    15  
 Ser Val Ser His Ser His Arg Arg Thr Ser Arg Arg Trp Asn Pro Asn  
                     20                    25                    30  
 Val Gln Arg Arg Lys Phe Tyr Val Pro Ser Glu Gly Arg Thr Ile Thr



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<221> CDS
<222> (101)..(283)
<223> RXA00698
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<400> 345  
ggtccgcctt gaagaggttg cagccccgctg tggcaagacc atcgaagagg tcgcaccagc 60

acgtattctg cgtgcacgcg caggtcagga ggcgtaagaa atg gcg ctg aag att 115  
Met Ala Leu Lys Ile  
1 5

act cag atc aaa ggc act gtg ggc acc aag ccc aag cat cgc gaa aat 163  
Thr Gln Ile Lys Gly Thr Val Gly Thr Lys Pro Lys His Arg Glu Asn  
10 15 20

ctt cgt tcc ctg ggt ctg aag cga atc cgc cac acc gtg atc cgc ccc      211  
Leu Arg Ser Leu Gly Leu Lys Arg Ile Arg His Thr Val Ile Arg Pro

25                          30                          35

gat acc cca gag gta cgt ggc atg atc ctg gca gtt cgc cac ctg atc 259  
Asp Thr Pro Glu Val Arg Gly Met Ile Leu Ala Val Arg His Leu Ile  
40 45 50

gtc gtc gaa gaa gtg gcg ggg gag taggtaacaa tgagcgaacc aat 306  
Val Val Glu Glu Val Ala Gly Glu  
55 60

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<210> 346
<211> 61
<212> PRT
<213> Corynebacterium glutamicum
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```
<400> 346
Met Ala Leu Lys Ile Thr Gln Ile Lys Gly Thr Val Gly Thr Lys Pro
  1             5             10             15
```

Lys His Arg Glu Asn Leu Arg Ser Leu Gly Leu Lys Arg Ile Arg His  
20 25 30

Thr Val Ile Arg Pro Asp Thr Pro Glu Val Arg Gly Met Ile Leu Ala  
35 40 45

Val Arg His Leu Ile Val Val Glu Glu Val Ala Gly Glu  
50 55 60

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<210> 347
<211> 387
<212> DNA
<213> Corynebacterium glutamicum
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<220>
<221> CDS
<222> (101) .. (364)
<223> RXA02633
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<400> 347  
ccaaatcatg gtgatgcata cttaccgaac ccaactcggg cactgatctgg catccgctgg 60

aaccgacctg aagtttcaat cctgaggga tgcgagagtaa atg aaa aag gat atc 115

Met Lys Lys Asp Ile  
1 5

cac cct gac tac cat gcg gta gtc ttc cag gac gca ggt act ggc ttc 163  
His Pro Asp Tyr His Ala Val Val Phe Gln Asp Ala Gly Thr Gly Phe  
10 15 20

cag ttc ctg acc aag tcc acc gct tcc agc gac cgc acc gtg tcc tgg 211  
Gln Phe Leu Thr Lys Ser Thr Ala Ser Ser Asp Arg Thr Val Ser Trp  
25 30 35

gaa gat ggt aac gag tac cca ctg atc gtc gtt gac gtc acc agc gag 259  
Glu Asp Gly Asn Glu Tyr Pro Leu Ile Val Val Asp Val Thr Ser Glu  
40 45 50

tct cac cca ttc tgg acc ggc gct cag cgt gtc atg gac acc gct ggt 307  
Ser His Pro Phe Trp Thr Gly Ala Gln Arg Val Met Asp Thr Ala Gly  
55 60 65

cgt gtt gag aag ttc gag cgt cgc ttc ggt ggc atg gct cgc cgc aag 355  
Arg Val Glu Lys Phe Glu Arg Arg Phe Gly Gly Met Ala Arg Arg Lys  
70 75 80 85

aag aag gca taggaggaa aacaatggca gtt 387  
Lys Lys Ala

<210> 348

<211> 88

<212> PRT

<213> Corynebacterium glutamicum

<400> 348

Met Lys Lys Asp Ile His Pro Asp Tyr His Ala Val Val Phe Gln Asp  
1 5 10 15

Ala Gly Thr Gly Phe Gln Phe Leu Thr Lys Ser Thr Ala Ser Ser Asp  
20 25 30

Arg Thr Val Ser Trp Glu Asp Gly Asn Glu Tyr Pro Leu Ile Val Val  
35 40 45

Asp Val Thr Ser Glu Ser His Pro Phe Trp Thr Gly Ala Gln Arg Val  
50 55 60

Met Asp Thr Ala Gly Arg Val Glu Lys Phe Glu Arg Arg Phe Gly Gly  
65 70 75 80

Met Ala Arg Arg Lys Lys Lys Ala  
85

<210> 349

<211> 285

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(262)

&lt;223&gt; RXA02636

&lt;400&gt; 349

tcactctgac cgtttccacc aaggggtctga aggtcattga ccgcgacggc atcgaagccg 60

ttgtgtctca gattcgcgca cgtggggaga agatctaaag atg gca cgt aat gat 115  
 Met Ala Arg Asn Asp  
 1 5

atc cgc cct atc atc aag ctg aag tct act gct ggc act ggt tac acc 163  
 Ile Arg Pro Ile Ile Lys Leu Lys Ser Thr Ala Gly Thr Gly Tyr Thr  
 10 15 20

tat gtc acc cgt aag aac aag cgc aac aac ccg gac cgt att tcc etc 211  
 Tyr Val Thr Arg Lys Asn Lys Arg Asn Asn Pro Asp Arg Ile Ser Leu  
 25 30 35

atg aag tac gat cca gta gtc cgt aag cac gtc gaa ttc cgc gag gag 259  
 Met Lys Tyr Asp Pro Val Val Arg Lys His Val Glu Phe Arg Glu Glu  
 40 45 50

cga taatcaatgg ctaagaagtc aaa 285  
 Arg

&lt;210&gt; 350

&lt;211&gt; 54

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 350

Met Ala Arg Asn Asp Ile Arg Pro Ile Ile Lys Leu Lys Ser Thr Ala  
 1 5 10 15

Gly Thr Gly Tyr Thr Tyr Val Thr Arg Lys Asn Lys Arg Asn Asn Pro  
 20 25 30

Asp Arg Ile Ser Leu Met Lys Tyr Asp Pro Val Val Arg Lys His Val  
 35 40 45

Glu Phe Arg Glu Glu Arg  
 50

&lt;210&gt; 351

&lt;211&gt; 264

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(241)

&lt;223&gt; RXA01423

&lt;400&gt; 351

ttcccccggt atagggttag cgcggaatc ttgcgcact ttgtccacta gaaccggtgt 60

gtccgggtgat ccgtcaacaa aatatctagg agtgtttcac atg gca aag ggc aag 115  
 Met Ala Lys Gly Lys  
 1 5

cgg acg ttc cag ccg aac aac cgt cgt cgt gca cgt gtt cac ggt ttc      163  
Arg Thr Phe Gln Pro Asn Asn Arg Arg Arg Ala Arg Val His Gly Phe  
                10                       15                              20

cgt ctt cgt atg cgt acc cgt gca ggt cgt gca att gtt gcg gct cgt 211  
Arg Leu Arg Met Arg Thr Arg Ala Gly Arg Ala Ile Val Ala Ala Arg  
25 30 35

cgt cgc aag ggt cgc gca aag ctg acc gcg taatttttta gcgtcaccac 261  
Arg Arg Lys Gly Arg Ala Lys Leu Thr Ala  
40 45

aat 264

<210> 352

<211> 47

<212> PRT

<213> Corynebacterium glutamicum

<400> 352

Met Ala Lys Gly Lys Arg Thr Phe Gln Pro Asn Asn Arg Arg Arg Ala  
1 5 10 15

Arg Val His Gly Phe Arg Leu Arg Met Arg Thr Arg Ala Gly Arg Ala  
20 25 30

Ile Val Ala Ala Arg Arg Arg Lys Gly Arg Ala Lys Leu Thr Ala  
35 40 45

&lt;210&gt; 353

<211> 315

<212> DNA

<213> *Corynebacterium glutamicum*

 $\langle 220 \rangle$ 

<221> CDS

<222> (101) . . (292)

<223> RXA02419

<400> 353

gaaacccgcg caaagcagga cggacgaaac atgacaatgg ttctcgggtcc ggtgcgcaag 60

ggcaagaaat aatcacgaat aggggtttaag gacaactttc atg aag aac aag acc 115  
Met Lys Asn Lys Thr  
1 5

cac aag ggc acc gca aag cgc gtt aag gtg act ggc tcc ggc aag ctg    163  
His Lys Gly Thr Ala Lys Arg Val Lys Val Thr Gly Ser Gly Lys Leu  
                10                    15                    20

gtt cgc gag cag gca aac cgc cgc cac ctt ctc gag ggc aag tca tct 211  
Val Arg Glu Gln Ala Asn Arg Arg His Leu Leu Glu Gly Lys Ser Ser  
25 30 35

acc cgc act cgt cgc ctg aag ggc atc gtt gag gtt gac aag gcc gac 259  
Thr Arg Thr Arg Arg Leu Lys Gly Ile Val Glu Val Asp Lys Ala Asp  
40 45 50

acc aag cgc atg aag cgc ctg ctc ggc aag gct taagtttaaa accttcgcct 312  
 Thr Lys Arg Met Lys Arg Leu Leu Gly Lys Ala  
 55 60

aaa

315

&lt;210&gt; 354

&lt;211&gt; 64

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 354

Met Lys Asn Lys Thr His Lys Gly Thr Ala Lys Arg Val Lys Val Thr  
 1 5 10 15

Gly Ser Gly Lys Lys Leu Val Arg Glu Gln Ala Asn Arg Arg His Leu Leu  
 20 25 30

Glu Gly Lys Ser Ser Thr Arg Thr Arg Arg Leu Lys Gly Ile Val Glu  
 35 40 45

Val Asp Lys Ala Asp Thr Lys Arg Met Lys Arg Leu Leu Gly Lys Ala  
 50 55 60

&lt;210&gt; 355

&lt;211&gt; 1581

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1558)

&lt;223&gt; RXA02190

&lt;400&gt; 355

gcctgaacgt gagatcaaaa ccccgctctat acaggggcatt tgaaagatac tgcattcctgt 60

ccattatccta atttctctatc catttcggag caattttacat atg ccc acc aac aat 115  
 Met Pro Thr Asn Asn  
 1 5

gca cct cag gta gcc atc aac gac att ggc tct gct gag gac ttc ctt 163  
 Ala Pro Gln Val Ala Ile Asn Asp Ile Gly Ser Ala Glu Asp Phe Leu  
 10 15 20

gca gca atc gac gca acc atc aag tac ttc aac gat ggc gat atc gtt 211  
 Ala Ala Ile Asp Ala Thr Ile Lys Tyr Phe Asn Asp Gly Asp Ile Val  
 25 30 35

gaa ggc acc gtg gta aag gtc gat cgt gac gag gta ctt etc gac atc 259  
 Glu Gly Thr Val Val Lys Val Asp Arg Asp Glu Val Leu Leu Asp Ile  
 40 45 50

gga tac aag acc gag ggt gtc atc cca tcc cgc gag ctg tcc atc aag 307  
 Gly Tyr Lys Thr Glu Gly Val Ile Pro Ser Arg Glu Leu Ser Ile Lys  
 55 60 65



cac gat gtc gat cca gac gag gtc gtc gaa gtc ggc gac caa att gac 355  
 His Asp Val Asp Pro Asp Glu Val Val Glu Val Gly Asp Gln Ile Asp  
 70 75 80 85

gca ctt gtc ctc acc aag gaa gac aaa gaa ggt cgt ctg atc ctt tcc 403  
 Ala Leu Val Leu Thr Lys Glu Asp Lys Glu Gly Arg Leu Ile Leu Ser  
 90 95 100

aag aag cgt gct cag tac gag cgt gct tgg ggc gcc atc gag gag ctc 451  
 Lys Lys Arg Ala Gln Tyr Glu Arg Ala Trp Gly Ala Ile Glu Glu Leu  
 105 110 115

aag gaa aag gac gag cca gtt acc ggt acc gtc atc gag gtc gtc aag 499  
 Lys Glu Lys Asp Glu Pro Val Thr Gly Thr Val Ile Glu Val Val Lys  
 120 125 130

ggt ggc ctc atc atc gac atc ggt ctc cgt ggc ttc ctg cct gca tcc 547  
 Gly Gly Leu Ile Ile Asp Ile Gly Leu Arg Gly Phe Leu Pro Ala Ser  
 135 140 145

ctc gtt gag atg cgt cgc gtc cgc gac ctg gat ccg tac atc ggc cag 595  
 Leu Val Glu Met Arg Arg Val Arg Asp Leu Asp Pro Tyr Ile Gly Gln  
 150 155 160 165

gag ctc gaa gct aag atc atc gag ctg gac aag aac cgc aac aac gtc 643  
 Glu Leu Glu Ala Lys Ile Ile Glu Leu Asp Lys Asn Arg Asn Asn Val  
 170 175 180

gtt ctg tcc cgt cgc gca ttc ctc gag cag acc cag tct gag gtc cgc 691  
 Val Leu Ser Arg Arg Ala Phe Leu Glu Gln Thr Gln Ser Glu Val Arg  
 185 190 195

tcc gag ttc ctg cac cag ctc cag aag ggc cag gtc cgc aag ggc gtc 739  
 Ser Glu Phe Leu His Gln Leu Gln Lys Gly Gln Val Arg Lys Gly Val  
 200 205 210

gtc tct tcc atc gtc aac ttc ggc gca ttc gtc gat ctc ggc ggt gtc 787  
 Val Ser Ser Ile Val Asn Phe Gly Ala Phe Val Asp Leu Gly Gly Val  
 215 220 225

gac gga ctg gtt cac gtt tcc gag ctg tcc tgg aag cac atc gac cac 835  
 Asp Gly Leu Val His Val Ser Glu Leu Ser Trp Lys His Ile Asp His  
 230 235 240 245

cca tct gag gtt gtc acc gtc ggc gac gaa gtc acc gtt gag gtt ctc 883  
 Pro Ser Glu Val Val Thr Val Gly Asp Glu Val Thr Val Glu Val Leu  
 250 255 260

gag gtc gat ctc gac cgc gag cgc gtc tcc ctg tcc ctg aag gct acc 931  
 Glu Val Asp Leu Asp Arg Glu Arg Val Ser Leu Ser Leu Lys Ala Thr  
 265 270 275

cag gaa gac cca tgg cgc gtc ttc gct cgc act cac gct gtc ggc cag 979  
 Gln Glu Asp Pro Trp Arg Val Phe Ala Arg Thr His Ala Val Gly Gln  
 280 285 290

atc gtt cca ggc aag gtc acc aag ctg gtt cca ttc ggt cgc ttc gtt 1027  
 Ile Val Pro Gly Lys Val Thr Lys Leu Val Pro Phe Gly Ala Phe Val  
 295 300 305

cgc gtc gaa gag ggc atc gaa ggc ctc gtc cac atc tcc gag ctg gct 1075  
 Arg Val Glu Glu Gly Ile Glu Gly Leu Val His Ile Ser Glu Leu Ala 325  
 310 315 320

cag cgc cac gtc gag gtt ccg gac cag gtt gtc gca gtt ggc gaa gag 1123  
 Gln Arg His Val Glu Val Pro Asp Gln Val Val Ala Val Gly Glu Glu 340  
 330 335

gtc atg gtc aag gtc atc gac atc gat ctc gag cgt cgt cgt atc tcc 1171  
 Val Met Val Lys Val Ile Asp Ile Asp Leu Glu Arg Arg Arg Ile Ser 355  
 345 350

ctg tcc ctc aag cag gct gac gag gac tac acc gaa gag ttc gac cca 1219  
 Leu Ser Leu Lys Gln Ala Asp Glu Asp Tyr Thr Glu Glu Phe Asp Pro 370  
 360 365

tcc aag tac gga atg gct gac tcc tac gac gag cag ggt aac tac atc 1267  
 Ser Lys Tyr Gly Met Ala Asp Ser Tyr Asp Glu Gln Gly Asn Tyr Ile 385  
 375 380

ttc cct gag ggc ttc gac gcc gag acc aac gaa tgg ctc gaa ggc ttc 1315  
 Phe Pro Glu Gly Phe Asp Ala Glu Thr Asn Glu Trp Leu Glu Gly Phe 405  
 390 395 400

gat gag cag cgt cag gct tgg gaa gct cgc tac gcc gag tcc gag cgt 1363  
 Asp Glu Gln Arg Gln Ala Trp Glu Ala Arg Tyr Ala Glu Ser Glu Arg 420  
 410 415

cgc ttc acc gct cac acc gct cag atc gag cgt cgt cgt cag cag gct 1411  
 Arg Phe Thr Ala His Thr Ala Gln Ile Glu Arg Arg Arg Gln Gln Ala 435  
 425 430

gaa gag gca gct gcc gag gct ccg gcc ggc aac tac tcc act gat tct 1459  
 Glu Glu Ala Ala Ala Glu Ala Pro Ala Gly Asn Tyr Ser Thr Asp Ser 450  
 440 445

gca gaa gat gca cct gca gca gaa gca gtt gaa gag tcc gct ggc tcc 1507  
 Ala Glu Asp Ala Pro Ala Ala Glu Ala Val Glu Glu Ser Ala Gly Ser 465  
 455 460 465

ctc gct tcc gat gag cag ctc gct gct ctc cgc gag aag ctc gca ggt 1555  
 Leu Ala Ser Asp Glu Gln Leu Ala Ala Leu Arg Glu Lys Leu Ala Gly 485  
 470 475 480

aac taatagtccc tgcacctctt aag 1581  
 Asn

&lt;210&gt; 356

&lt;211&gt; 486

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 356

Met Pro Thr Asn Asn Ala Pro Gln Val Ala Ile Asn Asp Ile Gly Ser  
 1 5 10 15

Ala Glu Asp Phe Leu Ala Ala Ile Asp Ala Thr Ile Lys Tyr Phe Asn  
 20 25 30

Asp Gly Asp Ile Val Glu Gly Thr Val Val Lys Val Asp Arg Asp Glu  
 35 40 45  
 Val Leu Leu Asp Ile Gly Tyr Lys Thr Glu Gly Val Ile Pro Ser Arg  
 50 55 60  
 Glu Leu Ser Ile Lys His Asp Val Asp Pro Asp Glu Val Val Glu Val  
 65 70 75 80  
 Gly Asp Gln Ile Asp Ala Leu Val Leu Thr Lys Glu Asp Lys Glu Gly  
 85 90 95  
 Arg Leu Ile Leu Ser Lys Lys Arg Ala Gln Tyr Glu Arg Ala Trp Gly  
 100 105 110  
 Ala Ile Glu Glu Leu Lys Glu Lys Asp Glu Pro Val Thr Gly Thr Val  
 115 120 125  
 Ile Glu Val Val Lys Gly Gly Leu Ile Ile Asp Ile Gly Leu Arg Gly  
 130 135 140  
 Phe Leu Pro Ala Ser Leu Val Glu Met Arg Arg Val Arg Asp Leu Asp  
 145 150 155 160  
 Pro Tyr Ile Gly Gln Glu Leu Glu Ala Lys Ile Ile Glu Leu Asp Lys  
 165 170 175  
 Asn Arg Asn Asn Val Val Leu Ser Arg Arg Ala Phe Leu Glu Gln Thr  
 180 185 190  
 Gln Ser Glu Val Arg Ser Glu Phe Leu His Gln Leu Gln Lys Gly Gln  
 195 200 205  
 Val Arg Lys Gly Val Val Ser Ser Ile Val Asn Phe Gly Ala Phe Val  
 210 215 220  
 Asp Leu Gly Gly Val Asp Gly Leu Val His Val Ser Glu Leu Ser Trp  
 225 230 235 240  
 Lys His Ile Asp His Pro Ser Glu Val Val Thr Val Gly Asp Glu Val  
 245 250 255  
 Thr Val Glu Val Leu Glu Val Asp Leu Asp Arg Glu Arg Val Ser Leu  
 260 265 270  
 Ser Leu Lys Ala Thr Gln Glu Asp Pro Trp Arg Val Phe Ala Arg Thr  
 275 280 285  
 His Ala Val Gly Gln Ile Val Pro Gly Lys Val Thr Lys Leu Val Pro  
 290 295 300  
 Phe Gly Ala Phe Val Arg Val Glu Glu Gly Ile Glu Gly Leu Val His  
 305 310 315 320  
 Ile Ser Glu Leu Ala Gln Arg His Val Glu Val Pro Asp Gln Val Val  
 325 330 335  
 Ala Val Gly Glu Glu Val Met Val Lys Val Ile Asp Ile Asp Leu Glu  
 340 345 350  
 Arg Arg Arg Ile Ser Leu Ser Leu Lys Gln Ala Asp Glu Asp Tyr Thr

355					360					365					
Glu	Glu	Phe	Asp	Pro	Ser	Lys	Tyr	Gly	Met	Ala	Asp	Ser	Tyr	Asp	Glu
370					375					380					
Gln	Gly	Asn	Tyr	Ile	Phe	Pro	Glu	Gly	Phe	Asp	Ala	Glu	Thr	Asn	Glu
385					390					395					
Trp	Leu	Glu	Gly	Phe	Asp	Glu	Gln	Arg	Gln	Ala	Trp	Glu	Ala	Arg	Tyr
405					410					415					
Ala	Glu	Ser	Glu	Arg	Arg	Phe	Thr	Ala	His	Thr	Ala	Gln	Ile	Glu	Arg
420					425					430					
Arg	Arg	Gln	Gln	Ala	Glu	Glu	Ala	Ala	Ala	Glu	Ala	Pro	Ala	Gly	Asn
435					440					445					
Tyr	Ser	Thr	Asp	Ser	Ala	Glu	Asp	Ala	Pro	Ala	Ala	Glu	Ala	Val	Glu
450					455					460					
Glu	Ser	Ala	Gly	Ser	Leu	Ala	Ser	Asp	Glu	Gln	Leu	Ala	Ala	Leu	Arg
465					470					475					
Glu	Lys	Leu	Ala	Gly	Asn										
485															

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<212> DNA
<213> Corynebacterium glutamicum
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<222> (101)..(838)
<223> RXN01912
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ggtgacactt	tgccaccaga	cccgccgctg	gaacccaaag	atg	cgt	cgt	ttc	atc											115	
				Met	Arg	Arg	Phe	Ile												
				1				5												
ttc	acc	gag	cgt	aac	ggc	atc	tac	atc	att	gac	ctt	cag	cag	acc	ctg			163		
Phe	Thr	Glu	Arg	Asn	Gly	Ile	Tyr	Ile	Ile	Asp	Leu	Gln	Gln	Thr	Leu					
				10					15					20						
acc	tac	atc	gat	cag	gct	ttc	gag	ttc	gtc	aag	gaa	acc	ggt	gct	cac			211		
Thr	Tyr	Ile	Asp	Gln	Ala	Phe	Glu	Phe	Val	Lys	Glu	Thr	Val	Ala	His					
				25				30					35							
ggt	ggc	acc	ggt	ctt	ttc	ggt	ggt	acc	aaa	aag	cag	gct	cag	gaa	gct			259		
Gly	Gly	Thr	Val	Leu	Phe	Val	Gly	Thr	Lys	Lys	Gln	Ala	Gln	Glu	Ala					
			40				45				50									
ggt	cag	ggt	gag	gca	gac	cgc	ggt	ggt	atg	cct	tac	gtg	aac	cac	cgt			307		
Val	Gln	Val	Glu	Ala	Asp	Arg	Val	Gly	Met	Pro	Tyr	Val	Asn	His	Arg					
			55			60					65									
tggt	ctc	ggc	ggc	atg	ctg	acc	aac	ttc	cag	acc	ggt	tcc	aag	cgt	ctg			355		

Trp Leu Gly Gly Met Leu Thr Asn Phe Gln Thr Val Ser Lys Arg Leu  
 70 75 80 85  
 aac cgc atg aag gaa ctg cag gca atg gat gct gca gaa aac ggc tac 403  
 Asn Arg Met Lys Glu Leu Gln Ala Met Asp Ala Ala Glu Asn Gly Tyr  
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 gag ggt cgc acc aag cgc gaa gtt ctc atg ctg acc cgt gag cgc acc 451  
 Glu Gly Arg Thr Lys Arg Glu Val Leu Met Leu Thr Arg Glu Arg Thr  
 105 110 115  
 aag ctg gag cgc gtc ctc ggt ggt atc gca gag atg acc cgc gtg cct 499  
 Lys Leu Glu Arg Val Leu Gly Gly Ile Ala Glu Met Thr Arg Val Pro  
 120 125 130  
 tcc gca ctg tgg atc att gac acc aac aag gag cac atc gct gtc gct 547  
 Ser Ala Leu Trp Ile Ile Asp Thr Asn Lys Glu His Ile Ala Val Ala  
 135 140 145  
 gag gct cac aag ctg aac atc cca gtt gtt gcc atc ctg gac acc aac 595  
 Glu Ala His Lys Leu Asn Ile Pro Val Val Ala Ile Leu Asp Thr Asn  
 150 155 160 165  
 tgt gac cca gac gtt gtt gac ttc cca gtt cct ggt aac gac gac gca 643  
 Cys Asp Pro Asp Val Val Asp Phe Pro Val Pro Gly Asn Asp Asp Ala  
 170 175 180  
 atc cgc tcc acc gca ctg ctt tcc cgc gtt atc tcc acc gct gtg gaa 691  
 Ile Arg Ser Thr Ala Leu Leu Ser Arg Val Ile Ser Thr Ala Val Glu  
 185 190 195  
 gag ggt aag aag gca cgc gag gag cgt cag ctg gca gct gct aag gat 739  
 Glu Gly Lys Lys Ala Arg Glu Glu Arg Gln Leu Ala Ala Ala Lys Asp  
 200 205 210  
 gca gca ggc gac gca aag cct gag gca gag gaa gca cca gca gca gct 787  
 Ala Ala Gly Asp Ala Lys Pro Glu Ala Glu Glu Ala Pro Ala Ala Ala  
 215 220 225  
 gag gct gaa gag gca cct gca gct gag gct gaa gag gca cct gca gct 835  
 Glu Ala Glu Glu Ala Pro Ala Ala Glu Ala Glu Glu Ala Pro Ala Ala  
 230 235 240 245  
 gag taagctgcc ttaactgcag ttt 861  
 Glu

&lt;210&gt; 358

&lt;211&gt; 246

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 358

Met Arg Arg Phe Ile Phe Thr Glu Arg Asn Gly Ile Tyr Ile Ile Asp  
 1 5 10 15

Leu Gln Gln Thr Leu Thr Tyr Ile Asp Gln Ala Phe Glu Phe Val Lys  
 20 25 30

Glu Thr Val Ala His Gly Gly Thr Val Leu Phe Val Gly Thr Lys Lys

35 40 45

Gln Ala Gln Glu Ala Val Gln Val Glu Ala Asp Arg Val Gly Met Pro  
50 55 60

Tyr Val Asn His Arg Trp Leu Gly Gly Met Leu Thr Asn Phe Gln Thr  
65 70 75 80

Val Ser Lys Arg Leu Asn Arg Met Lys Glu Leu Gln Ala Met Asp Ala  
85 90 95

Ala Glu Asn Gly Tyr Glu Gly Arg Thr Lys Arg Glu Val Leu Met Leu  
100 105 110

Thr Arg Glu Arg Thr Lys Leu Glu Arg Val Leu Gly Gly Ile Ala Glu  
115 120 125

Met Thr Arg Val Pro Ser Ala Leu Trp Ile Ile Asp Thr Asn Lys Glu  
130 135 140

His Ile Ala Val Ala Glu Ala His Lys Leu Asn Ile Pro Val Val Ala  
145 150 155 160

Ile Leu Asp Thr Asn Cys Asp Pro Asp Val Val Asp Phe Pro Val Pro  
165 170 175

Gly Asn Asp Asp Ala Ile Arg Ser Thr Ala Leu Leu Ser Arg Val Ile  
180 185 190

Ser Thr Ala Val Glu Glu Gly Lys Lys Ala Arg Glu Glu Arg Gln Leu  
195 200 205

Ala Ala Ala Lys Asp Ala Ala Gly Asp Ala Lys Pro Glu Ala Glu Glu  
210 215 220

Ala Pro Ala Ala Ala Glu Ala Glu Glu Ala Pro Ala Ala Glu Ala Glu  
225 230 235 240

Glu Ala Pro Ala Ala Glu  
245

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<213> Corynebacterium glutamicum

<220>  
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<222> (101)..(871)  
<223> FRXA01912

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Met Arg Arg Phe Ile  
1 5  
ttc acc gag cgt aac ggc atc tac atc att gag ctt cag cag acc ctg 163  
Phe Thr Glu Arg Asn Gly Ile Tyr Ile Ile Asp Leu Gln Gln Thr Leu

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acc	tac	atc	gat	cag	gct	ttc	gag	ttc	gtc	aag	gaa	acc	gtt	gct	cac	211														
Thr	Tyr	Ile	Asp	Gln	Ala	Phe	Glu	Phe	Val	Lys	Glu	Thr	Val	Ala	His															
25										30										35										
ggg	ggc	acc	gtt	ctt	ttc	gtt	ggg	acc	aaa	aag	cag	gct	cag	gaa	gct	259														
Gly	Gly	Thr	Val	Leu	Phe	Val	Gly	Thr	Lys	Lys	Gln	Ala	Gln	Glu	Ala															
40										45										50										
gtt	cag	gtt	gag	gca	gac	cgc	gtt	ggg	atg	cct	tac	gtg	aac	cac	cgt	307														
Val	Gln	Val	Glu	Ala	Asp	Arg	Val	Gly	Met	Pro	Tyr	Val	Asn	His	Arg															
55										60										65										
tgg	ctc	ggc	ggc	atg	ctg	acc	aac	ttc	cag	acc	gtt	tcc	aag	cgt	ctg	355														
Trp	Leu	Gly	Gly	Met	Leu	Thr	Asn	Phe	Gln	Thr	Val	Ser	Lys	Arg	Leu															
70										75										80										
aac	cgc	atg	aag	gaa	ctg	cag	gca	atg	gat	gct	gca	gaa	aac	ggc	tac	403														
Asn	Arg	Met	Lys	Glu	Leu	Gln	Ala	Met	Asp	Ala	Ala	Glu	Asn	Gly	Tyr															
90										95										100										
gag	ggg	cgc	acc	aag	cgc	gaa	gtt	ctc	atg	ctg	acc	cgt	gag	cgc	acc	451														
Glu	Gly	Arg	Thr	Lys	Arg	Glu	Val	Leu	Met	Leu	Thr	Arg	Glu	Arg	Thr															
105										110										115										
aag	ctg	gag	cgc	gtc	ctc	ggg	ggg	atc	gca	gag	atg	acc	cgc	gtg	cct	499														
Lys	Leu	Glu	Arg	Val	Leu	Gly	Gly	Ile	Ala	Glu	Met	Thr	Arg	Val	Pro															
120										125										130										
tcc	gca	ctg	tgg	atc	att	gac	acc	aac	aag	gag	cac	atc	gct	gtc	gct	547														
Ser	Ala	Leu	Trp	Ile	Ile	Asp	Thr	Asn	Lys	Glu	His	Ile	Ala	Val	Ala															
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gag	gct	cac	aag	ctg	aac	atc	cca	gtt	gtt	gcc	atc	ctg	gac	acc	aac	595														
Glu	Ala	His	Lys	Leu	Asn	Ile	Pro	Val	Val	Ala	Ile	Leu	Asp	Thr	Asn															
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tgt	gac	cca	gac	gtt	gtt	gac	ttc	cca	gtt	cct	ggg	aac	gac	gac	gca	643														
Cys	Asp	Pro	Asp	Val	Val	Asp	Phe	Pro	Val	Pro	Gly	Asn	Asp	Asp	Ala															
170										175										180										
atc	cgc	tcc	acc	gca	ctg	ctt	tcc	cgc	gtt	atc	tcc	acc	gct	gtg	gaa	691														
Ile	Arg	Ser	Thr	Ala	Leu	Leu	Ser	Arg	Val	Ile	Ser	Thr	Ala	Val	Glu															
185										190										195										
gag	ggg	aag	aag	gca	cgc	gag	gag	cgt	cag	ctg	gca	gct	gct	aag	gat	739														
Glu	Gly	Lys	Lys	Glu	Ala	Arg	Glu	Glu	Arg	Gln	Leu	Ala	Ala	Lys	Asp															
200										205										210										
gca	gca	ggc	gac	gca	aag	cct	gag	gca	gag	gaa	gca	cca	gca	gca	gct	787														
Ala	Ala	Gly	Asp	Ala	Lys	Pro	Glu	Ala	Glu	Glu	Ala	Pro	Ala	Ala	Ala															
215										220										225										
gag	gct	gaa	gag	gca	cct	gca	gct	gag	gct	gaa	gaa	cac	ctg	cag	ctg	835														
Glu	Ala	Glu	Glu	Ala	Pro	Ala	Ala	Glu	Ala	Glu	Glu	His	Leu	Gln	Leu															
230										235										240										
agt	aag	ctg	ccc	tta																										

aaagccccca cga

894

&lt;210&gt; 360

&lt;211&gt; 257

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 360

Met Arg Arg Phe Ile Phe Thr Glu Arg Asn Gly Ile Tyr Ile Ile Asp  
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Leu Gln Gln Thr Leu Thr Tyr Ile Asp Gln Ala Phe Glu Phe Val Lys  
 20 25 30

Glu Thr Val Ala His Gly Gly Thr Val Leu Phe Val Gly Thr Lys Lys  
 35 40 45

Gln Ala Gln Glu Ala Val Gln Val Glu Ala Asp Arg Val Gly Met Pro  
 50 55 60

Tyr Val Asn His Arg Trp Leu Gly Gly Met Leu Thr Asn Phe Gln Thr  
 65 70 75 80

Val Ser Lys Arg Leu Asn Arg Met Lys Glu Leu Gln Ala Met Asp Ala  
 85 90 95

Ala Glu Asn Gly Tyr Glu Gly Arg Thr Lys Arg Glu Val Leu Met Leu  
 100 105 110

Thr Arg Glu Arg Thr Lys Leu Glu Arg Val Leu Gly Gly Ile Ala Glu  
 115 120 125

Met Thr Arg Val Pro Ser Ala Leu Trp Ile Ile Asp Thr Asn Lys Glu  
 130 135 140

His Ile Ala Val Ala Glu Ala His Lys Leu Asn Ile Pro Val Val Ala  
 145 150 155 160

Ile Leu Asp Thr Asn Cys Asp Pro Asp Val Val Asp Phe Pro Val Pro  
 165 170 175

Gly Asn Asp Asp Ala Ile Arg Ser Thr Ala Leu Leu Ser Arg Val Ile  
 180 185 190

Ser Thr Ala Val Glu Glu Gly Lys Lys Ala Arg Glu Glu Arg Gln Leu  
 195 200 205

Ala Ala Ala Lys Asp Ala Ala Gly Asp Ala Lys Pro Glu Ala Glu Glu  
 210 215 220

Ala Pro Ala Ala Ala Glu Ala Glu Glu Ala Pro Ala Ala Glu Ala Glu  
 225 230 235 240

Glu His Leu Gln Leu Ser Lys Leu Pro Leu Thr Ala Val Ser Ala Val  
 245 250 255

Ser



<210> 361  
 <211> 737  
 <212> DNA  
 <213> *Corynebacterium glutamicum*

<220>  
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 <222> (1)..(714)  
 <223> RXA02041

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Arg Leu Gly Ile Thr Ser Asp Trp Lys Ser His Trp Tyr Ala Asp Lys
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tct tac gct gac tac gtc gca gaa gac atc aag att cgc gaa ttc ctg 96
Ser Tyr Ala Asp Tyr Val Ala Glu Asp Ile Lys Ile Arg Glu Phe Leu
20 25 30

tcc aag ggc ctc gac cgt gcc ggc atc gcc gac gtc gtc atc gag cgc 144
Ser Lys Gly Leu Asp Arg Ala Gly Ile Ala Asp Val Val Ile Glu Arg
35 40 45

acc cgc gac cgc gtt cgc gta gac atc cac acc gct cgc cca gcc atc 192
Thr Arg Asp Arg Val Arg Val Asp Ile His Thr Ala Arg Pro Gly Ile
50 55 60

gtc att ggt cgt cgt ggc gct gag gct gac cgc atc cgc cgt gag ctc 240
Val Ile Gly Arg Arg Gly Ala Glu Ala Asp Arg Ile Arg Arg Glu Leu
65 70 75 80

gag aag ctc acc ggc aag cag gtt gcc ctc aac atc ctc gag gtc aag 288
Glu Lys Leu Thr Gly Lys Gln Val Ala Leu Asn Ile Leu Glu Val Lys
85 90 95

aac gtc gat gct aac gct aag ctg gtg gca cag tcc atc gct gag cag 336
Asn Val Asp Ala Asn Ala Lys Leu Val Ala Gln Ser Ile Ala Glu Gln
100 105 110

ctg acc aac cgc gtg gca ttc cgt cgc gca atg cgc aag gct atc cag 384
Leu Thr Asn Arg Val Ala Phe Arg Arg Ala Met Arg Lys Ala Ile Gln
115 120 125

tct gca atg cgt cag cca cag gtt aag ggc atc aag gtc gtg tgc tcc 432
Ser Ala Met Arg Gln Pro Gln Val Lys Gly Ile Lys Val Val Cys Ser
130 135 140

ggc cgt ctc ggc ggt gcc gag atg tcc cgc acc gag cgc tac cac gaa 480
Gly Arg Leu Gly Gly Ala Glu Met Ser Arg Thr Glu Arg Tyr His Glu
145 150 155 160

ggc cgc gtt cca ctg cac acc ctt cgc gca gaa atc gat tac gcc acc 528
Gly Arg Val Pro Leu His Thr Leu Arg Ala Glu Ile Asp Tyr Gly Thr
165 170 175

tac gag gct cac acc act ttc gga cgc atc ggc gtc aag gtg tgg atc 576
Tyr Glu Ala His Thr Thr Phe Gly Arg Ile Gly Val Lys Val Trp Ile
180 185 190

tac aag ggt gac gtc gtt ggt gga cgt cgc gag agc gag atc aat gca 624

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Tyr Lys Gly Asp Val Val Gly Gly Arg Arg Glu Ser Glu Ile Asn Ala  
195 200 205

ccc gca gag cgt cgc ggc cgc ggc gac cgc aac gca cgt ccg cgt cgt 672  
Pro Ala Glu Arg Arg Gly Arg Gly Asp Arg Asn Ala Arg Pro Arg Arg  
210 215 220

ggt ggc cag cgt cgt cag cgt gct gag cag aag cag gag ggc 714  
Gly Gly Gln Arg Arg Gln Arg Ala Glu Gln Lys Gln Glu Gly  
225 230 235

taaacatgct tattcctaag cgc 737

<210> 362

<211> 238

<212> PRT

<213> Corynebacterium glutamicum

<400> 362

Arg Leu Gly Ile Thr Ser Asp Trp Lys Ser His Trp Tyr Ala Asp Lys  
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Ser Tyr Ala Asp Tyr Val Ala Glu Asp Ile Lys Ile Arg Glu Phe Leu  
20 25 30

Ser Lys Gly Leu Asp Arg Ala Gly Ile Ala Asp Val Val Ile Glu Arg  
35 40 45

Thr Arg Asp Arg Val Arg Val Asp Ile His Thr Ala Arg Pro Gly Ile  
50 55 60

Val Ile Gly Arg Arg Gly Ala Glu Ala Asp Arg Ile Arg Arg Glu Leu  
65 70 75 80

Glu Lys Leu Thr Gly Lys Gln Val Ala Leu Asn Ile Leu Glu Val Lys  
85 90 95

Asn Val Asp Ala Asn Ala Lys Leu Val Ala Gln Ser Ile Ala Glu Gln  
100 105 110

Leu Thr Asn Arg Val Ala Phe Arg Arg Ala Met Arg Lys Ala Ile Gln  
115 120 125

Ser Ala Met Arg Gln Pro Gln Val Lys Gly Ile Lys Val Val Cys Ser  
130 135 140

Gly Arg Leu Gly Gly Ala Glu Met Ser Arg Thr Glu Arg Tyr His Glu  
145 150 155 160

Gly Arg Val Pro Leu His Thr Leu Arg Ala Glu Ile Asp Tyr Gly Thr  
165 170 175

Tyr Glu Ala His Thr Thr Phe Gly Arg Ile Gly Val Lys Val Trp Ile  
180 185 190

Tyr Lys Gly Asp Val Val Gly Gly Arg Arg Glu Ser Glu Ile Asn Ala  
195 200 205

Pro Ala Glu Arg Arg Gly Arg Gly Asp Arg Asn Ala Arg Pro Arg Arg  
210 215 220

Gly Gly Gln Arg Arg Gln Arg Ala Glu Gln Lys Gln Glu Gly  
 225 230 235

<210> 363  
 <211> 726  
 <212> DNA  
 <213> *Corynebacterium glutamicum*

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 <222> (101)...(703)  
 <223> RXA00672

<400> 363  
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 Met Ala Arg Tyr Thr  
 1 5  
 ggc cca gca acc cgt aaa tcc cgt cgt ctg cgc gtc gac ctt gtt ggt 163  
 Gly Pro Ala Thr Arg Lys Ser Arg Arg Leu Arg Val Asp Leu Val Gly  
 10 15 20  
 gga gac atg gcg ttt gag cgc cgt cct tac cct cca gga cag gca ggc 211  
 Gly Asp Met Ala Phe Glu Arg Arg Pro Tyr Pro Pro Gly Gln Ala Gly  
 25 30 35  
 cgt gca cgc atc aag gag tcc gag tac ctg ctg cag ctc cag gag aag 259  
 Arg Ala Arg Ile Lys Glu Ser Glu Tyr Leu Leu Gln Leu Gln Glu Lys  
 40 45 50  
 cag aag gct cgt ttc atc tac gcc gtc atg gaa aag cag ttc cgt cgt 307  
 Gln Lys Ala Arg Phe Ile Tyr Glu Val Met Glu Lys Gln Phe Arg Arg  
 55 60 65  
 tac tac gcc gag gct aac cgt cgc gca gcc aag acc ggt gag aac ctg 355  
 Tyr Tyr Ala Glu Ala Asn Arg Arg Ala Gly Lys Thr Gly Glu Asn Leu  
 70 75 80 85  
 gtc gtc ctg ctc gag tcc cgc ctc gac aac gtc gtg tac cgc gca ggt 403  
 Val Val Leu Leu Glu Ser Arg Leu Asp Asn Val Val Tyr Arg Ala Gly  
 90 95 100  
 ctg gca aac acc cgt cgc cag gct cgt cag ctt gtt tcc cac ggt cac 451  
 Leu Ala Asn Thr Arg Arg Gln Ala Arg Gln Leu Val Ser His Gly His  
 105 110 115  
 ttc acc gtg aac gcc aag gca atc gac gtt cca tct ttc cgc gtt tct 499  
 Phe Thr Val Asn Gly Lys Ala Ile Asp Val Pro Ser Phe Arg Val Ser  
 120 125 130  
 cag tac gac atc atc aat gtt cgt gag aag tcc cag aag atg aac tgg 547  
 Gln Tyr Asp Ile Ile Asn Val Arg Glu Lys Ser Gln Lys Met Asn Trp  
 135 140 145  
 ttc gaa gag gct cag gac aac ctg gcc gac gca gtc gtc cca gct tgg 595  
 Phe Glu Glu Ala Gln Asp Asn Leu Ala Asp Ala Val Val Pro Ala Trp  
 150 155 160 165

ctc cag gtc gtt cct gag aac ctt cgt atc ctc gtg cac cag ctc cca 643  
 Leu Gln Val Val Pro Glu Asn Leu Arg Ile Leu Val His Gln Leu Pro  
                   170                  175                  180

gag cgc gca cag atc gat atc cca ctg caa gag cag ctc atc gtc gag 691  
 Glu Arg Ala Gln Ile Asp Ile Pro Leu Gln Glu Gln Leu Ile Val Glu  
                   185                  190                  195

ttc tac tgc aag tagtttttgc ttaccggct gcc 726  
 Phe Tyr Ser Lys  
                   200

&lt;210&gt; 364

&lt;211&gt; 201

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 364

Met Ala Arg Tyr Thr Gly Pro Ala Thr Arg Lys Ser Arg Arg Leu Arg  
           1                  5                  10                  15

Val Asp Leu Val Gly Gly Asp Met Ala Phe Glu Arg Arg Pro Tyr Pro  
                   20                  25                  30

Pro Gly Gln Ala Gly Arg Ala Arg Ile Lys Glu Ser Glu Tyr Leu Leu  
                   35                  40                  45

Gln Leu Gln Glu Lys Gln Lys Ala Arg Phe Ile Tyr Gly Val Met Glu  
                   50                  55                  60

Lys Gln Phe Arg Arg Tyr Tyr Ala Glu Ala Asn Arg Arg Ala Gly Lys  
                   65                  70                  75                  80

Thr Gly Glu Asn Leu Val Val Leu Leu Glu Ser Arg Leu Asp Asn Val  
                   85                  90                  95

Val Tyr Arg Ala Gly Leu Ala Asn Thr Arg Arg Gln Ala Arg Gln Leu  
                   100                  105                  110

Val Ser His Gly His Phe Thr Val Asn Gly Lys Ala Ile Asp Val Pro  
                   115                  120                  125

Ser Phe Arg Val Ser Gln Tyr Asp Ile Ile Asn Val Arg Glu Lys Ser  
                   130                  135                  140

Gln Lys Met Asn Trp Phe Glu Glu Ala Gln Asp Asn Leu Ala Asp Ala  
                   145                  150                  155                  160

Val Val Pro Ala Trp Leu Gln Val Val Pro Glu Asn Leu Arg Ile Leu  
                   165                  170                  175

Val His Gln Leu Pro Glu Arg Ala Gln Ile Asp Ile Pro Leu Gln Glu  
                   180                  185                  190

Gln Leu Ile Val Glu Phe Tyr Ser Lys  
                   195                  200

&lt;210&gt; 365

<211> 756  
<212> DNA  
<213> *Corynebacterium glutamicum*

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<220>
<221> CDS
<222> (101)..(733)
<223> RXA00697
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tgatgacctt ttctaagaac atcaacggaa ggattgcgta	atg ccg gga cgt gaa Met Pro Gly Arg Glu	115
cgg cgt gac ggc gga cgc tcc gcc gac gac aac aag caa aac gat cgc	10 15 20	163
Arg Arg Asp Gly Gly Arg Ser Ala Asp Asn Lys Gln Asn Asp Arg		
aac gag cgt cgt ggc gga ggc cgc cgc gat gac cgt cgc aat cag cag	25 30 35	211
Asn Glu Arg Arg Gly Gly Gly Arg Arg Asp Asp Arg Arg Asn Gln Gln		
cag gac gag cgc tca cag tac atc gag cgt gta gtc acc atc aac cgt	40 45 50	259
Gln Asp Glu Arg Ser Gln Tyr Ile Glu Arg Val Val Thr Ile Asn Arg		
gtg tcc aag gtc gtc aag ggt ggt cgt cgc ttc agc ttc acc gca ctt	55 60 65	307
Val Ser Lys Val Val Lys Gly Gly Arg Arg Phe Ser Phe Thr Ala Leu		
gtc atc gtt ggc gac ggc aag gga atg gtc ggt gtc ggt tac ggc aag	70 75 80 85	355
Val Ile Val Val Gly Asp Gly Lys Gly Met Val Gly Val Gly Tyr Gly Lys		
gcc aag gaa gtt cct gcc gca atc cag aag ggt gca gaa gag gct cgt	90 95 100	403
Ala Lys Glu Val Pro Ala Ala Ile Gln Lys Gly Ala Glu Glu Ala Arg		
aag aac ttc ttc cgc gtc cca atg gtc aac ggc acc atc acc cac cca	105 110 115	451
Lys Asn Phe Phe Arg Val Pro Met Val Asn Gly Thr Ile Thr His Pro		
gtt cag ggc gaa aag gca gcc ggc atc gtt atg ctg aag cca gct gct	120 125 130	499
Val Gln Gly Glu Lys Ala Ala Gly Ile Val Met Leu Lys Pro Ala Ala		
cca ggt acc ggt gtt atc gcc ggt ggc gca gca cgt cca gtt ctt gag	135 140 145	547
Pro Gly Thr Gly Val Ile Ala Gly Gly Ala Ala Arg Pro Val Leu Glu		
tgc gca ggt atc caa gac atc ctg tcc aag tcc ctt ggt tct gac aac	150 155 160	595
Cys Ala Gly Ile Gln Asp Ile Leu Ser Lys Ser Leu Gly Ser Asp Asn		
gct atc aac gtc gtc cac gca act gtg gat ggc ctg aag cag ctg gtc	170 175	643
Ala Ile Asn Val Val His Ala Thr Val Asp Gly Leu Lys Gln Leu Val		
cgc cct gaa gag gtt gca gcc cgc cgt ggc aag acc atc gaa gag gtc		691

Arg Pro Glu Glu Val Ala Ala Arg Arg Gly Lys Thr Ile Glu Glu Val  
 185 190 195

gca cca gca cgt att ctg cgt gca cgc gca ggt cag gag gcg  
 Ala Pro Ala Arg Ile Leu Arg Ala Arg Ala Gly Gln Glu Ala  
 200 205 210

733

taagaaatgg cgctgaagat tac

756

&lt;210&gt; 366

&lt;211&gt; 211

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 366

Met Pro Gly Arg Glu Arg Arg Asp Gly Gly Arg Ser Ala Asp Asp Asn  
 1 5 10 15

Lys Gln Asn Asp Arg Asn Glu Arg Arg Gly Gly Gly Arg Arg Asp Asp  
 20 25 30

Arg Arg Asn Gln Gln Gln Asp Glu Arg Ser Gln Tyr Ile Glu Arg Val  
 35 40 45

Val Thr Ile Asn Arg Val Ser Lys Val Val Lys Gly Gly Arg Arg Phe  
 50 55 60

Ser Phe Thr Ala Leu Val Ile Val Gly Asp Gly Lys Gly Met Val Gly  
 65 70 75 80

Val Gly Tyr Gly Lys Ala Lys Glu Val Pro Ala Ala Ile Gln Lys Gly  
 85 90 95

Ala Glu Glu Ala Arg Lys Asn Phe Phe Arg Val Pro Met Val Asn Gly  
 100 105 110

Thr Ile Thr His Pro Val Gln Gly Glu Lys Ala Ala Gly Ile Val Met  
 115 120 125

Leu Lys Pro Ala Ala Pro Gly Thr Gly Val Ile Ala Gly Gly Ala Ala  
 130 135 140

Arg Pro Val Leu Glu Cys Ala Gly Ile Gln Asp Ile Leu Ser Lys Ser  
 145 150 155 160

Leu Gly Ser Asp Asn Ala Ile Asn Val Val His Ala Thr Val Asp Gly  
 165 170 175

Leu Lys Gln Leu Val Arg Pro Glu Glu Val Ala Ala Arg Arg Gly Lys  
 180 185 190

Thr Ile Glu Glu Val Ala Pro Ala Arg Ile Leu Arg Ala Arg Ala Gly  
 195 200 205

Gln Glu Ala  
 210

&lt;210&gt; 367

&lt;211&gt; 390

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(367)

&lt;223&gt; RXN00545

&lt;400&gt; 367

gctgacgcaa cgaccctcct gctatgccaa cgacggcatg gccgaaaaaa caattactag 60

accataggag gtgatgaggt ccgtgcgtca atacgaactt atg atc att ctc gat 115  
 Met Ile Ile Leu Asp  
 1 5

cct tct cag gat gag cgc act gtt gcc cgg tcc ctg gat aaa ttc ctc 163  
 Pro Ser Gln Asp Glu Arg Thr Val Ala Pro Ser Leu Asp Lys Phe Leu  
 10 15 20

gag gtt gtc cgc aag gac aag ggt gac gtt gtg aag gtt gat gtt tgg 211  
 Glu Val Val Arg Lys Asp Lys Gly Asp Val Val Lys Val Asp Val Trp  
 25 30 35

gac aag cgc cgt ctt gca tac cca atc gac aag aag gaa gag ggc gtt 259  
 Gly Lys Arg Arg Leu Ala Tyr Pro Ile Asp Lys Lys Glu Glu Gly Val  
 40 45 50

gac gcc gtc gtc gat ctc aag tgt gag tct gcg acc gta ctc gag ctc 307  
 Tyr Ala Val Val Asp Leu Lys Cys Glu Ser Ala Thr Val Leu Glu Leu  
 55 60 65

gat cgt gtt ctg aac ctg aat gat ggt gtc ctg cgc acc aag gtt ctg 355  
 Asp Arg Val Leu Asn Leu Asn Asp Gly Val Leu Arg Thr Lys Val Leu  
 70 75 80 85

aga ctc gac aag taaagaactt taaggctcta gag 390  
 Arg Leu Asp Lys

&lt;210&gt; 368

&lt;211&gt; 89

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 368

Met Ile Ile Leu Asp Pro Ser Gln Asp Glu Arg Thr Val Ala Pro Ser  
 1 5 10 15

Leu Asp Lys Phe Leu Glu Val Val Arg Lys Asp Lys Gly Asp Val Val  
 20 25 30

Lys Val Asp Val Trp Gly Lys Arg Arg Leu Ala Tyr Pro Ile Asp Lys  
 35 40 45

Lys Glu Glu Gly Val Tyr Ala Val Val Asp Leu Lys Cys Glu Ser Ala  
 50 55 60

Thr Val Leu Glu Leu Asp Arg Val Leu Asn Leu Asn Asp Gly Val Leu  
 65 70 75 80

Arg Thr Lys Val Leu Arg Leu Asp Lys  
85

<210> 369  
<211> 355  
<212> DNA  
<213> *Corynebacterium glutamicum*

<220>  
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<222> (101)..(355)  
<223> FRXA00545

<400> 369  
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accataggag gtgatgaggt ccgtgcgtca atacgaactt atg atc att ctc gat 115  
Met Ile Ile Leu Asp  
1 5  
cct tct cag gat gag cgc act gtt gcc cgg tcc ctg gat aaa ttc ctc 163  
Pro Ser Gln Asp Glu Arg Thr Val Ala Pro Ser Leu Asp Lys Phe Leu  
10 15 20  
gag gtt gtc cgc aag gac aag ggt gac gtt gtg aag gtt gat gtt tgg 211  
Glu Val Val Arg Lys Asp Lys Gly Asp Val Val Lys Val Asp Val Trp  
25 30 35  
ggc aag cgc cgt ctt gca tac cca atc gac aag aag gaa gag ggc gtt 259  
Gly Lys Arg Arg Leu Ala Tyr Pro Ile Asp Lys Lys Glu Glu Gly Val  
40 45 50  
tac gcc gtc gtc gat ctc aag tgt gag tct gcg acc gta ctc gag ctc 307  
Tyr Ala Val Val Asp Leu Lys Cys Glu Ser Ala Thr Val Leu Glu Leu  
55 60 65  
gat cgt gtt ctg aac ctg aat gat ggt gtc ctg cgc acc aag gtt ctg 355  
Asp Arg Val Leu Asn Leu Asn Asp Gly Val Leu Arg Thr Lys Val Leu  
70 75 80 85

<210> 370  
<211> 85  
<212> PRT  
<213> *Corynebacterium glutamicum*

<400> 370  
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Leu Asp Lys Phe Leu Glu Val Val Arg Lys Asp Lys Gly Asp Val Val 30  
20 25  
Lys Val Asp Val Trp Gly Lys Arg Arg Leu Ala Tyr Pro Ile Asp Lys 40  
35 45  
Lys Glu Glu Gly Val Tyr Ala Val Val Asp Leu Lys Cys Glu Ser Ala 60  
50 55 60  
Thr Val Leu Glu Leu Asp Arg Val Leu Asn Leu Asn Asp Gly Val Leu



65

70

75

80

Arg Thr Lys Val Leu  
85

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<210> 371
<211> 588
<212> DNA
<213> Corynebacterium glutamicum
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ggctcgttcc cgctacggcg cgaagagggg ataattaaaa atg cgt aaa tca gca 115  
Met Arg Lys Ser Ala  
1 5

gct cct aag cgt cca gta gtt cag gac cct gta tac aag tcc gag ctc 163  
Ala Pro Lys Arg Pro Val Val Gln Asp Pro Val Tyr Lys Ser Glu Leu  
10 15 20

gtt acc cag ctc gta aac aag atc ctc atc ggt ggc aag aag tcc acc 211  
Val Thr Gln Leu Val Asn Lys Ile Leu Ile Gly Gly Lys Lys Ser Thr  
25 30 35

gca gag cgc atc gtc tac ggt gca ctc gag atc tgc cgt gag aag acc 259  
Ala Glu Arg Ile Val Tyr Gly Ala Leu Glu Ile Cys Arg Glu Lys Thr  
40 45 50

ggc acc gat cca gta gga acc ctc gag aag gct ctc ggc aac gtg cgt 307  
Gly Thr Asp Pro Val Gly Thr Leu Glu Lys Ala Leu Gly Asn Val Arg  
55 60 65

cca gac ctc gaa gtt cgt tcc cgc cgt gtt ggt ggc gct acc tac cag 355  
Pro Asp Leu Glu Val Arg Ser Arg Arg Val Gly Gly Ala Thr Tyr Gln  
70 75 80 85

gtg cca gtg gat gtt cgc cca gag cgc gca aac acc ctc gca ctg cgt 403  
Val Pro Val Asp Val Arg Pro Glu Arg Ala Asn Thr Leu Ala Leu Arg  
90 95 100

tgg ttg gta acc ttc acc cgt cag cgt cgt gag aac acc atg atc gag 451  
Trp Leu Val Thr Phe Thr Arg Gln Arg Arg Glu Asn Thr Met Ile Glu  
105 110 115

cgt ctt gca aac gaa ctt ctg gat gca gcc aac ggc ctt ggc gct tcc 499  
Arg Leu Ala Asn Glu Leu Leu Asp Ala Ala Asn Gly Leu Gly Ala Ser  
120 125 130

gtg aag cgt cgc gaa gac acc cac aag atg gca gag gcc aac cgc gcc 547  
Val Lys Arg Arg Glu Asp Thr His Lys Met Ala Glu Ala Asn Arg Ala  
135 140 145

ttc gct cac tac cgc tgg tagtactgcc aagacatgaa agc 588  
Phe Ala His Tyr Arg Trp

150

155

<210> 372  
 <211> 155  
 <212> PRT  
 <213> *Corynebacterium glutamicum*

<400> 372  
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 Tyr Lys Ser Glu Leu Val Thr Gln Leu Val Asn Lys Ile Leu Ile Gly  
 20 25 30  
 Gly Lys Lys Ser Thr Ala Glu Arg Ile Val Tyr Gly Ala Leu Glu Ile  
 35 40 45  
 Cys Arg Glu Lys Thr Gly Thr Asp Pro Val Gly Thr Leu Glu Lys Ala  
 50 55 60  
 Leu Gly Asn Val Arg Pro Asp Leu Glu Val Arg Ser Arg Arg Val Gly  
 65 70 75 80  
 Gly Ala Thr Tyr Gln Val Pro Val Asp Val Arg Pro Glu Arg Ala Asn  
 85 90 95  
 Thr Leu Ala Leu Arg Trp Leu Val Thr Phe Thr Arg Gln Arg Arg Glu  
 100 105 110  
 Asn Thr Met Ile Glu Arg Leu Ala Asn Glu Leu Leu Asp Ala Ala Asn  
 115 120 125  
 Gly Leu Gly Ala Ser Val Lys Arg Arg Glu Asp Thr His Lys Met Ala  
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 Glu Ala Asn Arg Ala Phe Ala His Tyr Arg Trp  
 145 150 155

<210> 373  
 <211> 519  
 <212> DNA  
 <213> *Corynebacterium glutamicum*

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 <223> RXA00694

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 ggaagggaac cccaacgaga aaggcatcag gtcgtctcta atg aca atg act gat 115  
 Met Thr Met Thr Asp  
 1 5  
 cca atc gcc gac atg ctg tgg cgc gtg cgc aat gct agc aat gcg cac 163  
 Pro Ile Ala Asp Met Leu Ser Arg Val Arg Asn Ala Ser Asn Ala His  
 10 15 20

cac gac acc gtg tcc atg cca tcc tcc aag atc aag gca aac atc gcc 211  
 His Asp Thr Val Ser Met Pro Ser Ser Lys Ile Lys Ala Asn Ile Ala  
 25 30 35

gag atc ttg aag cag gaa ggc tac atc gct aac tac acc gtt gag gat 259  
 Glu Ile Leu Lys Gln Glu Gly Tyr Ile Ala Asn Tyr Thr Val Glu Asp  
 40 45 50

gca aag gtc ggc aag acc ctg tcc ctg gag ctg aag tac agc aac acc 307  
 Ala Lys Val Gly Lys Thr Leu Ser Leu Glu Leu Lys Tyr Ser Asn Thr  
 55 60 65

cgt gag cgc tcc atc gct ggt ctg cgc cgc gtt tcc aag cct ggt ctg 355  
 Arg Glu Arg Ser Ile Ala Gly Leu Arg Arg Val Ser Lys Pro Gly Leu  
 70 75 80 85

cgt gta tac gct aag tcc acc aat ctg cca cag gtt ctg ggc ggc ctt 403  
 Arg Val Tyr Ala Lys Ser Thr Asn Leu Pro Gln Val Leu Gly Gly Leu  
 90 95 100

ggc gtg gct atc att tcc acg tca cag ggc ctg ctg acc gac cgt cag 451  
 Gly Val Ala Ile Ile Ser Thr Ser Gln Gly Leu Leu Thr Asp Arg Gln  
 105 110 115

gct acc gag aag ggc gta ggc gga gaa gtc ctg gcc tac gtc tgg 496  
 Ala Thr Glu Lys Gly Val Gly Gly Glu Val Leu Ala Tyr Val Trp  
 120 125 130

taatagggag gattgactaa ata 519

<210> 374  
 <211> 132  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 374  
 Met Thr Met Thr Asp Pro Ile Ala Asp Met Leu Ser Arg Val Arg Asn  
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Ala Ser Asn Ala His His Asp Thr Val Ser Met Pro Ser Ser Lys Ile  
 20 25 30

Lys Ala Asn Ile Ala Glu Ile Leu Lys Gln Glu Gly Tyr Ile Ala Asn  
 35 40 45

Tyr Thr Val Glu Asp Ala Lys Val Gly Lys Thr Leu Ser Leu Glu Leu  
 50 55 60

Lys Tyr Ser Asn Thr Arg Glu Arg Ser Ile Ala Gly Leu Arg Arg Val  
 65 70 75 80

Ser Lys Pro Gly Leu Arg Val Tyr Ala Lys Ser Thr Asn Leu Pro Gln  
 85 90 95

Val Leu Gly Gly Leu Gly Val Ala Ile Ile Ser Thr Ser Gln Gly Leu  
 100 105 110

Leu Thr Asp Arg Gln Ala Thr Glu Lys Gly Val Gly Gly Glu Val Leu  
 115 120 125

Ala Tyr Val Trp  
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<210> 375  
<211> 492  
<212> DNA  
<213> *Corynebacterium glutamicum*

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<221> CDS  
<222> (101)..(469)  
<223> RXN02038

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agaagcctga ggcctacgag atcaagaag tggcccagta atg tca gag cct atc 115  
Met Ser Glu Pro Ile  
1 5  
cag aac gag aac gta gag agc aac gtc gca gac gct gct gac atc gct 163  
Gln Asn Glu Asn Val Glu Ser Asn Val Ala Asp Ala Ala Asp Ile Ala  
10 15 20  
gca gca acc gct gca acc gag gag ttc acc aac acc atc ggc gat gca 211  
Ala Ala Thr Ala Ala Thr Glu Glu Phe Thr Asn Thr Ile Gly Asp Ala  
25 30 35  
att gct act gct tcc gaa gaa gag acc atc gag gct gca cca gta gta 259  
Ile Ala Thr Ala Ser Glu Glu Thr Ile Glu Ala Ala Pro Val Val  
40 45 50  
ctc gac ggc cca atc cag acc gtt ggt cgc cgt aag cgc gcc atc gtt 307  
Leu Asp Gly Pro Ile Gln Thr Val Gly Arg Arg Lys Arg Ala Ile Val  
55 60 65  
cgc gtc cgc ctt gta gct ggc tcc ggc gag ttc aag tgc aac ggt cgc 355  
Arg Val Arg Leu Val Ala Gly Ser Gly Glu Phe Lys Cys Asn Gly Arg  
70 75 80 85  
acc ctg gaa gag tac ttc cct aac aag ctg cac cag cag ctg atc aag 403  
Thr Leu Glu Glu Tyr Phe Pro Asn Lys Leu His Gln Gln Leu Ile Lys  
90 95 100  
gct cct ttg gtc ctt ctg gac cgc ctg aac caa tgc aac atc gag gct 451  
Ala Pro Leu Val Leu Leu Asp Arg Leu Asn Gln Cys Asn Ile Glu Ala  
105 110 115  
tct ata aag gga cct aaa tagatcgcc aggttatggc aat 492  
Ser Ile Lys Gly Pro Lys  
120

<210> 376  
<211> 123  
<212> PRT  
<213> *Corynebacterium glutamicum*

<400> 376  
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gct cct  
Ala Pro

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<400> 378
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  1             5             10             15
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Ala Ala Asp Ile Ala Ala Ala Thr Ala Ala Thr Glu Glu Phe Thr Asn  
20 25 30

Thr Ile Gly Asp Ala Ile Ala Thr Ala Ser Glu Glu Glu Thr Ile Glu  
35 40 45

Ala Ala Pro Val Val Leu Asp Gly Pro Ile Gln Thr Val Gly Arg Arg  
50 55 60

Lys Arg Ala Ile Val Arg Val Arg Leu Val Ala Gly Ser Gly Glu Phe  
65 70 75 80

Lys Cys Asn Gly Arg Thr Leu Glu Glu Tyr Phe Pro Asn Lys Leu His  
85 90 95

Gln Gln Leu Ile Lys Ala Pro  
100

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<210> 379
<211> 426
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
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<223> RXA01287
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Val Ala Gly Gln Lys  
1 5

atc cgc att agg ctc aag gcc tac gac cac gaa gcg att gat gcg tct 163  
Ile Arg Ile Arg Leu Lys Ala Tyr Asp His Glu Ala Ile Asp Ala Ser  
10 15 20

gca cgc aag atc gtt gag acg gtc acc cgt acg ggt gcc cga gtc gtt 211  
Ala Arg Lys Ile Val Glu Thr Val Thr Arg Thr Gly Ala Arg Val Val  
25 30 35

gga cgc gtc cct ttg cct acc gaa aag aac gta tac gcc gtt att cgt 259  
 Gly Pro Val Pro Leu Pro Thr Glu Lys Asn Val Tyr Ala Val Ile Arg  
                   40                  45                  50

tct cca cat aag tac aag gac tct cgc gag cac ttc gag atg cgc act 307  
 Ser Pro His Lys Tyr Lys Asp Ser Arg Glu His Phe Glu Met Arg Thr  
                   55                  60                  65

cac aag cgc ctg atc gac atc ctc gac ccg acg ccg aag act gtt gat 355  
 His Lys Arg Leu Ile Asp Ile Leu Asp Pro Thr Pro Lys Thr Val Asp  
                   70                  75                  80                  85

gcc ctt atg cgc atc gac ctt ccg gcc agc gtc gac gtg aac att cag 403  
 Ala Leu Met Arg Ile Asp Leu Pro Ala Ser Val Asp Val Asn Ile Gln  
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tgatcgacgg aatttttggc agc 426

<210> 380  
 <211> 101  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 380  
 Val Ala Gly Gln Lys Ile Arg Ile Arg Leu Lys Ala Tyr Asp His Glu  
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Ala Ile Asp Ala Ser Ala Arg Lys Ile Val Glu Thr Val Thr Arg Thr  
                   20                  25                  30

Gly Ala Arg Val Val Gly Pro Val Pro Leu Pro Thr Glu Lys Asn Val  
                   35                  40                  45

Tyr Ala Val Ile Arg Ser Pro His Lys Tyr Lys Asp Ser Arg Glu His  
                   50                  55                  60

Phe Glu Met Arg Thr His Lys Arg Leu Ile Asp Ile Leu Asp Pro Thr  
                   65                  70                  75                  80

Pro Lys Thr Val Asp Ala Leu Met Arg Ile Asp Leu Pro Ala Ser Val  
                   85                  90                  95

Asp Val Asn Ile Gln  
                   100

<210> 381  
 <211> 113  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (1)..(90)  
 <223> RXA00673

<400> 381  
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1 5 10 15 90  
 cag cca cac aac ggc tgc cgt cca cca aag cgt cgt cgc gtt  
 Gln Pro His Asn Gly Cys Arg Pro Pro Lys Arg Arg Arg Val  
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<210> 382  
 <211> 30  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 382  
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 Gln Pro His Asn Gly Cys Arg Pro Pro Lys Arg Arg Arg Val  
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<210> 383  
 <211> 489  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(466)  
 <223> RXA01280

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 Met Pro Thr Ile Gln  
 1 5

cag ctg gtc cgt aag gcc cgc cac gat aag tcc gac aag gtg gct acc 163  
 Gln Leu Val Arg Lys Ala Arg His Asp Lys Ser Asp Lys Val Ala Thr  
 10 15 20

gag gca ctg aag ggt tcc cct cag cgt cgt ggc gta tgc acc cgt gtg 211  
 Ala Ala Leu Lys Gly Ser Pro Gln Arg Arg Gly Val Cys Thr Arg Val  
 25 30 35

tac acc acc acc cct aag aag cct aac tct gct ctt cgt aag gtc gct 259  
 Tyr Thr Thr Thr Pro Lys Lys Pro Asn Ser Ala Leu Arg Lys Val Ala  
 40 45 50

cgt gtg cgc ctt acc tcc ggc atc gag gtt tcc gct tac atc cct ggt 307  
 Arg Val Arg Leu Thr Ser Gly Ile Glu Val Ser Ala Tyr Ile Pro Gly  
 55 60 65

gag ggc cac aac ctg cag gag cac tcc atg gtg ctc gtt cgc ggt ggt 355  
 Glu Gly His Asn Leu Gln Glu His Ser Met Val Leu Val Arg Gly Gly  
 70 75 80 85

cgt gtt aag gac ctc cca ggt gtc cgt tac aag atc gtc cgt ggc gca 403  
 Arg Val Lys Asp Leu Pro Gly Val Arg Tyr Lys Ile Val Arg Gly Ala



	90		95		100	
ctg gat acc cag ggt gtt aag gac cgc aag cag gct cgt tcc cgc tac						451
Leu Asp Thr Gln Gly Val Lys Asp Arg Lys Gln Ala Arg Ser Arg Tyr						
	105		110		115	

ggc gcg aag agg gga taattaaaaa tgcgtaaatc agc 489  
 Gly Ala Lys Arg Gly  
 120

&lt;210&gt; 384

&lt;211&gt; 122

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 384

Met Pro Thr Ile Gln Gln Leu Val Arg Lys Ala Arg His Asp Lys Ser	
1 5 10 15	

Asp Lys Val Ala Thr Ala Ala Leu Lys Gly Ser Pro Gln Arg Gly	
20 25 30	

Val Cys Thr Arg Val Tyr Thr Thr Pro Lys Lys Pro Asn Ser Ala	
35 40 45	

Leu Arg Lys Val Ala Arg Val Arg Leu Thr Ser Gly Ile Glu Val Ser	
50 55 60	

Ala Tyr Ile Pro Gly Glu Gly His Asn Leu Gln Glu His Ser Met Val	
65 70 75 80	

Leu Val Arg Gly Gly Arg Val Lys Asp Leu Pro Gly Val Arg Tyr Lys	
85 90 95	

Ile Val Arg Gly Ala Leu Asp Thr Gln Gly Val Lys Asp Arg Lys Gln	
100 105 110	

Ala Arg Ser Arg Tyr Gly Ala Lys Arg Gly	
115 120	

&lt;210&gt; 385

&lt;211&gt; 426

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(403)

&lt;223&gt; RXA02637

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agtcgctaag cacgtcgaat tccgcgagga gcgataatca atg gct aag aag tca	115
Met Ala Lys Lys Ser	
1 5	

aag atc gcc aag aac gag aag cgc aag gaa atc gtc gcc cgc tac gcg	163
Lys Ile Ala Lys Asn Glu Lys Arg Lys Glu Ile Val Ala Arg Tyr Ala	

	10	15	20	
gag cgt cgc gct gag ctc aag gca att atc agt aac cca aac acc tct				211
Glu Arg Arg Ala Glu Leu Lys Ala Ile Ile Ser Asn Pro Asn Thr Ser				
	25	30	35	
gac gag gat cgt ctg gat gca cag ttc gaa ctg aac agc cag cca cgt				259
Asp Glu Asp Arg Leu Asp Ala Gln Phe Glu Leu Asn Ser Gln Pro Arg				
	40	45	50	
gat gct gct gct gtc cgc gtt cgt aac cgc gac tca cac gat ggt cgc				307
Asp Ala Ala Val Arg Val Arg Asn Arg Asp Ser His Asp Gly Arg				
	55	60	65	
cca cgc ggc tac ctc cgt aag ttc ggt ctt tcc cgt gtc cgt atg cgc				355
Pro Arg Gly Tyr Leu Arg Lys Phe Gly Leu Ser Arg Val Arg Met Arg				
	70	75	80	85
gag atg gct cac cgt ggt gag ctg cgg ggc gtt cgt aag tcc agc tgg				403
Glu Met Ala His Arg Gly Glu Leu Pro Gly Val Arg Lys Ser Ser Trp				
	90	95	100	
taagggagtt tttaaccaatg aag				426
<210> 386				
<211> 101				
<212> PRT				
<213> Corynebacterium glutamicum				
<400> 386				
Met Ala Lys Lys Ser Lys Ile Ala Lys Asn Glu Lys Arg Lys Glu Ile				15
	1	5	10	
Val Ala Arg Tyr Ala Glu Arg Arg Ala Glu Leu Lys Ala Ile Ile Ser				30
	20	25		
Asn Pro Asn Thr Ser Asp Glu Asp Arg Leu Asp Ala Gln Phe Glu Leu				45
	35	40		
Asn Ser Gln Pro Arg Asp Ala Ala Val Arg Val Arg Asn Arg Asp				60
	50	55		
Ser His Asp Gly Arg Pro Arg Gly Tyr Leu Arg Lys Phe Gly Leu Ser				80
	65	70	75	
Arg Val Arg Met Arg Glu Met Ala His Arg Gly Glu Leu Pro Gly Val				95
	85	90		
Arg Lys Ser Ser Trp				100

&lt;210&gt; 387

&lt;211&gt; 390

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(367)

&lt;223&gt; RXA01487

&lt;400&gt; 387

gtccgcagca gttgtgaaaa gtacacacat catccgggtt tatcttgat gaatgagtga 60

aaatttttca tgcggactga aataactttt aggagacacc atg gct ctt act tct 115  
 Met Ala Leu Thr Ser 5  
 1

gag cag aag aag tcc atc ctt tcc gag ttc ggc ctc cac gag acc gac 163  
 Glu Gln Lys Lys Ser Ile Leu Ser Glu Phe Gly Leu His Glu Thr Asp 20  
 10 15

acc ggt tcc cca gaa gca cag atc gcg ctt ctg acc aac cgc atc aac 211  
 Thr Gly Ser Pro Glu Ala Gln Ile Ala Leu Leu Thr Asn Arg Ile Asn 35  
 25 30

aac ctc acc gag cac ctc aag ttc cac aag cac gat cac cac tcc cgt 259  
 Asn Leu Thr Glu His Leu Lys Phe His Lys His Asp His His Ser Arg 50  
 40 45

cgt ggt ctg ctg ctg ctc gtt ggt cgt cgt cgt ggt ctg ctg aag tac 307  
 Arg Gly Leu Leu Leu Val Gly Arg Arg Arg Gly Leu Leu Lys Tyr 60 65  
 55

ctg gct gac aac aac gtt gat cgc tac cgt gat ctg atc gca cgc ctc 355  
 Leu Ala Asp Asn Asn Val Asp Arg Tyr Arg Asp Leu Ile Ala Arg Leu 85  
 70 75 80

ggc ctg cgt cga taagcctggt tttccagtc ttt 390  
 Gly Leu Arg Arg

&lt;210&gt; 388

&lt;211&gt; 89

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 388

Met Ala Leu Thr Ser Glu Gln Lys Lys Ser Ile Leu Ser Glu Phe Gly  
 1 5 10 15

Leu His Glu Thr Asp Thr Gly Ser Pro Glu Ala Gln Ile Ala Leu Leu  
 20 25 30

Thr Asn Arg Ile Asn Asn Leu Thr Glu His Leu Lys Phe His Lys His  
 35 40 45

Asp His His Ser Arg Arg Gly Leu Leu Leu Val Gly Arg Arg Arg  
 50 55 60

Gly Leu Leu Lys Tyr Leu Ala Asp Asn Asn Val Asp Arg Tyr Arg Asp  
 65 70 75 80

Leu Ile Ala Arg Leu Gly Leu Arg Arg  
 85

&lt;210&gt; 389

&lt;211&gt; 618

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(595)

&lt;223&gt; RXA02752

&lt;400&gt; 389

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ccggaggagt cacgcgcagg ttaaacaaga agggctgaac cggctcacca gcacacgggtg 60
agtgactgta ctgcccagtg acctagtgag gaaaattcac atg gct gta aag att 115
                               Met Ala Val Lys Ile
                               1 5

aag ctc cag cgc ctc ggc aag atc cgt acc cgg cac tac cgc gtt gtc 163
Lys Leu Gln Arg Leu Gly Lys Ile Arg Thr Pro His Tyr Arg Val Val
                               10 15 20

atc gct gat gca cgc acc aag cgc gac ggc aag gtt atc gag aac atc 211
Ile Ala Asp Ala Arg Thr Lys Arg Asp Gly Lys Val Ile Glu Asn Ile
                               25 30 35

ggt atc tac gag cca aag gct gag cct tcc gta atc aag atc aac tcc 259
Gly Ile Tyr Glu Pro Lys Ala Glu Pro Ser Val Ile Lys Ile Asn Ser
                               40 45 50

gag cgt cgc cag cac tgg ctc tcc gtt ggc gct cag cca acc gag gct 307
Glu Arg Ala Gln His Trp Leu Ser Val Gly Ala Gln Pro Thr Glu Ala
                               55 60 65

gtt gca cgc ctg ctc aag gtg acc ggc gac tgg cag aag ttc aag ggc 355
Val Ala Ala Leu Leu Lys Val Thr Gly Asp Trp Gln Lys Phe Lys Gly
                               70 75 80 85

atc gag ggc gca gaa ggc acc ctc cgt gtt gca gag cct aag cca tcc 403
Ile Glu Gly Ala Glu Gly Thr Leu Arg Val Ala Glu Pro Lys Pro Ser
                               90 95 100

aag ctt gag ctg ttc aac cag gct ctt tct gag gct aac aac ggc cca 451
Lys Leu Glu Leu Phe Asn Gln Ala Leu Ser Glu Ala Asn Asn Gly Pro
                               105 110 115

acc gct gaa gcc atc act gaa aag aag aag gct cgc gag gac aag 499
Thr Ala Glu Ala Ile Thr Glu Lys Lys Lys Lys Ala Arg Glu Asp Lys
                               120 125 130

gaa gct aag gaa gca gct gag aag gct gct gct gaa aag gct gcc gct 547
Glu Ala Lys Glu Ala Ala Glu Lys Ala Ala Ala Glu Lys Ala Ala Ala
                               135 140 145

gca gag tcc gaa gag gct cca gct gag gaa gct gct gca gaa gag gca 595
Ala Glu Ser Glu Glu Ala Pro Ala Glu Glu Ala Ala Ala Glu Glu Ala
                               150 155 160 165

taagccactt ttgtttgtac ttc 618

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&lt;210&gt; 390

&lt;211&gt; 165

&lt;212&gt; PRT

## &lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 390

Met Ala Val Lys Ile Lys Leu Gln Arg Leu Gly Lys Ile Arg Thr Pro  
 1 5 10 15

His Tyr Arg Val Val Ile Ala Asp Ala Arg Thr Lys Arg Asp Gly Lys  
 20 25 30

Val Ile Glu Asn Ile Gly Ile Tyr Glu Pro Lys Ala Glu Pro Ser Val  
 35 40 45

Ile Lys Ile Asn Ser Glu Arg Ala Gln His Trp Leu Ser Val Gly Ala  
 50 55 60

Gln Pro Thr Glu Ala Val Ala Ala Leu Leu Lys Val Thr Gly Asp Trp  
 65 70 75 80

Gln Lys Phe Lys Gly Ile Glu Gly Ala Glu Gly Thr Leu Arg Val Ala  
 85 90 95

Glu Pro Lys Pro Ser Lys Leu Glu Leu Phe Asn Gln Ala Leu Ser Glu  
 100 105 110

Ala Asn Asn Gly Pro Thr Ala Glu Ala Ile Thr Glu Lys Lys Lys Lys  
 115 120 125

Ala Arg Glu Asp Lys Glu Ala Lys Glu Ala Ala Glu Lys Ala Ala Ala  
 130 135 140

Glu Lys Ala Ala Ala Ala Glu Ser Glu Glu Ala Pro Ala Glu Glu Ala  
 145 150 155 160

Ala Ala Glu Glu Ala  
 165

&lt;210&gt; 391

&lt;211&gt; 384

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(361)

&lt;223&gt; RXA02389

&lt;400&gt; 391

gttgacattt atgccaagca gtttatttaa aactgcggga gaaacactcc tcgatgggtt 60

tgtacacaac tttaactaga aagttcaaga ggtatttgcg atg gca aac atc aag 115  
 Met Ala Asn Ile Lys  
 1 5

tct cag atc aag cgt aac aag acc aac gag aag gct cgt ctg cgt aac 163  
 Ser Gln Ile Lys Arg Asn Lys Thr Asn Glu Lys Ala Arg Leu Arg Asn  
 10 15 20

cag gca gtt cgc tcc gca gtc cgc acc gag atc cgc aag ttc aac gct 211  
 Gln Ala Val Arg Ser Ala Val Arg Thr Glu Ile Arg Lys Phe Asn Ala  
 25 30 35

gcg att gaa gca ggc gac aag gat gca gct cag gct cag ctc cgt acc 259  
 Ala Ile Glu Ala Gly Asp Lys Asp Ala Ala Gln Ala Gln Leu Arg Thr  
           40                          45                          50

gct tcc cgc gca ctg gac aag gca gta acc aag ggt gtc ttc cac atc 307  
 Ala Ser Arg Ala Leu Asp Lys Ala Val Thr Lys Gly Val Phe His Ile  
           55                          60                          65

aac aac gct gct aac aag aag tcc aac atg gct acc gct ttc aac aag 355  
 Asn Asn Ala Ala Asn Lys Lys Ser Asn Met Ala Thr Ala Phe Asn Lys  
           70                          75                          80                          85

ctt ggc taatttttgg ctcttttgaa aat 384  
 Leu Gly

&lt;210&gt; 392

&lt;211&gt; 87

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 392

Met Ala Asn Ile Lys Ser Gln Ile Lys Arg Asn Lys Thr Asn Glu Lys  
           1                          5                          10                          15

Ala Arg Leu Arg Asn Gln Ala Val Arg Ser Ala Val Arg Thr Glu Ile  
                           20                          25                          30

Arg Lys Phe Asn Ala Ala Ile Glu Ala Gly Asp Lys Asp Ala Ala Gln  
           35                          40                          45

Ala Gln Leu Arg Thr Ala Ser Arg Ala Leu Asp Lys Ala Val Thr Lys  
           50                          55                          60

Gly Val Phe His Ile Asn Asn Ala Ala Asn Lys Lys Ser Asn Met Ala  
           65                          70                          75                          80

Thr Ala Phe Asn Lys Leu Gly  
                           85

&lt;210&gt; 393

&lt;211&gt; 1137

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101) .. (1114)

&lt;223&gt; RXA00671

<400> 393  
 gccccgggtg cacaggaatc ttctgatttt ccaaaccatcc ttcatgggttt tagaaacctt 60

taccgacgtc aaatagcgtt cgctactcaa ggagagtcca atg ctc att tca cag 115  
   Met Leu Ile Ser Gln  
   1                          5

cgc cca acc atc acc gag gaa ttt gtt aat aac gca cgt tcc cgg ttt 163

Arg	Pro	Thr	Ile	Thr	Glu	Glu	Phe	Val	Asn	Asn	Ala	Arg	Ser	Arg	Phe	
				10					15					20		
gtc	atc	gag	cca	ctg	gag	cca	ggg	ttt	ggc	tac	acc	ctc	ggg	aac	tcc	211
Val	Ile	Glu	Pro	Leu	Glu	Pro	Gly	Phe	Gly	Tyr	Thr	Leu	Gly	Asn	Ser	
				25				30					35			
ctg	cgc	cgt	acc	ctg	ctg	tcc	tcc	att	cct	gga	gca	gca	gta	acc	agc	259
Leu	Arg	Arg	Thr	Leu	Leu	Ser	Ser	Ile	Pro	Gly	Ala	Ala	Val	Thr	Ser	
		40					45					50				
gtc	aag	att	gac	ggg	gta	ctc	cac	gag	ttc	acc	acc	atc	agc	ggg	gtt	307
Val	Lys	Ile	Asp	Gly	Val	Leu	His	Glu	Phe	Thr	Thr	Ile	Ser	Gly	Val	
		55				60					65					
aag	gaa	gat	gtc	tct	gac	atc	atc	ttg	aac	atc	aag	gga	ttg	gtt	ttg	355
Lys	Glu	Asp	Val	Ser	Asp	Ile	Ile	Leu	Asn	Ile	Lys	Gly	Leu	Val	Leu	
	70				75				80					85		
tct	tct	gat	tcc	gat	gag	cca	gtt	gtt	atg	cag	ctg	gtc	aag	gaa	ggc	403
Ser	Ser	Asp	Ser	Asp	Glu	Pro	Val	Val	Met	Gln	Leu	Val	Lys	Glu	Gly	
				90					95					100		
cca	gga	gtt	gta	act	gca	ggg	gac	att	cag	cca	cca	gca	ggc	gtg	gag	451
Pro	Gly	Val	Val	Thr	Ala	Gly	Asp	Ile	Gln	Pro	Pro	Ala	Gly	Val	Glu	
				105				110					115			
atc	cac	aac	ccg	gat	ctg	cac	att	gca	acc	ctg	aac	gag	acc	gcc	aag	499
Ile	His	Asn	Pro	Asp	Leu	His	Ile	Ala	Thr	Leu	Asn	Glu	Thr	Ala	Lys	
		120					125					130				
att	gag	atc	gag	ctc	atc	gtc	gag	cgt	gga	cgt	ggc	tac	gtt	ccc	gca	547
Ile	Glu	Ile	Glu	Leu	Ile	Val	Glu	Arg	Gly	Arg	Gly	Tyr	Val	Pro	Ala	
		135				140					145					
act	gtt	act	gca	acc	ggg	gga	gag	atc	ggc	cgc	att	ccg	gtc	gat	cag	595
Thr	Val	Thr	Ala	Thr	Gly	Gly	Glu	Ile	Gly	Arg	Ile	Pro	Val	Asp	Gln	
	150				155				160					165		
atc	tac	tcc	cca	gta	ctg	aag	gtc	agc	tac	aag	gtt	gaa	gct	act	cgt	643
Ile	Tyr	Ser	Pro	Val	Leu	Lys	Val	Ser	Tyr	Lys	Val	Glu	Ala	Thr	Arg	
				170				175					180			
gtt	gag	cag	cgc	acc	gac	ttt	gac	aag	ctg	gtc	atc	gac	gtt	gag	acc	691
Val	Glu	Gln	Arg	Thr	Asp	Phe	Asp	Lys	Leu	Val	Ile	Asp	Val	Glu	Thr	
				185				190				195				
aag	aac	tct	att	acc	gca	cgt	gac	gcc	ctg	ggg	tcg	gca	ggg	aag	acc	739
Lys	Asn	Ser	Ile	Thr	Ala	Arg	Asp	Ala	Leu	Ala	Ser	Ala	Gly	Lys	Thr	
		200					205					210				
ctg	gtt	gag	ctg	ttc	ggc	ctc	gca	cgc	gag	ctg	aac	atc	gca	ggc	gag	787
Leu	Val	Glu	Leu	Phe	Gly	Leu	Ala	Arg	Glu	Leu	Asn	Ile	Ala	Ala	Glu	
		215				220					225					
ggc	atc	gag	atc	gga	cca	tct	oct	cag	gag	acc	gag	tac	atc	gct	ggc	835
Gly	Ile	Glu	Ile	Gly	Pro	Ser	Pro	Gln	Glu	Thr	Glu	Tyr	Ile	Ala	Ala	
	230				235				240					245		
tac	agc	atg	cca	atc	gag	gat	ctg	gac	ttc	tct	gtc	cgt	tcc	tac	aac	883
Tyr	Ser	Met	Pro	Ile	Glu	Asp	Leu	Asp	Phe	Ser	Val	Arg	Ser	Tyr	Asn	

250	255	260	
tgc ctc aag cgc gaa gac atc cac acc gtg ggt gaa ctc gca gag cgc			931
Cys Leu Lys Arg Glu Asp Ile His Thr Val Gly Glu Leu Ala Glu Arg			
265	270	275	
gct gag tcc gat ttg ctg gat atc cgc aac ttc gga cag aag tcg atc			979
Ala Glu Ser Asp Leu Leu Asp Ile Arg Asn Phe Gly Gln Lys Ser Ile			
280	285	290	
aac gag gta aag atc aag ctt gct ggc ctg ggt ctg acc ctg aag gat			1027
Asn Glu Val Lys Ile Lys Leu Ala Gly Leu Gly Leu Thr Leu Lys Asp			
295	300	305	
gct cct gaa gac ttc gat cct tca act ctt gaa ggt tat gac gcc gaa			1075
Ala Pro Glu Asp Phe Asp Pro Ser Thr Leu Glu Gly Tyr Asp Ala Glu			
310	315	320	325
act ggt ggc tac atc gat gtc gag gcg gaa gat tcc gag taagtcgcat			1124
Thr Gly Gly Tyr Ile Asp Val Glu Ala Glu Asp Ser Glu			
330	335		
ggtccaattc atg			1137
<210> 394			
<211> 338			
<212> PRT			
<213> Corynebacterium glutamicum			
<400> 394			
Met Leu Ile Ser Gln Arg Pro Thr Ile Thr Glu Glu Phe Val Asn Asn			
1	5	10	15
Ala Arg Ser Arg Phe Val Ile Glu Pro Leu Glu Pro Gly Phe Gly Tyr			
20	25	30	
Thr Leu Gly Asn Ser Leu Arg Arg Thr Leu Leu Ser Ser Ile Pro Gly			
35	40	45	
Ala Ala Val Thr Ser Val Lys Ile Asp Gly Val Leu His Glu Phe Thr			
50	55	60	
Thr Ile Ser Gly Val Lys Glu Asp Val Ser Asp Ile Ile Leu Asn Ile			
65	70	75	80
Lys Gly Leu Val Leu Ser Ser Asp Ser Asp Glu Pro Val Val Met Gln			
85	90	95	
Leu Val Lys Glu Gly Pro Gly Val Val Thr Ala Gly Asp Ile Gln Pro			
100	105	110	
Pro Ala Gly Val Glu Ile His Asn Pro Asp Leu His Ile Ala Thr Leu			
115	120	125	
Asn Glu Thr Ala Lys Ile Glu Ile Glu Leu Ile Val Glu Arg Gly Arg			
130	135	140	
Gly Tyr Val Pro Ala Thr Val Thr Ala Thr Gly Gly Glu Ile Gly Arg			
145	150	155	160



Ile Pro Val Asp Gln Ile Tyr Ser Pro Val Leu Lys Val Ser Tyr Lys  
 165 170 175

Val Glu Ala Thr Arg Val Glu Gln Arg Thr Asp Phe Asp Lys Leu Val  
 180 185 190

Ile Asp Val Glu Thr Lys Asn Ser Ile Thr Ala Arg Asp Ala Leu Ala  
 195 200 205

Ser Ala Gly Lys Thr Leu Val Glu Leu Phe Gly Leu Ala Arg Glu Leu  
 210 215 220

Asn Ile Ala Ala Glu Gly Ile Glu Ile Gly Pro Ser Pro Gln Glu Thr  
 225 230 235

Glu Tyr Ile Ala Ala Tyr Ser Met Pro Ile Glu Asp Leu Asp Phe Ser  
 245 250 255

Val Arg Ser Tyr Asn Cys Leu Lys Arg Glu Asp Ile His Thr Val Gly  
 260 265 270

Glu Leu Ala Glu Arg Ala Glu Ser Asp Leu Leu Asp Ile Arg Asn Phe  
 275 280 285

Gly Gln Lys Ser Ile Asn Glu Val Lys Ile Lys Leu Ala Gly Leu Gly  
 290 295 300

Leu Thr Leu Lys Asp Ala Pro Glu Asp Phe Asp Pro Ser Thr Leu Glu  
 305 310 315 320

Gly Tyr Asp Ala Glu Thr Gly Gly Tyr Ile Asp Val Glu Ala Glu Asp  
 325 330 335

Ser Glu

<210> 395  
 <211> 489  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(466)  
 <223> RXN02981

<400> 395  
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ggggaaaacc atcgcaacaa ccggaaaggg taactgccac atg gca cgt cta gct 115  
 Met Ala Arg Leu Ala  
 1 5

ggt gtt gac ctc cca cgc aac aag cgt atg gaa gtc gct ctc acc tac 163  
 Gly Val Asp Leu Pro Arg Asn Lys Arg Met Glu Val Ala Leu Thr Tyr  
 10 15 20

atc tac gga atc ggc cca gcc cgt tcc aag cag ctt ctc gag gag acc 211  
 Ile Tyr Gly Ile Gly Pro Ala Arg Ser Lys Gln Leu Leu Glu Glu Thr  
 25 30 35

gga atc tcc cca gac ctg cgc acc gac aac ctc act gat gag cag atc 259  
 Gly Ile Ser Pro Asp Leu Arg Thr Asp Asn Leu Thr Asp Glu Gln Ile  
 40 45 50  
 gct gct ctt cgt gac gtt att gaa ggc acc tgg aag gtc gag ggt gac 307  
 Ala Ala Leu Arg Asp Val Ile Glu Gly Thr Trp Lys Val Glu Gly Asp  
 55 60 65  
 ctc cgc cgc cag gta caa gct gac atc cgt cgc aag atc gaa atc ggc 355  
 Leu Arg Arg Gln Val Gln Ala Asp Ile Arg Arg Lys Ile Glu Ile Gly  
 70 75 80 85  
 tgc tac cag ggt att cgc cac cgc cgt ggc ctg cct gtt cgt ggt cag 403  
 Cys Tyr Gln Gly Ile Arg His Arg Arg Gly Leu Pro Val Arg Gly Gln  
 90 95 100  
 cgc acc aag acc aat gcg cgt act cgt aag ggt cct aag aag acg atc 451  
 Arg Thr Lys Thr Asn Ala Arg Thr Arg Lys Gly Pro Lys Lys Thr Ile  
 105 110 115  
 gcc gga aag aag aag taaaaatgcc tcctaaagca cgc 489  
 Ala Gly Lys Lys Lys  
 120

&lt;210&gt; 396

&lt;211&gt; 122

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 396

Met Ala Arg Leu Ala Gly Val Asp Leu Pro Arg Asn Lys Arg Met Glu  
 1 5 10 15

Val Ala Leu Thr Tyr Ile Tyr Gly Ile Gly Pro Ala Arg Ser Lys Gln  
 20 25 30

Leu Leu Glu Thr Gly Ile Ser Pro Asp Leu Arg Thr Asp Asn Leu  
 35 40 45

Thr Asp Glu Gln Ile Ala Ala Leu Arg Asp Val Ile Glu Gly Thr Trp  
 50 55 60

Lys Val Glu Gly Asp Leu Arg Arg Gln Val Gln Ala Asp Ile Arg Arg  
 65 70 75 80

Lys Ile Glu Ile Gly Cys Tyr Gln Gly Ile Arg His Arg Arg Gly Leu  
 85 90 95

Pro Val Arg Gly Gln Arg Thr Lys Thr Asn Ala Arg Thr Arg Lys Gly  
 100 105 110

Pro Lys Lys Thr Ile Ala Gly Lys Lys Lys  
 115 120

&lt;210&gt; 397

&lt;211&gt; 372

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(349)

&lt;223&gt; RXN03139

&lt;400&gt; 397

tccgtaagtt cgggtctttcc cgtgtccgta tgcgcgagat ggctcacgt ggtgagctgc 60

cgggcggttcg taagtccagc tggtaaggga gtttttacca atg aag cag cgt aac 115  
 Met Lys Gln Arg Asn  
 1 5

aac gct aag cgc gtc cgc ctt gag cag act cgc cgc cca aag aag aac 163  
 Asn Ala Lys Arg Val Arg Leu Glu Gln Thr Arg Arg Pro Lys Lys Asn  
 10 15 20

ccg ctg aag gca gcg gcc atc gag aag gtg gac tac aag gac atc aac 211  
 Pro Leu Lys Ala Ala Gly Ile Glu Lys Val Asp Tyr Lys Asp Ile Asn  
 25 30 35

acc ctt cgt cag ttc atc tcc gac cgc cac aag atc cgt tca cgt cgt 259  
 Thr Leu Arg Gln Phe Ile Ser Asp Arg His Lys Ile Arg Ser Arg Arg  
 40 45 50

gtc acc ggt ctg acc ccg cag cag cag cgc gag gtt gca acc gcc gtg 307  
 Val Thr Gly Leu Thr Pro Gln Gln Gln Arg Glu Val Ala Thr Ala Val  
 55 60 65

aag aac gca cgc gaa atg gct ctc ctg ccg ttc acc agc cgc 349  
 Lys Asn Ala Arg Glu Met Ala Leu Leu Pro Phe Thr Ser Arg  
 70 75 80

taagactggg aataacgtaa cag 372

&lt;210&gt; 398

&lt;211&gt; 83

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 398

Met Lys Gln Arg Asn Asn Ala Lys Arg Val Arg Leu Glu Gln Thr Arg  
 1 5 10 15

Arg Pro Lys Lys Asn Pro Leu Lys Ala Ala Gly Ile Glu Lys Val Asp  
 20 25 30

Tyr Lys Asp Ile Asn Thr Leu Arg Gln Phe Ile Ser Asp Arg His Lys  
 35 40 45

Ile Arg Ser Arg Arg Val Thr Gly Leu Thr Pro Gln Gln Gln Arg Glu  
 50 55 60

Val Ala Thr Ala Val Lys Asn Ala Arg Glu Met Ala Leu Leu Pro Phe  
 65 70 75 80

Thr Ser Arg

<210> 399  
 <211> 525  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(502)  
 <223> RXN00673

<400> 399  
 gccaccgcgcg tggcctgcct gttcgtgggc agcgcaccaa gaccaatgcg cgtactcgta 60  
 aggggtcctaa gaagacgacg gccggaaaga agaagtaaaa atg cct cct aaa gca 115  
 Met Pro Pro Lys Ala  
 1 5  
 cgc act aac gcg cgc cgc aca ggc cgt cgc gtt gta aaa aag aac gtt 163  
 Arg Thr Asn Ala Arg Arg Thr Gly Arg Arg Val Val Lys Lys Asn Val  
 10 15 20  
 gct aac ggc aac gct tac atc aag tcc acc ttt aac aac acc atc gtt 211  
 Ala Asn Gly Asn Ala Tyr Ile Lys Ser Thr Phe Asn Asn Thr Ile Val  
 25 30 35  
 tcg atc act gat acc aac ggt gct gta atc tct tgg gct tcc tct ggg 259  
 Ser Ile Thr Asp Thr Asn Gly Ala Val Ile Ser Trp Ala Ser Ser Gly  
 40 45 50  
 cac gtc gga ttc aag ggc tca cgt aag tcc act cgc ttc gct gct cag 307  
 His Val Gly Phe Lys Gly Ser Arg Lys Ser Thr Pro Phe Ala Ala Gln  
 55 60 65  
 atg gct gca gag aac gct gcc cgc aag gca atg gat cac ggc atg aag 355  
 Met Ala Ala Glu Asn Ala Ala Arg Lys Ala Met Asp His Gly Met Lys  
 70 75 80 85  
 aag gtt gac gtt ttc gtc aag ggc cca gga tca ggc cgc gag act gca 403  
 Lys Val Asp Val Phe Val Lys Gly Pro Gly Ser Gly Arg Glu Thr Ala  
 90 95 100  
 atc cgt tcc ett cag gct gca ggc ctg gag atc ggt tca atc tcc gac 451  
 Ile Arg Ser Leu Gln Ala Ala Gly Leu Glu Ile Gly Ser Ile Ser Asp  
 105 110 115  
 gtg acc cca cag cca cac aac ggc tgc cgt cca cca aag cgt cgt cgc 499  
 Val Thr Pro Gln Pro His Asn Gly Cys Arg Pro Pro Lys Arg Arg Arg  
 120 125 130  
 gtt taataggga gaaaggtaa tac 525  
 Val

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 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 400  
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 atc gac gga aaa gta tgg gac ctc aag tac cgc ctc cgc ccc gac cta 403  
 Ile Asp Gly Lys Val Trp Asp Leu Lys Tyr Arg Leu Arg Pro Asp Leu  
 90 95 100  
 tgg ggc aat gga tac gcc acg gaa atc tcc aac gcc gca aca ctg gcc 451  
 Trp Gly Asn Gly Tyr Ala Thr Glu Ile Ser Asn Ala Ala Thr Leu Ala  
 105 110 115  
 acc aag cgt atc gac gac agc ctc cca ctc acg gcc agg gtg act acc 499  
 Thr Lys Arg Ile Asp Asp Ser Leu Pro Leu Thr Ala Arg Val Thr Thr  
 120 125 130  
 aac cac cct gcc tca ttc cgt att ttg gaa aaa ctg gga ctc acc ccc 547  
 Asn His Pro Ala Ser Phe Arg Ile Leu Glu Lys Leu Gly Leu Thr Pro  
 135 140 145  
 gta tgg gaa ggc cga cga gtc gga acg gaa gat gac ccc aac gag cct 595  
 Val Trp Glu Gly Arg Arg Val Gly Thr Glu Asp Asp Pro Asn Glu Pro  
 150 155 160 165  
 gat gtg aga att tat tct gac cgt cgc cta tgg gat gaa att ctt gaa 643  
 Asp Val Arg Ile Tyr Ser Asp Arg Pro Leu Ser Asp Glu Ile Leu Glu  
 170 175 180  
 atg ctc aag caa cga cca tagaccagaa aatctcacc ctt 684  
 Met Leu Lys Gln Arg Pro  
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 <213> *Corynebacterium glutamicum*  
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 Trp Glu His Arg Pro Gln Ala Arg His Thr Asn Val Arg Val Thr Arg  
 35 40 45  
 Asp Ile Ile Lys Arg Thr Asn Glu Ser Trp Gly Lys Lys Asp Leu Gly  
 50 55 60  
 Pro Trp Gly Val Tyr Leu Arg Asp Arg Pro Ser Glu Phe Val Gly Val  
 65 70 75 80  
 Gly Gly Val Glu Leu Ile Asp Gly Lys Val Trp Asp Leu Lys Tyr Arg  
 85 90 95  
 Leu Arg Pro Asp Leu Trp Gly Asn Gly Tyr Ala Thr Glu Ile Ser Asn  
 100 105 110  
 Ala Ala Thr Leu Ala Thr Lys Arg Ile Asp Asp Ser Leu Pro Leu Thr  
 115 120 125

Ala Arg Val Thr Thr Asn His Pro Ala Ser Phe Arg Ile Leu Glu Lys  
130 135 140

Leu Gly Leu Thr Pro Val Trp Glu Gly Arg Arg Val Gly Thr Glu Asp  
145 150 155 160

Asp Pro Asn Glu Pro Asp Val Arg Ile Tyr Ser Asp Arg Pro Leu Ser  
165 170 175

Asp Glu Ile Leu Glu Met Leu Lys Gln Arg Pro  
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<210> 403

<211> 1128

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1105)

<223> RXN00897

<400> 403

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Met Thr Pro Ser Leu  
1 5

ccc cgt ttc cgc agc cag aaa cct gcc gtc gcc gat cgt gtt gtt gca 163  
Pro Arg Phe Arg Ser Gln Lys Pro Ala Val Gly Asp Arg Val Val Ala  
10 15 20

cgt cgc cgg att cct ggt gcc aat gtg cat tgg aca gat gtc att ggc 211  
Arg Arg Arg Ile Pro Gly Ala Asn Val His Trp Thr Asp Val Ile Gly  
25 30 35

cat gtg att ggg gtg gat ccg ttg gtg gtt cgc ccg cag tgc gtt ggt 259  
His Val Ile Gly Val Asp Pro Leu Val Val Arg Pro Gln Ser Val Gly  
40 45 50

ggg atg ccg tct gat gcg gaa gaa att gtc att cct gat gat cag ctt 307  
Gly Met Pro Ser Asp Ala Glu Glu Ile Val Ile Pro Asp Asp Gln Leu  
55 60 65

gag gtg att aag att ttg tgc ccg cgc acc att agg aat tgc gat att 355  
Glu Val Ile Lys Ile Leu Ser Pro Arg Thr Ile Arg Asn Ser Asp Ile  
70 75 80 85

cgt gcg gtg gag gtt gcc acg gcg aag gcc ttt ccg ggg ctg gtc aat 403  
Arg Ala Val Glu Val Ala Thr Ala Lys Ala Phe Pro Gly Leu Val Asn  
90 95 100

gag tgg cat gat ggt tgg ctg ctg cgt gcc ggt gat gcc att gcg gag 451  
Glu Trp His Asp Gly Trp Leu Leu Arg Ala Gly Asp Gly Ile Ala Glu  
105 110 115

cgt tct aat tct gcg tgc cca ctc gcc cca agt gtc ggt tct gag ccg 499  
Arg Ser Asn Ser Ala Ser Pro Leu Gly Pro Ser Val Gly Ser Glu Pro

120	125	130	
gta ccg atg gag gat att tgc cgg ttt tat gca cgt cac gat ctc ccc Val Pro Met Glu Asp Ile Ser Arg Phe Tyr Ala Arg His Asp Leu Pro 135 140 145			547
gtg aag ctg cac att ccg gag cgg att ggt cgg cct gcg cag aaa gtc Val Lys Leu His Ile Pro Glu Arg Ile Gly Arg Pro Ala Gln Lys Val 150 155 160 165			595
att gac gcc gat ccc cag aaa tgg gtg atg ggc cgg gag att ttg gtg Ile Asp Ala Asp Pro Gln Lys Trp Val Met Gly Pro Glu Ile Leu Val 170 175 180			643
atg acg aaa tct ttg gac cat gtg gag tgc cac gaa ttg ccc ggt ggc Met Thr Lys Ser Leu Asp His Val Glu Ser His Glu Leu Pro Gly Gly 185 190 195			691
cta gaa ttt agc gtc gat aag cag cct gac cag gag tgg ctg ggc atg Leu Glu Phe Ser Val Asp Lys Gln Pro Asp Gln Glu Trp Leu Gly Met 200 205 210			739
tac cat ttc cgc gga cag gcg ttg ccc gct cac gcc ctt gag ctt ttg Tyr His Phe Arg Gly Gln Ala Leu Pro Ala His Ala Leu Glu Leu Leu 215 220 225			787
cgc acg caa atc gag ggc cgc atg ggg ttc ggg cgc ctg acc acg ccg Arg Thr Gln Ile Glu Gly Arg Met Gly Phe Gly Arg Leu Thr Thr Pro 230 235 240 245			835
gcg ggg caa acc gtc gcg atc acg cgc gcc acc atc acg gct gcg gag Ala Gly Gln Thr Val Ala Ile Thr Arg Ala Thr Ile Thr Ala Ala Glu 250 255 260			883
gag cgc ata ttt ttg ggc tat tca gcg gtc gag gtg gat cct gct ttt Glu Arg Ile Phe Leu Gly Tyr Ser Ala Val Glu Val Asp Pro Ala Phe 265 270 275			931
cga cgt cag ggg ctg ggc acc gcg ctc ggc tgc cgc atc cag gag tgg Arg Arg Gln Gly Leu Gly Thr Ala Leu Gly Ser Arg Ile Gln Glu Trp 280 285 290			979
ggc gcc gag caa cac gca cag gag gca tat ctc cag gtt gtc gcc cat Gly Ala Glu Gln His Ala Gln Glu Ala Tyr Leu Gln Val Val Ala His 295 300 305			1027
aat gaa gca ggt atc ggc ctg tat caa aag ctc ggg ttc agt gaa cac Asn Glu Ala Gly Ile Gly Leu Tyr Gln Lys Leu Gly Phe Ser Glu His 310 315 320 325			1075
cac cga cac cgg tac gcc gaa cgg aaa ttc taaaatccaa aacagctagg His Arg His Arg Tyr Ala Glu Arg Lys Phe 330 335			1125
gta			1128

&lt;210&gt; 404

&lt;211&gt; 335

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum



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 Thr Asp Val Ile Gly His Val Ile Gly Val Asp Pro Leu Val Val Arg  
 35 40 45  
 Pro Gln Ser Val Gly Gly Met Pro Ser Asp Ala Glu Glu Ile Val Ile  
 50 55 60  
 Pro Asp Asp Gln Leu Glu Val Ile Lys Ile Leu Ser Pro Arg Thr Ile  
 65 70 75 80  
 Arg Asn Ser Asp Ile Arg Ala Val Glu Val Ala Thr Ala Lys Ala Phe  
 85 90 95  
 Pro Gly Leu Val Asn Glu Trp His Asp Gly Trp Leu Leu Arg Ala Gly  
 100 105 110  
 Asp Gly Ile Ala Glu Arg Ser Asn Ser Ala Ser Pro Leu Gly Pro Ser  
 115 120 125  
 Val Gly Ser Glu Pro Val Pro Met Glu Asp Ile Ser Arg Phe Tyr Ala  
 130 135 140  
 Arg His Asp Leu Pro Val Lys Leu His Ile Pro Glu Arg Ile Gly Arg  
 145 150 155 160  
 Pro Ala Gln Lys Val Ile Asp Ala Asp Pro Gln Lys Trp Val Met Gly  
 165 170 175  
 Pro Glu Ile Leu Val Met Thr Lys Ser Leu Asp His Val Glu Ser His  
 180 185 190  
 Glu Leu Pro Gly Gly Leu Glu Phe Ser Val Asp Lys Gln Pro Asp Gln  
 195 200 205  
 Glu Trp Leu Gly Met Tyr His Phe Arg Gly Gln Ala Leu Pro Ala His  
 210 215 220  
 Ala Leu Glu Leu Leu Arg Thr Gln Ile Glu Gly Arg Met Gly Phe Gly  
 225 230 235 240  
 Arg Leu Thr Thr Pro Ala Gly Gln Thr Val Ala Ile Thr Arg Ala Thr  
 245 250 255  
 Ile Thr Ala Ala Glu Glu Arg Ile Phe Leu Gly Tyr Ser Ala Val Glu  
 260 265 270  
 Val Asp Pro Ala Phe Arg Arg Gln Gly Leu Gly Thr Ala Leu Gly Ser  
 275 280 285  
 Arg Ile Gln Glu Trp Gly Ala Glu Gln His Ala Gln Glu Ala Tyr Leu  
 290 295 300  
 Gln Val Val Ala His Asn Glu Ala Gly Ile Gly Leu Tyr Gln Lys Leu  
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Gly Phe Ser Glu His His Arg His Arg Tyr Ala Glu Arg Lys Phe  
325 330 335

<210> 405

<211> 2322

<212> DNA

<213> *Corynebacterium glutamicum*

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<223> RXN01380

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cggcgtcaaa gatgaacaag tgcaggccgc catcaagctc ttg gat gaa gga aac 115  
Leu Asp Glu Gly Asn  
1 5

acc gtt ccg ttc atc gcc agg tac cgc aag gaa atc act ggg gga ctc 163  
Thr Val Pro Phe Ile Ala Arg Tyr Arg Lys Glu Ile Thr Gly Gly Leu  
10 15 20

gat gat acc caa ctg cgt gac ctg gaa gaa cgc ctc agt tac ctc cgt 211  
Asp Asp Thr Gln Leu Arg Asp Leu Glu Arg Leu Ser Tyr Leu Arg  
25 30 35

gag ctg gag gat cgt aaa caa agc atc ctc gcc gcg att gag gaa caa 259  
Glu Leu Glu Asp Arg Lys Gln Ser Ile Leu Ala Ala Ile Glu Glu Gln  
40 45 50

ggc aaa ctc acc gac gat tta cgc tcg ctg att ttg gga tgc gac acc 307  
Gly Lys Leu Thr Asp Asp Leu Arg Ser Leu Ile Leu Gly Cys Asp Thr  
55 60 65

aag gct cgc ctg gag gat ctg tac ctg cgc ttc aaa aaa cgc cgc aag 355  
Lys Ala Arg Leu Glu Asp Leu Tyr Leu Pro Phe Lys Lys Arg Arg Lys  
70 75 80 85

acg aag gcc gat atc gct agg gag gcg ggc ctg gag ggg ctc gtc gat 403  
Thr Lys Ala Asp Ile Ala Arg Glu Ala Gly Leu Glu Gly Leu Val Asp  
90 95 100

aag ctt atc gac gcc ccg tcc ctc gac gcc gca gcg cag gca gct gca 451  
Lys Leu Ile Asp Ala Pro Ser Leu Asp Ala Ala Ala Gln Ala Ala Ala  
105 110 115

ttt acg act gag ggc ttt gag gat tcc aaa aaa gtt ttg gat ggc gct 499  
Phe Thr Thr Glu Gly Phe Glu Asp Ser Lys Lys Val Leu Asp Gly Ala  
120 125 130

cgc gcc att ttg att gac cgc ttc gcg ctc gat gcc gat ttg gtg ggc 547  
Arg Ala Ile Leu Ile Asp Arg Phe Ala Leu Asp Ala Asp Leu Val Gly  
135 140 145

gag gtg cgt gag caa atg tat cgc gcg ggt tcc atg gcg gca tcg gtg 595  
Glu Val Arg Glu Gln Met Tyr Arg Ala Gly Ser Met Ala Ala Ser Val  
150 155 160 165

gtg	gcg	ggc	aag	gag	cag	gaa	ggc	gca	aag	ttc	aag	gac	tac	ttt	gag	643
Val	Ala	Gly	Lys	Glu	Gln	Glu	Gly	Ala	Lys	Phe	Lys	Asp	Tyr	Phe	Glu	
170																
ttt	tcc	gaa	cct	ttt	gac	aag	ctt	cca	tct	cac	cga	att	ttg	gcg	ctg	691
Phe	Ser	Glu	Pro	Phe	Asp	Lys	Leu	Pro	Ser	His	Arg	Ile	Leu	Ala	Leu	
185																
ctg	cgc	ggt	gaa	aac	gaa	ggt	gtg	ctg	agc	ctc	aac	ctc	gat	gcg	ggc	739
Leu	Arg	Gly	Glu	Asn	Glu	Gly	Val	Leu	Ser	Leu	Asn	Leu	Asp	Ala	Gly	
200																
gac	gac	ata	atc	tac	gaa	ggt	ttg	atc	gcc	gac	cga	ttc	tcc	ctg	gac	787
Asp	Asp	Ile	Ile	Tyr	Glu	Gly	Leu	Ile	Ala	Asp	Arg	Phe	Ser	Leu	Asp	
215																
acc	cac	act	tct	agc	tgg	ctg	gct	gag	gct	gtg	cgc	tgg	ggt	tgg	cgc	835
Thr	His	Thr	Ser	Ser	Trp	Leu	Ala	Glu	Ala	Val	Arg	Trp	Gly	Trp	Arg	
230																
acc	aaa	ctg	tat	gtg	tcc	tcc	gga	ttg	gat	gtg	cgc	atg	cgt	ctg	aaa	883
Thr	Lys	Leu	Tyr	Val	Ser	Ser	Gly	Leu	Asp	Val	Arg	Met	Arg	Leu	Lys	
250																
gaa	aaa	gca	gag	gaa	ggc	gca	ctc	gat	gtg	ttt	gcc	acc	aac	ctc	cgc	931
Glu	Lys	Ala	Glu	Glu	Gly	Ala	Leu	Asp	Val	Phe	Ala	Thr	Asn	Leu	Arg	
265																
gac	ggt	ctc	ctt	gca	gct	ccc	gct	ggc	cag	cgc	tcc	aca	att	ggc	ctt	979
Asp	Val	Leu	Leu	Ala	Ala	Pro	Ala	Gly	Gln	Arg	Ser	Thr	Ile	Gly	Leu	
280																
gac	ccg	gga	ttc	cgc	aac	ggt	gtg	aaa	gta	gct	gtc	gtg	gat	tcc	acc	1027
Asp	Pro	Gly	Phe	Arg	Asn	Gly	Val	Lys	Val	Ala	Val	Val	Asp	Ser	Thr	
295																
ggt	aag	gat	ggt	gcc	acc	acg	atc	gtc	tac	cca	cac	cag	ccc	caa	aac	1075
Gly	Lys	Asp	Val	Ala	Thr	Thr	Ile	Val	Tyr	Pro	His	Gln	Pro	Gln	Asn	
310																
cgc	tgg	aag	gaa	gcc	gta	tcc	gaa	ctg	gct	aac	ctg	tgc	gcg	acc	cac	1123
Arg	Trp	Lys	Glu	Ala	Val	Ser	Glu	Leu	Ala	Asn	Leu	Cys	Ala	Thr	His	
330																
ggt	gtg	gaa	ctc	atg	gcg	atc	ggc	aac	gga	acc	gcc	tcg	agg	gaa	acg	1171
Gly	Val	Glu	Leu	Met	Ala	Ile	Gly	Asn	Gly	Thr	Ala	Ser	Arg	Glu	Thr	
345																
gaa	aaa	ctc	gcc	ggc	gaa	gta	gct	gac	atg	atc	aaa	gcc	gca	ggt	ggc	1219
Glu	Lys	Leu	Ala	Gly	Glu	Val	Ala	Asp	Met	Ile	Lys	Ala	Ala	Gly	Gly	
360																
acg	cga	cca	acc	ccc	gtg	gtg	gtc	tcc	gaa	tcg	ggc	gca	tcc	gtg	tac	1267
Thr	Arg	Pro	Thr	Pro	Val	Val	Val	Ser	Glu	Ser	Gly	Ala	Ser	Val	Tyr	
375																
tcg	gca	tca	ccg	atc	gca	gcc	gaa	gaa	ttc	ccc	gac	atg	gac	gtc	tcc	1315
Ser	Ala	Ser	Pro	Ile	Ala	Ala	Glu	Glu	Phe	Pro	Asp	Met	Asp	Val	Ser	
390																
405																

ctc cgc ggt gca gtt tct atc gcg agg cga ctc cag gat cca ctg gcg 1363  
 Leu Arg Gly Ala Val Ser Ile Ala Arg Arg Leu Gln Asp Pro Leu Ala  
 410 415 420

gag ctc gtc aag att gag ccc aaa gcc atc gga gtc gcc cag tac caa 1411  
 Glu Leu Val Lys Ile Glu Pro Lys Ala Ile Gly Val Gly Gln Tyr Gln  
 425 430 435

cac gat gtc aac cag gtt gca ctt gcc aaa acc ctt gat ggt gtc gtc 1459  
 His Asp Val Asn Gln Val Ala Leu Ala Lys Thr Leu Asp Gly Val Val  
 440 445 450

gaa gac gca gta aac gca gtc gga gtt aac ctc aac acc gca tcc gca 1507  
 Glu Asp Ala Val Asn Ala Val Gly Val Asn Leu Asn Thr Ala Ser Ala  
 455 460 465

cca ctt ctt acc cga gtt gcc gga gtg acc tcc acc ttg gca aac aat 1555  
 Pro Leu Leu Thr Arg Val Ala Gly Val Thr Ser Thr Leu Ala Asn Asn  
 470 475 480 485

atc gtg gcc tac cgc aac gaa aac ggt gga ttc tcc tcc cga aaa gaa 1603  
 Ile Val Ala Tyr Arg Asn Glu Asn Gly Gly Phe Ser Ser Arg Lys Glu  
 490 495 500

ctg aac aaa gtt cct cgc ctg gga ccc aaa gcc ttt gaa cag tgt gct 1651  
 Leu Asn Lys Val Pro Arg Leu Gly Pro Lys Ala Phe Glu Gln Cys Ala  
 505 510 515

ggc ttc ctc cgc att tct gga tcc acc gac cct ctc gac gcc tcc gct 1699  
 Gly Phe Leu Arg Ile Ser Gly Ser Thr Asp Pro Leu Asp Ala Ser Ala  
 520 525 530

gtt cac ccc gag gcg tac cca gtt gtt cgc aac att gcg aaa gcc aca 1747  
 Val His Pro Glu Ala Tyr Pro Val Val Arg Asn Ile Ala Lys Ala Thr  
 535 540 545

gga ttg gat gtc tcg gga ctg atc gga aac tct gcg gtg ctc acc aaa 1795  
 Gly Leu Asp Val Ser Gly Leu Ile Gly Asn Ser Ala Val Leu Thr Lys  
 550 555 560 565

ttg aag ccc gct gat ttc gct gat gaa cga ttc gcc atc ccc acc gtc 1843  
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 570 575 580

acc gac atc atc gcc gag ctg gat aaa ccc gga cgt gac ccc cgc cca 1891  
 Thr Asp Ile Ile Ala Glu Leu Asp Lys Pro Gly Arg Asp Pro Arg Pro  
 585 590 595

gaa ttc aaa acc gcc agc ttc aaa gaa gcc gtg gag aaa atc tcc gac 1939  
 Glu Phe Lys Thr Ala Ser Phe Lys Glu Gly Val Glu Lys Ile Ser Asp  
 600 605 610

ctc aca ccc gcc atg atc ctg gaa gga act gtc acc aac gtt gcg gcg 1987  
 Leu Thr Pro Gly Met Ile Leu Glu Gly Thr Val Thr Asn Val Ala Ala  
 615 620 625

ttc gcc gca ttc gtt gac gtg gga gtg cac cga gat gcc ctc gtt cac 2035  
 Phe Gly Ala Phe Val Asp Val Gly Val His Arg Asp Gly Leu Val His  
 630 635 640 645

gtt tcc gcg atg agc gac aaa ttc atc tcc aac ccc cac gaa gtt gtt 2083

Val Ser Ala Met Ser Asp Lys Phe Ile Ser Asn Pro His Glu Val Val  
650 655 660

cgc tct ggt gag gtc gtg aag gta aag gtc atg gaa gtt gac gtc gac 2131  
Arg Ser Gly Glu Val Val Lys Val Lys Val Met Glu Val Asp Val Asp  
665 670 675

cgc aaa cgc atc ggc ctt tcc ctc cgc ttg acc gat gaa ccc ggt gcc 2179  
Arg Lys Arg Ile Gly Leu Ser Leu Arg Leu Thr Asp Glu Pro Gly Ala  
680 685 690

cca gct ccg caa aag cgc gga aac cga cca gcc aaa cag cag cga gct 2227  
Pro Ala Pro Gln Lys Arg Gly Asn Arg Pro Ala Lys Gln Gln Arg Ala  
695 700 705

ccg caa aaa cag tcc gct aag ccc gcc aca ggt tcc atg gca gat gct 2275  
Pro Gln Lys Gln Ser Ala Lys Pro Ala Thr Gly Ser Met Ala Asp Ala  
710 715 720 725

tta cga cgc gcc ggc ctc ggt ggc taaggcaact ttcaaacc aa gcg 2322  
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730

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<211> 733  
<212> PRT  
<213> Corynebacterium glutamicum

<400> 406  
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Leu Ser Tyr Leu Arg Glu Leu Glu Asp Arg Lys Gln Ser Ile Leu Ala  
35 40 45

Ala Ile Glu Glu Gln Gly Lys Leu Thr Asp Asp Leu Arg Ser Leu Ile  
50 55 60

Leu Gly Cys Asp Thr Lys Ala Arg Leu Glu Asp Leu Tyr Leu Pro Phe  
65 70 75 80

Lys Lys Arg Arg Lys Thr Lys Ala Asp Ile Ala Arg Glu Ala Gly Leu  
85 90 95

Glu Gly Leu Val Asp Lys Leu Ile Asp Ala Pro Ser Leu Asp Ala Ala  
100 105 110

Ala Gln Ala Ala Ala Phe Thr Thr Glu Gly Phe Glu Asp Ser Lys Lys  
115 120 125

Val Leu Asp Gly Ala Arg Ala Ile Leu Ile Asp Arg Phe Ala Leu Asp  
130 135 140

Ala Asp Leu Val Gly Glu Val Arg Glu Gln Met Tyr Arg Ala Gly Ser  
145 150 155 160

Met Ala Ala Ser Val Val Ala Gly Lys Glu Gln Glu Gly Ala Lys Phe

[illegible]

Ser Ser Arg Lys Glu Leu Asn Lys Val Pro Arg Leu Gly Pro Lys Ala  
500 505 510

Phe Glu Gln Cys Ala Gly Phe Leu Arg Ile Ser Gly Ser Thr Asp Pro  
515 520 525

Leu Asp Ala Ser Ala Val His Pro Glu Ala Tyr Pro Val Val Arg Asn  
530 535 540

Ile Ala Lys Ala Thr Gly Leu Asp Val Ser Gly Leu Ile Gly Asn Ser  
545 550 555 560

Ala Val Leu Thr Lys Leu Lys Pro Ala Asp Phe Ala Asp Glu Arg Phe  
565 570 575

Gly Ile Pro Thr Val Thr Asp Ile Ile Ala Glu Leu Asp Lys Pro Gly  
580 585 590

Arg Asp Pro Arg Pro Glu Phe Lys Thr Ala Ser Phe Lys Glu Gly Val  
595 600 605

Glu Lys Ile Ser Asp Leu Thr Pro Gly Met Ile Leu Glu Gly Thr Val  
610 615 620

Thr Asn Val Ala Ala Phe Gly Ala Phe Val Asp Val Gly Val His Arg  
625 630 635 640

Asp Gly Leu Val His Val Ser Ala Met Ser Asp Lys Phe Ile Ser Asn  
645 650 655

Pro His Glu Val Val Arg Ser Gly Glu Val Val Lys Val Lys Val Met  
660 665 670

Glu Val Asp Val Asp Arg Lys Arg Ile Gly Leu Ser Leu Arg Leu Thr  
675 680 685

Asp Glu Pro Gly Ala Pro Ala Pro Gln Lys Arg Gly Asn Arg Pro Ala  
690 695 700

Lys Gln Gln Arg Ala Pro Gln Lys Gln Ser Ala Lys Pro Ala Thr Gly  
705 710 715 720

Ser Met Ala Asp Ala Leu Arg Arg Ala Gly Leu Gly Gly  
725 730

<210> 407

<211> 1286

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(1263)

<223> RXA00157

<400> 407

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 Val Gln Thr Glu Ala Ala Ile Ala Ala Asn Ser Glu Gln Leu Asn Val  
 20 25 30

ttg act acc aat cgc agt acc ttg gtt gcc cag cgt gat ggg gct gag 144  
 Leu Thr Thr Asn Arg Ser Thr Leu Val Ala Gln Arg Asp Gly Ala Glu  
 35 40 45

cgc aac ttg gcc atc gct cgt gcg cag gcg gat aat ctg caa ggt cag 192  
 Arg Asn Leu Ala Ile Ala Arg Ala Gln Ala Asp Asn Leu Gln Gly Gln  
 50 55 60

cgt gct gag tac gag gaa ttc cag cag gca gag cag gct cgc atc cag 240  
 Arg Ala Glu Tyr Glu Glu Phe Gln Gln Ala Glu Gln Ala Arg Ile Gln  
 65 70 75 80

gcg gaa gcg gaa gct cag gct gct gcg gag gag aag cgt cgt gcc gat 288  
 Ala Glu Ala Glu Ala Gln Ala Ala Ala Glu Glu Lys Arg Arg Ala Asp  
 85 90 95

gag gct gct gca cag gca gcc gct gaa gct caa gaa gct gcc cag caa 336  
 Glu Ala Ala Ala Gln Ala Ala Ala Glu Ala Gln Glu Ala Ala Gln Gln  
 100 105 110

gct cag gcg gcg gag gaa gcc caa gcc gcg caa gca gct gag aca gca 384  
 Ala Gln Ala Ala Glu Glu Ala Gln Ala Ala Gln Ala Ala Glu Thr Ala  
 115 120 125

caa gcc caa gcc gcg caa gct gcg gaa acc caa gct gca caa gcc gcg 432  
 Gln Ala Gln Ala Ala Gln Ala Ala Glu Thr Gln Ala Ala Gln Ala Ala  
 130 135 140

caa gct cag gca gaa gcg aat gat cgt gcc gcc gcg caa cag cgt gct 480  
 Gln Ala Gln Ala Glu Ala Asn Asp Arg Ala Ala Ala Gln Gln Arg Ala  
 145 150 155 160

gca gag gct caa gca gca gcg gaa cag gcg caa cgt gag gct gac gct 528  
 Ala Glu Ala Gln Ala Ala Ala Glu Gln Ala Gln Arg Glu Ala Asp Ala  
 165 170 175

cag gcg gcc aac gat gcc caa gct cag gca ctg cgt gaa cag gcg ctc 576  
 Gln Ala Ala Asn Asp Ala Gln Ala Gln Ala Leu Arg Glu Gln Ala Leu  
 180 185 190

acc gca gcc tcc atc gct gcg gct gct cta att gcg gcg agc cag tcc 624  
 Thr Ala Ala Ser Ile Ala Ala Ala Ala Leu Ile Ala Ser Gln Ser  
 195 200 205

agc cat gcc act act caa aat cct tac cca act gat gaa gac gcg gat 672  
 Ser His Ala Thr Thr Gln Asn Pro Tyr Pro Thr Asp Glu Asp Ala Asp  
 210 215 220

ccg acc gat att gcg gac atc caa gcc cca acg cag cca ggt acg ggt 720  
 Pro Thr Asp Ile Ala Asp Ile Gln Gly Pro Thr Gln Pro Gly Thr Gly  
 225 230 235 240

gag tct gga gat tcc cag agc aac tcc agc gac aac gat tcc aca gcc 768  
 Glu Ser Gly Asp Ser Gln Ser Asn Ser Ser Asp Asn Asp Ser Thr Gly  
 245 250 255



aac gat tcc aca ggc tct gac tct tca gat tca gat tcc tcc ggc aac 816  
 Asn Asp Ser Thr Gly Ser Asp Ser Ser Asp Ser Asp Ser Ser Gly Asn  
 260 265 270  
 gat tct tca gag gtt att tcc ggc gat cgt tcc gct cag att gag act 864  
 Asp Ser Ser Glu Val Ile Ser Gly Asp Arg Ser Ala Gln Ile Glu Thr  
 275 280 285  
 gtg att gcg cgc gcc atg agc cag ttg ggt gtg cag tac gca tgg ggt 912  
 Val Ile Ala Arg Ala Met Ser Gln Leu Gly Val Gln Tyr Ala Trp Gly  
 290 295 300  
 ggc ggt aac gct aat ggc cca act ctg ggt atc cgt gac ggt ggc gtg 960  
 Gly Gly Asn Ala Asn Gly Pro Thr Leu Gly Ile Arg Asp Gly Gly Val  
 305 310 315 320  
 gcg gac tct tac ggc gat tac aac aag gtt ggc ttc gac tgc tct gga 1008  
 Ala Asp Ser Tyr Gly Asp Tyr Asn Lys Val Gly Phe Asp Cys Ser Gly  
 325 330 335  
 ctg acc ttg tat gcg ttt gcg ggt gtg gga att tca ctt cct cac tac 1056  
 Leu Thr Leu Tyr Ala Phe Ala Gly Val Gly Ile Ser Leu Pro His Tyr  
 340 345 350  
 acg ggc tac cag tac cag cac ggc acc aag gtg tgc cct tct gag atg 1104  
 Thr Gly Tyr Gln Tyr Gln His Gly Thr Lys Val Ser Pro Ser Glu Met  
 355 360 365  
 caa cgt ggc gat ctg atc ttc tat ggt ccg gga gcg tct cag cac gtg 1152  
 Gln Arg Gly Asp Leu Ile Phe Tyr Gly Pro Gly Ala Ser Gln His Val  
 370 375 380  
 gca att tac ctc ggt gat ggt cag atg att gag gct ccg aat tgc ggt 1200  
 Ala Ile Tyr Leu Gly Asp Gly Gln Met Ile Glu Ala Pro Asn Ser Gly  
 385 390 395 400  
 tct gtc gtg aag att tct cct gtt cgc tgg agc gga atg acc gag agc 1248  
 Ser Val Val Lys Ile Ser Pro Val Arg Trp Ser Gly Met Thr Glu Ser  
 405 410 415  
 gtg gta cgc ctc att tagtttcctc ctatgaatct tga 1286  
 Val Val Arg Leu Ile  
 420

&lt;210&gt; 408

&lt;211&gt; 421

&lt;212&gt; PR

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 408

Ala Arg Ile Val Ala Glu Gln Arg Glu Ala Glu Ala Val Glu Lys Lys  
 1 5 10 15

Val Gln Thr Glu Ala Ala Ile Ala Ala Asn Ser Glu Gln Leu Asn Val  
 20 25 30

Leu Thr Thr Asn Arg Ser Thr Leu Val Ala Gln Arg Asp Gly Ala Glu  
 35 40 45

Arg Asn Leu Ala Ile Ala Arg Ala Gln Ala Asp Asn Leu Gln Gly Gln

50	55	60
Arg Ala Glu Tyr Glu Glu Phe Gln Gln Ala Glu Gln Ala Arg Ile Gln 65 70 75 80		
Ala Glu Ala Glu Ala Gln Ala Ala Ala Glu Glu Lys Arg Arg Ala Asp 85 90 95		
Glu Ala Ala Ala Gln Ala Ala Ala Glu Ala Gln Glu Ala Ala Gln Gln 100 105 110		
Ala Gln Ala Ala Glu Glu Ala Gln Ala Ala Gln Ala Ala Glu Thr Ala 115 120 125		
Gln Ala Gln Ala Ala Gln Ala Ala Glu Thr Gln Ala Ala Gln Ala Ala 130 135 140		
Gln Ala Gln Ala Glu Ala Asn Asp Arg Ala Ala Ala Gln Gln Arg Ala 145 150 155 160		
Ala Glu Ala Gln Ala Ala Ala Glu Gln Ala Gln Arg Glu Ala Asp Ala 165 170 175		
Gln Ala Ala Asn Asp Ala Gln Ala Gln Ala Leu Arg Glu Gln Ala Leu 180 185 190		
Thr Ala Ala Ser Ile Ala Ala Ala Ala Leu Ile Ala Ala Ser Gln Ser 195 200 205		
Ser His Ala Thr Thr Gln Asn Pro Tyr Pro Thr Asp Glu Asp Ala Asp 210 215 220		
Pro Thr Asp Ile Ala Asp Ile Gln Gly Pro Thr Gln Pro Gly Thr Gly 225 230 235 240		
Glu Ser Gly Asp Ser Gln Ser Asn Ser Ser Asp Asn Asp Ser Thr Gly 245 250 255		
Asn Asp Ser Thr Gly Ser Asp Ser Ser Asp Ser Asp Ser Ser Gly Asn 260 265 270		
Asp Ser Ser Glu Val Ile Ser Gly Asp Arg Ser Ala Gln Ile Glu Thr 275 280 285		
Val Ile Ala Arg Ala Met Ser Gln Leu Gly Val Gln Tyr Ala Trp Gly 290 295 300		
Gly Gly Asn Ala Asn Gly Pro Thr Leu Gly Ile Arg Asp Gly Gly Val 305 310 315 320		
Ala Asp Ser Tyr Gly Asp Tyr Asn Lys Val Gly Phe Asp Cys Ser Gly 325 330 335		
Leu Thr Leu Tyr Ala Phe Ala Gly Val Gly Ile Ser Leu Pro His Tyr 340 345 350		
Thr Gly Tyr Gln Tyr Gln His Gly Thr Lys Val Ser Pro Ser Glu Met 355 360 365		
Gln Arg Gly Asp Leu Ile Phe Tyr Gly Pro Gly Ala Ser Gln His Val 370 375 380		

Ala Ile Tyr Leu Gly Asp Gly Gln Met Ile Glu Ala Pro Asn Ser Gly  
385 390 395 400

Ser Val Val Lys Ile Ser Pro Val Arg Trp Ser Gly Met Thr Glu Ser  
405 410 415

Val Val Arg Leu Ile  
420

<210> 409

<211> 972

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(949)

<223> RXA00208

<400> 409

cggccaattt tttcttttgt ggggggtgcct cttacgcatt tcttgaattt ttgttaggct 60

tgcttaggtc agttaagat atatacgtata gaggttttcc atg aac act cca gcg 115  
Met Asn Thr Pro Ala  
1 5

ccc cgc aaa cga cgc gaa atg aaa atc aag aca gca acc gtc act ggt 163  
Pro Arg Lys Arg Arg Glu Met Lys Ile Lys Thr Ala Thr Val Thr Gly  
10 15 20

gtg cgt caa att tcc ccc gat ctc atc cgc ttc agc ttc gac tgc cca 211  
Val Arg Gln Ile Ser Pro Asp Leu Ile Arg Phe Ser Phe Asp Cys Pro  
25 30 35

gaa atc gtt ggc gcc gac ctg ggg ttc acg gac cat tac atc aag atc 259  
Glu Ile Val Gly Ala Asp Leu Gly Phe Thr Asp His Tyr Ile Lys Ile  
40 45 50

ctc ttc gtg cca gca ggt gcg gat tac tcc tgg cct ttc gac atg gca 307  
Leu Phe Val Pro Ala Gly Ala Asp Tyr Ser Trp Pro Phe Asp Met Ala  
55 60 65

gaa att gcg gaa acc cag ccc cgt gag ctg caa cca gtg cgc gcg acc 355  
Glu Ile Ala Glu Thr Gln Pro Arg Glu Leu Gln Pro Val Arg Arg Thr  
70 75 80 85

tac act ttc cgc acg gtt gac act gtc gca ggc aca ttt gac ata gat 403  
Tyr Thr Phe Arg Thr Val Asp Thr Val Ala Gly Thr Phe Asp Ile Asp  
90 95 100

ttc gtt gcg cac ggc acc gat ggc ctt gcc ggt cct tgg gcg cag cag 451  
Phe Val Ala His Gly Thr Asp Gly Leu Ala Gly Pro Trp Ala Gln Gln  
105 110 115

gca cag gta ggt gat gtc atc gcg ttc ggc ggc cca ggt ggc gca tgg 499  
Ala Gln Val Gly Asp Val Ile Ala Phe Gly Gly Pro Gly Gly Ala Trp  
120 125 130

aag cca gaa acc acc tat gag cac tac gtt ctc gca ggc gat gaa gcc 547

Lys Pro Glu Thr Thr Tyr Glu His Tyr Val Leu Ala Gly Asp Glu Ala  
 135 140 145

gca gca ccc gca att ttc gca gcc tta gaa cac cta ccc gcc ggc acc 595  
 Ala Ala Pro Ala Ile Phe Ala Ala Leu Glu His Leu Pro Ala Gly Thr  
 150 155 160 165

acc gcc aaa gcc ttc att gaa atc tcc tcc aac gaa gcg cgt ttc aac 643  
 Thr Ala Lys Ala Phe Ile Glu Ile Ser Ser Asn Glu Ala Arg Phe Asn  
 170 175 180

gcc cca gcc agc gac aac atc gag gtt gtc tgg gtg ccc cgc gac ggc 691  
 Ala Pro Ala Ser Asp Asn Ile Glu Val Val Trp Val Pro Arg Asp Gly  
 185 190 195

gcc acc cac ggt aca ttg ctt atc gac gcc ctc cgc cag gac ggc tac 739  
 Ala Thr His Gly Thr Leu Leu Ile Asp Ala Leu Arg Gln Asp Gly Tyr  
 200 205 210

cca acc aag aaa act tcc tgg ttc atc cac gga gtc gcc gaa atg gtg 787  
 Pro Thr Lys Lys Thr Ser Trp Phe Ile His Gly Val Ala Glu Met Val  
 215 220 225

aag gaa acc cgc aaa ttc ctc ttc gtg gaa ggc aac gta gac aaa gct 835  
 Lys Glu Thr Arg Lys Phe Leu Phe Val Glu Gly Asn Val Asp Lys Ala  
 230 235 240 245

gat gca tcc att tcc gga tac tgg cgc ctt ggc atg acc gaa gac cag 883  
 Asp Ala Ser Ile Ser Gly Tyr Trp Arg Leu Gly Met Thr Glu Asp Gln  
 250 255 260

tgg cag gcc tcc aag cgg gag ttc aat gag caa aat gag gca gaa gaa 931  
 Trp Gln Ala Ser Lys Arg Glu Phe Asn Glu Gln Asn Glu Ala Glu Glu  
 265 270 275

ctc gcg ctc agc aag gca taagggaag gggttctaga aag 972  
 Leu Ala Leu Ser Lys Ala  
 280

<210> 410  
 <211> 283  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 410  
 Met Asn Thr Pro Ala Pro Arg Lys Arg Arg Glu Met Lys Ile Lys Thr  
 1 5 10 15

Ala Thr Val Thr Gly Val Arg Gln Ile Ser Pro Asp Leu Ile Arg Phe  
 20 25 30

Ser Phe Asp Cys Pro Glu Ile Val Gly Ala Asp Leu Gly Phe Thr Asp  
 35 40 45

His Tyr Ile Lys Ile Leu Phe Val Pro Ala Gly Ala Asp Tyr Ser Trp  
 50 55 60

Pro Phe Asp Met Ala Glu Ile Ala Glu Thr Gln Pro Arg Glu Leu Gln  
 65 70 75 80

Pro Val Arg Arg Thr Tyr Thr Phe Arg Thr Val Asp Thr Val Ala Gly  
85 90 95

Thr Phe Asp Ile Asp Phe Val Ala His Gly Thr Asp Gly Leu Ala Gly  
100 105 110

Pro Trp Ala Gln Gln Ala Gln Val Gly Asp Val Ile Ala Phe Gly Gly  
115 120 125

Pro Gly Gly Ala Trp Lys Pro Glu Thr Thr Tyr Glu His Tyr Val Leu  
130 135 140

Ala Gly Asp Glu Ala Ala Pro Ala Ile Phe Ala Ala Leu Glu His  
145 150 155 160

Leu Pro Ala Gly Thr Thr Ala Lys Ala Phe Ile Glu Ile Ser Ser Asn  
165 170 175

Glu Ala Arg Phe Asn Ala Pro Ala Ser Asp Asn Ile Glu Val Val Trp  
180 185 190

Val Pro Arg Asp Gly Ala Thr His Gly Thr Leu Leu Ile Asp Ala Leu  
195 200 205

Arg Gln Asp Gly Tyr Pro Thr Lys Lys Thr Ser Trp Phe Ile His Gly  
210 215 220

Val Ala Glu Met Val Lys Glu Thr Arg Lys Phe Leu Phe Val Glu Gly  
225 230 235 240

Asn Val Asp Lys Ala Asp Ala Ser Ile Ser Gly Tyr Trp Arg Leu Gly  
245 250 255

Met Thr Glu Asp Gln Trp Gln Ala Ser Lys Arg Glu Phe Asn Glu Gln  
260 265 270

Asn Glu Ala Glu Glu Leu Ala Leu Ser Lys Ala  
275 280

<210> 411

<211> 411

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (26)..(388)

<223> RXA00967

<400> 411

caactagaaa atgactgggg gcgatatg ccg gtg cag gac gca ggc gaa cgc 52  
Met Pro Val Gln Asp Ala Gly Glu Arg  
1 5

aac aac aat gac cgg cca gtg atg ccg gga gag atc ctc cgt gag gaa 100  
Asn Asn Asn Asp Arg Pro Val Met Pro Gly Glu Ile Leu Arg Glu Glu  
10 15 20 25

ttc atg gag cct ttg ggg ctg tcc caa aac ggc ttg gcg cgg gca ata 148  
Phe Met Glu Pro Leu Gly Leu Ser Gln Asn Gly Leu Ala Arg Ala Ile

30	35	40	
gga gtg cca cca cgc agg att aat gag atc gtg cac ggc aaa cgc gca			196
Gly Val Pro Pro Arg Arg Ile Asn Glu Ile Val His Gly Lys Arg Ala			
45	50	55	
atc acg gca gac act gcg ctg cgt tta gct gct tat tta ggt ccc gat			244
Ile Thr Ala Asp Thr Ala Leu Arg Leu Ala Ala Tyr Leu Gly Pro Asp			
60	65	70	
cca cag ttt tgg ctc aac ttg cag acc cac tac gac ctg tgc gtg acg			292
Pro Gln Phe Trp Leu Asn Leu Gln Thr His Tyr Asp Leu Ser Val Thr			
75	80	85	
tat tta gat gcg cgc aca ctg ttg gaa gcg atc aag cct tat gat cgt			340
Tyr Leu Asp Ala Arg Thr Leu Leu Glu Ala Ile Lys Pro Tyr Asp Arg			
90	95	100	105
cag caa aat gtg gct cgg acc ctg aat ccg ctt cag gag agc tgc cag			388
Gln Gln Asn Val Ala Arg Thr Leu Asn Pro Leu Gln Glu Ser Ser Gln			
110	115	120	
taggagtcgc ctctgggtcgg ggc			411
<210> 412			
<211> 121			
<212> PRT			
<213> Corynebacterium glutamicum			
<400> 412			
Met Pro Val Gln Asp Ala Gly Glu Arg Asn Asn Asn Asp Arg Pro Val			
1	5	10	15
Met Pro Gly Glu Ile Leu Arg Glu Glu Phe Met Glu Pro Leu Gly Leu			
20	25	30	
Ser Gln Asn Gly Leu Ala Arg Ala Ile Gly Val Pro Pro Arg Arg Ile			
35	40	45	
Asn Glu Ile Val His Gly Lys Arg Ala Ile Thr Ala Asp Thr Ala Leu			
50	55	60	
Arg Leu Ala Ala Tyr Leu Gly Pro Asp Pro Gln Phe Trp Leu Asn Leu			
65	70	75	80
Gln Thr His Tyr Asp Leu Ser Val Thr Tyr Leu Asp Ala Arg Thr Leu			
85	90	95	
Leu Glu Ala Ile Lys Pro Tyr Asp Arg Gln Gln Asn Val Ala Arg Thr			
100	105	110	
Leu Asn Pro Leu Gln Glu Ser Ser Gln			
115	120		
<210> 413			
<211> 381			
<212> DNA			
<213> Corynebacterium glutamicum			

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(358)

&lt;223&gt; RXA01149

&lt;400&gt; 413

attttaaca agaaccctttt tcaaacattc tttttataag ttttttccat attggttgat 60

ccccaccat cgggatccct gatccacgaa aggagtgttc gtg gta gct ccg cag 115  
 Val Val Ala Pro Gln  
 1 5

tcc cgg aaa ccg cag cac cct ggt gag att ttg agt gaa cgt ttc ctc 163  
 Ser Arg Lys Pro Gln His Pro Gly Glu Ile Leu Ser Glu Arg Phe Leu  
 10 15 20

gaa ccc cga gga atc agc cac tac gat ctc gcc aaa acc ctc cac atc 211  
 Glu Pro Arg Gly Ile Ser His Tyr Asp Leu Ala Lys Thr Leu His Ile  
 25 30 35

acc gaa gca acc atc gcc aat ttc gtt gaa ggt cgc acc gac ctc acc 259  
 Thr Glu Ala Thr Ile Ala Asn Phe Val Glu Gly Arg Thr Asp Leu Thr  
 40 45 50

atc gga ctt gca gta cgc ctc tcc cgc tca ttc gat ttg agc aca cag 307  
 Ile Gly Leu Ala Val Arg Leu Ser Arg Ser Phe Asp Leu Ser Thr Gln  
 55 60 65

gaa tgg atc gca ctg cag cgc acc ttt gat cag gct cat cgt cga tct 355  
 Glu Trp Ile Ala Leu Gln Arg Thr Phe Asp Gln Ala His Arg Arg Ser  
 70 75 80 85

gct taaaagtttt tagcttcac gaa 381  
 Ala

&lt;210&gt; 414

&lt;211&gt; 86

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 414

Val Val Ala Pro Gln Ser Arg Lys Pro Gln His Pro Gly Glu Ile Leu  
 1 5 10 15

Ser Glu Arg Phe Leu Glu Pro Arg Gly Ile Ser His Tyr Asp Leu Ala  
 20 25 30

Lys Thr Leu His Ile Thr Glu Ala Thr Ile Ala Asn Phe Val Glu Gly  
 35 40 45

Arg Thr Asp Leu Thr Ile Gly Leu Ala Val Arg Leu Ser Arg Ser Phe  
 50 55 60

Asp Leu Ser Thr Gln Glu Trp Ile Ala Leu Gln Arg Thr Phe Asp Gln  
 65 70 75 80

Ala His Arg Arg Ser Ala  
 85

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<210> 415
<211> 1989
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (101)..(1966)  
<223> RXA01305
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<400> 415
ttctcaaggc tccctctcct ttaagttcgt ggccccagcg ccagcttttt tcataaaaaac 60
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tcaacaggca ctgtgggacc ccttcacttt gaaagacatc atg cgc ccc tct tcc 115  
Met Arg Pro Ser Ser  
1 5

cgg cca ctt ggc ctg gtc cta tgc acc gca ctg gca tca acg atc atc      163  
Arg Pro Leu Gly Leu Val Leu Cys Thr Ala Leu Ala Ser Thr Ile Ile  
                10                       15                              20

acc gtt ccc gca gcg tcc gcc cag gag cca gcg ctt ctc gat gcc tcc 211  
Thr Val Pro Ala Ala Ser Ala Gln Glu Pro Ala Leu Leu Asp Ala Ser  
25 30 35

gcc atc gcc cca cat acc gcc agc tac gcc tac tac gtt gat gca tgg 259  
Ala Ile Ala Pro His Thr Ala Ser Tyr Gly Tyr Tyr Val Asp Ala Trp  
40 45 50

gac acc aac gtt tcc act gat ctg aat cca tca agt aat gca gct gtt 307  
Asp Thr Asn Val Ser Thr Asp Leu Asn Pro Ser Ser Asn Ala Ala Val  
55 60 65

ggc gta ctg gag gaa atg ctt gag ctg tgg acc cca ggc gaa gaa tgg 355  
Gly Val Leu Glu Glu Met Leu Glu Leu Trp Thr Pro Gly Glu Glu Trp  
70 75 80 85

aac acc ggc gtc aag gtt gac ccc acc gtg ctg gat tcc aac atc gca 403  
Asn Thr Gly Val Lys Val Asp Pro Thr Val Leu Asp Ser Asn Ile Ala  
90 95 100

cag tct gtg gca atc tcc cag cag gcg acc gat gct cag caa gaa cgt 451  
Gln Ser Val Ala Ile Ser Gln Gln Ala Thr Asp Ala Gln Gln Glu Arg  
105 110 115

gct tgg gtt att gat cgc cgc aac cag aac tac acc gca acc gac ggt 499  
Ala Trp Val Ile Asp Arg Arg Asn Gln Asn Tyr Thr Ala Thr Asp Gly  
120 125 130

ctt ggc gca tac gca gat agt tac cgc gag acc gca cag gtg ggc acc 547  
 Leu Gly Ala Tyr Ala Asp Ser Tyr Arg Glu Thr Ala Gln Val Gly Thr  
 135 140 145

acc atc cct gac gtt gtt cca gct gat gcc acc acc gtg aag tac aac 595  
Thr Ile Pro Asp Val Val Pro Ala Asp Ala Thr Thr Val Lys Tyr Asn  
150 155 160 165

gat ggc ggc aat gtg aat ggc aat tgg gca gag acc ggt gga gaa ctc 643  
Asp Gly Gly Asn Val Asn Gly Asn Trp Ala Glu Thr Gly Gly Glu Leu  
170 175 180



gga tcc act gtt gat cta att gaa gct atc cgt cag cat gcc gca acc 691  
 Gly Ser Thr Val Asp Leu Ile Glu Ala Ile Arg Gln His Ala Ala Thr  
 185 190 195

agc aac aat gcc aag gcg tac tac caa tac cca cgc ccc tac cgc tgg 739  
 Ser Asn Asn Ala Lys Ala Tyr Tyr Gln Tyr Pro Arg Pro Tyr Arg Trp  
 200 205 210

act gaa tcc atc gaa cca gaa gcc tgg ggc gag gcc gtt gac atg cca 787  
 Thr Glu Ser Ile Glu Pro Glu Ala Trp Gly Glu Gly Val Asp Met Pro  
 215 220 225

gag tat gca aac cca ctg cgc aag gat gaa tcc gaa gct gcc agc gat 835  
 Glu Tyr Ala Asn Pro Leu Arg Lys Asp Glu Ser Glu Ala Ala Ser Asp  
 230 235 240 245

ggc ggt ttc cct tcc gga cac acc tcc gca gcc gcc atg gca acc aac 883  
 Gly Gly Phe Pro Ser Gly His Thr Ser Ala Gly Gly Met Ala Thr Asn  
 250 255 260

ggc ctg gct tac gct ttc cca cag caa tac gat aaa ctg ctc atg act 931  
 Gly Leu Ala Tyr Phe Pro Gln Gln Tyr Asp Lys Leu Leu Met Thr  
 265 270 275

gca cgc gaa atc ggc gaa agc cgc atc cag ctg gcc atg cac tct ccg 979  
 Ala Ala Glu Ile Gly Glu Ser Arg Ile Gln Leu Gly Met His Ser Pro  
 280 285 290

ctt gat gtt att ggc gcc cgt gtt cta tcc acc cgc att act gca ggt 1027  
 Leu Asp Val Ile Gly Gly Arg Val Leu Ser Thr Ala Ile Thr Ala Gly  
 295 300 305

gca ctt aat gat ccg aat ctc gac tgc gtg aag gct gaa gcc ttc gat 1075  
 Ala Leu Asn Asp Pro Asn Leu Asp Ser Val Lys Ala Glu Ala Phe Asp  
 310 315 320 325

gat gct cag gca tgg atc agt aac cag agc gac atc acc acc aac act 1123  
 Asp Ala Gln Ala Trp Ile Ser Asn Gln Ser Asp Ile Thr Thr Asn Thr  
 330 335 340

cgc gat ttt gat gag caa ctc gcc gag tac acc aac ttc ctc acc ttc 1171  
 Arg Asp Phe Asp Glu Gln Leu Ala Glu Tyr Thr Asn Phe Leu Thr Phe  
 345 350 355

ggc ttc gag cag tcc ggc gac acc acc caa gac atg cgc gtg cca aag 1219  
 Gly Phe Glu Gln Ser Gly Asp Thr Thr Gln Asp Met Arg Val Pro Lys  
 360 365 370

gga gct gag gct ctg ctg gaa acc cgc ctt ccg tac ctt gat gac gaa 1267  
 Gly Ala Glu Ala Leu Leu Glu Thr Arg Leu Pro Tyr Leu Asp Asp Glu  
 375 380 385

cag cgc cgt tgg gtt cta cat tcc act gcc ctc gag tcc ggt ttc cca 1315  
 Gln Arg Arg Trp Val Leu His Ser Thr Gly Leu Glu Ser Gly Phe Pro  
 390 395 400 405

gta ctt gat gat gcc gaa ggt tgg gcc cgt ctc aac ctc tac gct gcc 1363  
 Val Leu Asp Asp Ala Glu Gly Trp Gly Arg Leu Asn Leu Tyr Ala Ala  
 410 415 420

cag gct ggc tac agt gca ttc gat acc aac gtt gac gtc acc atg aat 1411  
 Gln Ala Gly Tyr Ser Ala Phe Asp Thr Asn Val Asp Val Thr Met Asn  
 425 430 435

gcc atc gac ggt ggc tac aac gcc aaa gac aac tgg caa aac gac atc 1459  
 Ala Ile Asp Gly Gly Tyr Asn Ala Lys Asp Asn Trp Gln Asn Asp Ile  
 440 445 450

gag ggc gca gga tcc ctg acc aag aac ggt tcc ggt gaa ctc acc ctg 1507  
 Glu Gly Ala Gly Ser Leu Thr Lys Asn Gly Ser Gly Glu Leu Thr Leu  
 455 460 465

tca ggt gac aac tcc tac acc ggt gga acc acc atc acc gcg ggc acc 1555  
 Ser Gly Asp Asn Ser Tyr Thr Gly Gly Thr Thr Ile Thr Ala Gly Thr  
 470 475 480 485

ttg gtt gct gca act gag tca gct ctg gga gca ggc gat ctc acc atc 1603  
 Leu Val Ala Ala Thr Glu Ser Ala Leu Gly Ala Gly Asp Leu Thr Ile  
 490 495 500

aac gat ggt gca acc ttg aag atc acc cag cct gtc acc gtg gat gga 1651  
 Asn Asp Gly Ala Thr Leu Lys Ile Thr Gln Pro Val Thr Val Asp Gly  
 505 510 515

acc gca aac ctg gga gga act ctg cac gtt gcc ctt cct gtt ggc acc 1699  
 Thr Ala Asn Leu Gly Gly Thr Leu His Val Ala Leu Pro Val Gly Thr  
 520 525 530

aac cac gtc acc gtg atc gat gct gca tca att tcc ggt gaa ttt gat 1747  
 Asn His Val Thr Val Ile Asp Ala Ala Ser Ile Ser Gly Glu Phe Asp  
 535 540 545

gag gtt att gtt gat ggc gca gtt gac gct cag gtg agc tac gac aac 1795  
 Glu Val Ile Val Asp Gly Ala Val Asp Ala Gln Val Ser Tyr Asp Asn  
 550 555 560 565

ggc tct gtc gtg att act aca ggc gca cct tct gat gac gta aag gaa 1843  
 Gly Ser Val Val Ile Thr Thr Gly Ala Pro Ser Asp Asp Val Lys Glu  
 570 575 580

act ggc tct tct gct ggc gga att ctt gcc atc gtg gca gcc ctg ggt 1891  
 Thr Gly Ser Ser Ala Gly Gly Ile Leu Ala Ile Val Ala Ala Leu Gly  
 585 590 595

ggc att gca gca ctg atc ttc ggt gca ttc acc cag ttt ggt ttc cca 1939  
 Gly Ile Ala Ala Leu Ile Phe Gly Ala Phe Thr Gln Phe Gly Phe Pro  
 600 605 610

cca gca atc aag gaa atg ttc gac ctt taagccttcg ccaacccac 1986  
 Pro Ala Ile Lys Glu Met Phe Asp Leu  
 615 620

ggc 1989

&lt;210&gt; 416

&lt;211&gt; 622

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 416

Met Arg Pro Ser Ser Arg Pro Leu Gly Leu Val Leu Cys Thr Ala Leu  
 1 5 10 15

Ala Ser Thr Ile Ile Thr Val Pro Ala Ala Ser Ala Gln Glu Pro Ala  
 20 25 30

Leu Leu Asp Ala Ser Ala Ile Ala Pro His Thr Ala Ser Tyr Gly Tyr  
 35 40 45

Tyr Val Asp Ala Trp Asp Thr Asn Val Ser Thr Asp Leu Asn Pro Ser  
 50 55 60

Ser Asn Ala Ala Val Gly Val Leu Glu Glu Met Leu Glu Leu Trp Thr  
 65 70 75 80

Pro Gly Glu Glu Trp Asn Thr Gly Val Lys Val Asp Pro Thr Val Leu  
 85 90 95

Asp Ser Asn Ile Ala Gln Ser Val Ala Ile Ser Gln Gln Ala Thr Asp  
 100 105 110

Ala Gln Gln Glu Arg Ala Trp Val Ile Asp Arg Arg Asn Gln Asn Tyr  
 115 120 125

Thr Ala Thr Asp Gly Leu Gly Ala Tyr Ala Asp Ser Tyr Arg Glu Thr  
 130 135 140

Ala Gln Val Gly Thr Thr Ile Pro Asp Val Val Pro Ala Asp Ala Thr  
 145 150 155 160

Thr Val Lys Tyr Asn Asp Gly Gly Asn Val Asn Gly Asn Trp Ala Glu  
 165 170 175

Thr Gly Gly Glu Leu Gly Ser Thr Val Asp Leu Ile Glu Ala Ile Arg  
 180 185 190

Gln His Ala Ala Thr Ser Asn Asn Ala Lys Ala Tyr Tyr Gln Tyr Pro  
 195 200 205

Arg Pro Tyr Arg Trp Thr Glu Ser Ile Glu Pro Glu Ala Trp Gly Glu  
 210 215 220

Gly Val Asp Met Pro Glu Tyr Ala Asn Pro Leu Arg Lys Asp Glu Ser  
 225 230 235 240

Glu Ala Ala Ser Asp Gly Gly Phe Pro Ser Gly His Thr Ser Ala Gly  
 245 250 255

Gly Met Ala Thr Asn Gly Leu Ala Tyr Ala Phe Pro Gln Gln Tyr Asp  
 260 265 270

Lys Leu Leu Met Thr Ala Ala Glu Ile Gly Glu Ser Arg Ile Gln Leu  
 275 280 285

Gly Met His Ser Pro Leu Asp Val Ile Gly Gly Arg Val Leu Ser Thr  
 290 295 300

Ala Ile Thr Ala Gly Ala Leu Asn Asp Pro Asn Leu Asp Ser Val Lys  
 305 310 315 320

Ala Glu Ala Phe Asp Asp Ala Gln Ala Trp Ile Ser Asn Gln Ser Asp

325	330	335
Ile Thr Thr Asn Thr Arg Asp Phe Asp Glu Gln Leu Ala Glu Tyr Thr 340 345 350		
Asn Phe Leu Thr Phe Gly Phe Glu Gln Ser Gly Asp Thr Thr Gln Asp 355 360 365		
Met Arg Val Pro Lys Gly Ala Glu Ala Leu Leu Glu Thr Arg Leu Pro 370 375 380		
Tyr Leu Asp Asp Glu Gln Arg Arg Trp Val Leu His Ser Thr Gly Leu 385 390 395 400		
Glu Ser Gly Phe Pro Val Leu Asp Asp Ala Glu Gly Trp Gly Arg Leu 405 410 415		
Asn Leu Tyr Ala Ala Gln Ala Gly Tyr Ser Ala Phe Asp Thr Asn Val 420 425 430		
Asp Val Thr Met Asn Ala Ile Asp Gly Gly Tyr Asn Ala Lys Asp Asn 435 440 445		
Trp Gln Asn Asp Ile Glu Gly Ala Gly Ser Leu Thr Lys Asn Gly Ser 450 455 460		
Gly Glu Leu Thr Leu Ser Gly Asp Asn Ser Tyr Thr Gly Gly Thr Thr 465 470 475 480		
Ile Thr Ala Gly Thr Leu Val Ala Ala Thr Glu Ser Ala Leu Gly Ala 485 490 495		
Gly Asp Leu Thr Ile Asn Asp Gly Ala Thr Leu Lys Ile Thr Gln Pro 500 505 510		
Val Thr Val Asp Gly Thr Ala Asn Leu Gly Gly Thr Leu His Val Ala 515 520 525		
Leu Pro Val Gly Thr Asn His Val Thr Val Ile Asp Ala Ala Ser Ile 530 535 540		
Ser Gly Glu Phe Asp Glu Val Ile Val Asp Gly Ala Val Asp Ala Gln 545 550 555 560		
Val Ser Tyr Asp Asn Gly Ser Val Val Ile Thr Thr Gly Ala Pro Ser 565 570 575		
Asp Asp Val Lys Glu Thr Gly Ser Ser Ala Gly Gly Ile Leu Ala Ile 580 585 590		
Val Ala Ala Leu Gly Gly Ile Ala Ala Leu Ile Phe Gly Ala Phe Thr 595 600 605		
Gln Phe Gly Phe Pro Pro Ala Ile Lys Glu Met Phe Asp Leu 610 615 620		

&lt;210&gt; 417

&lt;211&gt; 420

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(397)

&lt;223&gt; RXA01453

&lt;400&gt; 417

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 Met Ala Gln Lys Leu  
 1 5

tac ccg ccg att cac cct ggt gag att ctc atg gag gac ttc atc aag 163  
 Tyr Pro Pro Ile His Pro Gly Glu Ile Leu Met Glu Asp Phe Ile Lys  
 10 15 20

ggc ttc ggc ctc aca cag aac aag gtc gcc gta tcg atc ggg gtg cct 211  
 Gly Phe Gly Leu Thr Gln Asn Lys Val Ala Val Ser Ile Gly Val Pro  
 25 30 35

ccg cga cgc atc aac gag atc gtg cac ggc aag cga tcc atc acg gcc 259  
 Pro Arg Arg Ile Asn Glu Ile Val His Gly Lys Arg Ser Ile Thr Ala  
 40 45 50

gat acg gct ctg cgt ctc ggg cgg tac ttc ggt atc gac ccg cag ttc 307  
 Asp Thr Ala Leu Arg Leu Gly Arg Tyr Phe Gly Ile Asp Pro Gln Phe  
 55 60 65

tgg ctg agc ctt cag act cag tac gag ttg gag ctc gat cgc gac gcc 355  
 Trp Leu Ser Leu Gln Thr Gln Tyr Glu Leu Glu Leu Asp Arg Asp Ala  
 70 75 80 85

ggt gca gcg act tac gca cag atc acg ccg ctg aag gtc gcg 397  
 Gly Ala Ala Thr Tyr Ala Gln Ile Thr Pro Leu Lys Val Ala  
 90 95

tgagctcggg gccagaaaa cat 420

&lt;210&gt; 418

&lt;211&gt; 99

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 418

Met Ala Gln Lys Leu Tyr Pro Pro Ile His Pro Gly Glu Ile Leu Met  
 1 5 10 15

Glu Asp Phe Ile Lys Gly Phe Gly Leu Thr Gln Asn Lys Val Ala Val  
 20 25 30

Ser Ile Gly Val Pro Pro Arg Arg Ile Asn Glu Ile Val His Gly Lys  
 35 40 45

Arg Ser Ile Thr Ala Asp Thr Ala Leu Arg Leu Gly Arg Tyr Phe Gly  
 50 55 60

Ile Asp Pro Gln Phe Trp Leu Ser Leu Gln Thr Gln Tyr Glu Leu Glu  
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Lys Val Ala

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													Met	Lys	Glu	Thr	Asp					115
													1								5	
aac	cta	ctg	cgc	gaa	aac	tcc	cac	gac	cgc	gac	atc	tct	gaa	atc	gtc					163		
Asn	Leu	Leu	Arg	Glu	Asn	Ser	His	Asp	Arg	Asp	Ile	Ser	Glu	Ile	Val					163		
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gcc	acc	atc	act	gcc	ctt	gac	cac	cca	tca	ccc	tca	ctt	ctg	cga	ttc					211		
Ala	Thr	Ile	Thr	Ala	Leu	Asp	His	Pro	Ser	Pro	Ser	Leu	Leu	Arg	Phe					211		
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aca	gct	ttt	gtt	cca	gga	tca	gca	aac	aac	cca	gtg	tgg	gca	gaa	gcc					259		
Thr	Ala	Phe	Val	Pro	Gly	Ser	Ala	Asn	Asn	Pro	Val	Trp	Ala	Glu	Ala					259		
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aac	gtg	gca	atc	agg	ctt	tac	ctc	agc	gaa	gaa	ttc	gac	gac	gcc	acc					307		
Asn	Val	Ala	Ile	Arg	Leu	Tyr	Leu	Ser	Glu	Glu	Phe	Asp	Asp	Ala	Thr					307		
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cgc	gtc	tac	acc	gtc	cga	tcc	ttt	gat	gcc	gca	act	gaa	agc	atc	gtg					355		
Arg	Val	Tyr	Thr	Val	Arg	Ser	Phe	Asp	Ala	Ala	Thr	Glu	Ser	Ile	Val					355		
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gtg	gat	gtg	gtt	caa	cac	cac	gaa	agc	ccc	atg	atg	cgc	tgg	tca					403			
Val	Asp	Val	Val	Gln	His	His	Glu	Ser	Pro	Met	Met	Arg	Trp	Ser					403			
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gac	acc	gta	aaa	atc	aac	gac	acc	ctc	gtg	ctc	acc	gga	ccc	cgc	cca					451		
Asp	Thr	Val	Lys	Ile	Asn	Asp	Thr	Leu	Val	Leu	Thr	Gly	Pro	Arg	Pro					451		
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cac	ttt	gtc	atc	ccc	gaa	ggc	gaa	caa	gca	gca	ctc	ttc	ctt	gat	gac					499		
His	Phe	Val	Ile	Pro	Glu	Gly	Glu	Gln	Ala	Ala	Leu	Phe	Leu	Asp	Asp					499		
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acc	gcc	atc	ccc	gct	ctc	gcc	gct	att	ttg	gat	caa	tgg	cca	aca	gat					547		
Thr	Ala	Ile	Pro	Ala	Leu	Ala	Ala	Ile	Leu	Asp	Gln	Trp	Pro	Thr	Asp					547		
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ctt	cgt	ggc	aaa	gga	tgg	gtt	gtc	act	gac	gat	ccc	gca	gcc	ttc	gat					595		

Leu	Arg	Gly	Lys	Gly		Trp	Val	Val	Thr	Asp	Asp	Pro	Ala	Ala	Phe	Asp	
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gaa	cta	ccc	agc	atc	gac	gga	ctg	gaa	ctg	aac	ctg	ctc	gcg	cgg	gga		
Glu	Leu	Pro	Ser	Ile	Asp	Gly	Leu	Glu	Leu	Asn	Leu	Leu	Ala	Pro	Gly		
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tca	gat	cca	act	gtt	cag	cca	ctt	gcc	caa	cag	gca	tat	gac	ctg	gaa		691
Ser	Asp	Pro	Thr	Val	Gln	Pro	Leu	Ala	Gln	Gln	Ala	Tyr	Asp	Leu	Glu		
			185					190					195				
aac	cca	gaa	act	tac	gtg	gtg	tgg	gca	gcc	ggc	gag	cga	gat	gaa	ata		739
Asn	Pro	Glu	Thr	Tyr	Val	Val	Trp	Ala	Ala	Gly	Glu	Arg	Asp	Glu	Ile		
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aaa	tcc	atc	cgc	agg	cac	ttc	cgc	aag	cag	gtg	gga	ttg	gaa	aaa	gat		787
Lys	Ser	Ile	Arg	Arg	His	Phe	Arg	Lys	Gln	Val	Gly	Leu	Glu	Lys	Asp		
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gca	gtg	gcc	gtg	ttt	ggg	tac	tgg	aaa	tac	aac	acc	acc	aac	act	cag		835
Ala	Val	Ala	Val	Phe	Gly	Tyr	Trp	Lys	Tyr	Asn	Thr	Thr	Asn	Thr	Gln		
230				235					240					245			
atc	gat	gca	gtc	cgc	aaa	gaa	aac	tac	atg	aag	atg	ctc	tct	gaa	ggg		883
Ile	Asp	Ala	Val	Arg	Lys	Glu	Asn	Tyr	Met	Lys	Met	Leu	Ser	Glu	Gly		
			250					255						260			
cta	cag	ctg	gaa	aac	ttc	gac	gac	ctc	tca	ttg	gag	att	taaggggtcg				932
Leu	Gln	Leu	Glu	Asn	Phe	Asp	Asp	Leu	Ser	Leu	Glu	Ile					
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<212>	PRT																
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			20					25					30				
Ser	Leu	Leu	Arg	Phe	Thr	Ala	Phe	Val	Pro	Gly	Ser	Ala	Asn	Asn	Pro		
		35				40						45					
Val	Trp	Ala	Glu	Ala	Asn	Val	Ala	Ile	Arg	Leu	Tyr	Leu	Ser	Glu	Glu		
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Phe	Asp	Asp	Ala	Thr	Arg	Val	Tyr	Thr	Val	Arg	Ser	Phe	Asp	Ala	Ala		
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Thr	Glu	Ser	Ile	Val	Val	Asp	Val	Val	Gln	His	His	His	Glu	Ser	Pro		
			85					90						95			
Met	Met	Arg	Trp	Ser	Asp	Thr	Val	Lys	Ile	Asn	Asp	Thr	Leu	Val	Leu		
		100						105					110			</	

Thr Gly Pro Arg Pro His Phe Val Ile Pro Glu Gly Glu Gln Ala Ala  
 115 120 125  
 Leu Phe Leu Asp Asp Thr Ala Ile Pro Ala Leu Ala Ala Ile Leu Asp  
 130 135 140  
 Gln Trp Pro Thr Asp Leu Arg Gly Lys Gly Trp Val Val Thr Asp Asp  
 145 150 155 160  
 Pro Ala Ala Phe Asp Glu Leu Pro Ser Ile Asp Gly Leu Glu Leu Asn  
 165 170 175  
 Leu Leu Ala Pro Gly Ser Asp Pro Thr Val Gln Pro Leu Ala Gln Gln  
 180 185 190  
 Ala Tyr Asp Leu Glu Asn Pro Glu Thr Tyr Val Val Trp Ala Ala Gly  
 195 200 205  
 Glu Arg Asp Glu Ile Lys Ser Ile Arg Arg His Phe Arg Lys Gln Val  
 210 215 220  
 Gly Leu Glu Lys Asp Ala Val Ala Val Phe Gly Tyr Trp Lys Tyr Asn  
 225 230 235 240  
 Thr Thr Asn Thr Gln Ile Asp Ala Val Arg Lys Glu Asn Tyr Met Lys  
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 Glu Ile

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 <212> DNA  
 <213> *Corynebacterium glutamicum*

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 <222> (101)..(994)  
 <223> RXA01832

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 Met Ala Thr Ser Asn  
 1 5  
 cgg ata gct aat gct atg aac agt ttg gcc aag ctg gac agt tct atg 163  
 Arg Ile Ala Asn Ala Met Asn Ser Leu Ala Lys Leu Asp Ser Ser Met  
 10 15 20  
 caa cgc ggc ctt gat aat gcg ttg gcg ttt gtt ttc cgt ggt cgc gtt 211  
 Gln Arg Gly Leu Asp Asn Ala Leu Ala Phe Val Phe Arg Gly Arg Val  
 25 30 35  
 gtt cgc gct gag ctt gag gag ctt ttg aag caa gag gct gag gac aat 259  
 Val Pro Ala Glu Leu Glu Glu Leu Leu Lys Gln Glu Ala Glu Asp Asn





cgt att gtt agt ccc tagagggaga ggttgatcaa tgg  
 Arg Ile Val Ser Pro  
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1017

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 <212> PRT  
 <213> *Corynebacterium glutamicum*

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 Phe Arg Gly Arg Val Val Pro Ala Glu Leu Glu Glu Leu Lys Gln  
 35 40 45  
 Glu Ala Glu Asp Asn Val Val His Thr Glu Phe Gly Tyr Val Glu Ala  
 50 55 60  
 Pro Asn Val Phe Lys Val Ser Val Ser Pro Asn Asp Phe Ser Asn Leu  
 65 70 75 80  
 Val Asp Arg Phe Pro Asp Gln Pro Ala Arg Phe Gly Asp Gln Met  
 85 90 95  
 Arg Phe Cys Arg Asn Ser Gly Trp Thr Leu Val Gly Pro Val Ile Val  
 100 105 110  
 Leu Ile Glu Glu Asp Ser Ser Leu His Thr Gly Gln Leu Lys Ser Val  
 115 120 125  
 Ser Glu Lys Asp Pro Asp Pro Glu Leu Ser Ser Gly Tyr Leu Pro Leu  
 130 135 140  
 Glu Gly Asp Gly Ile Leu Pro Val Ala Glu Ser Glu Ser Lys Asn Val  
 145 150 155 160  
 Ser Asp Ser Ser Pro Tyr Thr Gly Thr Glu Phe Leu Pro Ala Gln Ser  
 165 170 175  
 Ala Asp Arg Pro Leu Val Gln Gly Val Pro Gln Ser Gln Val Asp Ala  
 180 185 190  
 Asn Arg Gln Ala Ala Met Lys Pro Ala Gly Pro Thr Val Thr Leu Leu  
 195 200 205  
 Leu Gln Asp Gly Ser Ser Arg Thr Tyr Leu Val Arg Glu Gly Ser Asn  
 210 215 220  
 Ile Ile Gly Arg Ser Asn Asp Ala Asp Leu Arg Leu Pro Asp Thr Gly  
 225 230 235 240  
 Val Ser Arg Gln His Val Glu Ile Thr Trp Asp Gly Arg Asp Ala Ile  
 245 250 255  
 Leu Val Asp Leu Lys Ser Thr Asn Gly Thr Thr Val Asn Asp Thr Pro

260

265

270

Val Asp Asn Trp Leu Leu Ala Asp Gly Asp Val Ile Thr Val Gly His  
 275 280 285

Ser Asn Ile Glu Val Arg Ile Val Ser Pro  
 290 295

&lt;210&gt; 423

&lt;211&gt; 690

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(667)

&lt;223&gt; RXA02533

&lt;400&gt; 423

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 Met Glu Asp Asp Leu  
 1 5

agt gct gct ctc gtc aaa gcg ctt ttc gac gcg cga acc caa cgc agg 163  
 Ser Ala Ala Leu Val Lys Ala Leu Phe Asp Ala Arg Thr Gln Arg Arg  
 10 15 20

ctc tct atc tcg gcg tta gct gaa tcc tcc ggt gtg tcg cga gca atg 211  
 Leu Ser Ile Ser Ala Leu Ala Glu Ser Ser Gly Val Ser Arg Ala Met  
 25 30 35

att tcc cgc gtg gaa aac gca gag gcg caa cca agc gct gca tta ctt 259  
 Ile Ser Arg Val Glu Asn Ala Glu Ala Gln Pro Ser Ala Ala Leu Leu  
 40 45 50

gga cgc ctt tcc ggt gca ttg ggt atg acg ctt tcg gag ctc att gca 307  
 Gly Arg Leu Ser Gly Ala Leu Gly Met Thr Leu Ser Glu Leu Ile Ala  
 55 60 65

cag gct gaa ggt ggc tat gac cgg ggc gct cgg cgg tca aag cag tct 355  
 Gln Ala Glu Gly Gly Tyr Asp Arg Gly Ala Arg Ser Lys Gln Ser  
 70 75 80 85

gta tgg aca gat cca gct acc ggt tac aca cgg cgt gca gtg tca cag 403  
 Val Trp Thr Asp Pro Ala Thr Gly Tyr Thr Arg Arg Ala Val Ser Gln  
 90 95 100

cag tca gaa tcc cca cta gaa cta gtg gaa gta atg ctg cct cct ggg 451  
 Pro Ser Glu Ser Pro Leu Glu Leu Val Glu Val Met Leu Pro Pro Gly  
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gcg gaa gtt ggc tac cca gct gat gct tat cgt ttc atg gat cag gtg 499  
 Ala Glu Val Gly Tyr Pro Ala Asp Ala Tyr Arg Phe Met Asp Gln Val  
 120 125 130

gtc tgg gta ctc gaa ggg gcc gtt cgt att act gaa ggt gaa gag gtc 547  
 Val Trp Val Leu Glu Gly Ala Val Arg Ile Thr Glu Gly Glu Glu Val  
 135 140 145

cac gaa ctt tca acg ggg gat tgt cta cgg ttt ggg cct ccg cga gat 595  
 His Glu Leu Ser Thr Gly Asp Cys Leu Arg Phe Gly Pro Pro Arg Asp  
 150 155 160 165

acc gac ttt gct aat ccc acc acc gta gcc act agg tat tta gtt gcc 643  
 Thr Asp Phe Ala Asn Pro Thr Thr Val Ala Thr Arg Tyr Leu Val Ala  
 170 175 180

ttg gac aag cgt gta cct cgt gct tgatataaca agtaaggaag cct 690  
 Leu Asp Lys Arg Val Pro Arg Ala  
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&lt;210&gt; 424

&lt;211&gt; 189

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 424

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 20 25 30

Val Ser Arg Ala Met Ile Ser Arg Val Glu Asn Ala Glu Ala Gln Pro  
 35 40 45

Ser Ala Ala Leu Leu Gly Arg Leu Ser Gly Ala Leu Gly Met Thr Leu  
 50 55 60

Ser Glu Leu Ile Ala Gln Ala Glu Gly Gly Tyr Asp Arg Gly Ala Arg  
 65 70 75 80

Arg Ser Lys Gln Ser Val Trp Thr Asp Pro Ala Thr Gly Tyr Thr Arg  
 85 90 95

Arg Ala Val Ser Gln Pro Ser Glu Ser Pro Leu Glu Leu Val Glu Val  
 100 105 110

Met Leu Pro Pro Gly Ala Glu Val Gly Tyr Pro Ala Asp Ala Tyr Arg  
 115 120 125

Phe Met Asp Gln Val Val Trp Val Leu Glu Gly Ala Val Arg Ile Thr  
 130 135 140

Glu Gly Glu Glu Val His Glu Leu Ser Thr Gly Asp Cys Leu Arg Phe  
 145 150 155 160

Gly Pro Pro Arg Asp Thr Asp Phe Ala Asn Pro Thr Thr Val Ala Thr  
 165 170 175

Arg Tyr Leu Val Ala Leu Asp Lys Arg Val Pro Arg Ala  
 180 185

&lt;210&gt; 425

&lt;211&gt; 1035

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

$\langle 220 \rangle$ 

<221> CDS

 $\langle 222 \rangle$  (101) .. (1012)

<223> RXN02727

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Val Val Leu Leu Pro  
1 5

ctg cta gtt cct caa ctg cag gtg cag cca cag ttg cag ctt cca agt 163  
Leu Leu Val Pro Gln Leu Gln Val Gln Pro Gln Leu Gln Leu Pro Ser  
10 15 20

ctg ttg acg agg cag cgc tgc gca agg aaa tca aag aga agc tgc gct 211  
Leu Leu Thr Arg Gln Arg Cys Ala Arg Lys Ser Lys Arg Ser Cys Ala  
25 30 35

ccg aat acg gca tcc aag ctc gat gat gcc tcc aag gcc gct cag aag 259  
Pro Asn Thr Ala Ser Lys Leu Asp Asp Ala Ser Lys Ala Ala Gln Lys  
40 45 50

gct caa aac gat gcg aag tcc gct caa gat cag cta cag cgt gca caa 307  
Ala Gln Asn Asp Ala Lys Ser Ala Gln Asp Gln Leu Gln Arg Ala Gln  
55 60 65

gct gac gca aag gca gct cgc gac gaa gct gaa aag gcc aag gct gaa 355  
Ala Asp Ala Lys Ala Ala Arg Asp Glu Ala Glu Lys Ala Lys Ala Glu  
70 75 80 85

gct aag tca gca gca tcc tcc agc acc act aag gca gca gcg gtt ggc 403  
Ala Lys Ser Ala Ala Ser Ser Ser Thr Thr Lys Ala Ala Ala Val Gly  
90 95 100

gct gtc ggc gct ggc acc gga gca gca gtt gct aca ggt gct gca aat 451  
Ala Val Gly Ala Gly Thr Gly Ala Ala Val Ala Thr Gly Ala Ala Asn  
105 110 115

gtg gac acc cac atg cag gca gcg aag gtt ctg gga ctc gca cag gaa 499  
Val Asp Thr His Met Gln Ala Ala Lys Val Leu Gly Leu Ala Gln Glu  
120 125 130

atg gca gac cgc ctg acc tca gag gct cgc tcc gaa tcc aag tcc atg 547  
Met Ala Asp Arg Leu Thr Ser Glu Ala Arg Ser Glu Ser Lys Ser Met  
135 140 145

ctg gac gag gct cgc gaa gca gca gag aag cag atc gag gaa gca aac 595  
Leu Asp Glu Ala Arg Glu Ala Ala Glu Lys Gln Ile Glu Glu Ala Asn  
150 155 160 165

agc acc tcc aac cgc act ctg gaa gat gct cgc gca aac gct gag aag 643  
Ser Thr Ser Asn Arg Thr Leu Glu Asp Ala Arg Ala Asn Ala Glu Lys  
170 175 180

cag atc gct gaa gcg cag aac cgc gct gac act ctg gtc aac gaa gct 691  
Gln Ile Ala Glu Ala Gln Asn Arg Ala Asp Thr Leu Val Asn Glu Ala  
185 190 195

gac gct aag gct aag aac ctg gtt tcc gaa gcc gag aag aag tcc gca 739  
 Asp Ala Lys Ala Lys Asn Leu Val Ser Glu Ala Glu Lys Lys Ser Ala  
 200 205 210

gcc acc ctg gcc gca tcc acc tct cgt gca gaa gct cag atc cgt caa 787  
 Ala Thr Leu Ala Ala Ser Thr Ser Arg Ala Glu Ala Gln Ile Arg Gln  
 215 220 225

gcc gag gac aag gca aac gcc ctc cag gca gac gca gag cgc aag cac 835  
 Ala Glu Asp Lys Ala Asn Ala Leu Gln Ala Asp Ala Glu Arg Lys His  
 230 235 240 245

acc gaa acc atg gct gca gtc aag gaa cag cag aat gct ctg gag acc 883  
 Thr Glu Thr Met Ala Ala Val Lys Glu Gln Asn Ala Leu Glu Thr  
 250 255 260

cgc atc cgc gaa ctg cag acc ttc gag cgt gag tac cgc acc cgt ctg 931  
 Arg Ile Ala Glu Leu Gln Thr Phe Glu Arg Glu Tyr Arg Thr Arg Leu  
 265 270 275

aag tcc ctc ctc gag ggc cag ctg gaa gaa ctc cac gca cgt ggc tcc 979  
 Lys Ser Leu Leu Glu Gly Gln Leu Glu Glu Leu His Ala Arg Gly Ser  
 280 285 290

tct gca cca acc aac aac aag cca tct ggt gag taaaaagaaa gattagttat 1032  
 Ser Ala Pro Thr Asn Asn Lys Pro Ser Gly Glu  
 295 300

ctt 1035

<210> 426  
 <211> 304  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 426  
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Leu Gln Leu Pro Ser Leu Leu Thr Arg Gln Arg Cys Ala Arg Lys Ser  
 20 25 30

Lys Arg Ser Cys Ala Pro Asn Thr Ala Ser Lys Leu Asp Asp Ala Ser  
 35 40 45

Lys Ala Ala Gln Lys Ala Gln Asn Asp Ala Lys Ser Ala Gln Asp Gln  
 50 55 60

Leu Gln Arg Ala Gln Ala Asp Ala Lys Ala Ala Arg Asp Glu Ala Glu  
 65 70 75 80

Lys Ala Lys Ala Glu Ala Lys Ser Ala Ala Ser Ser Ser Thr Thr Lys  
 85 90 95

Ala Ala Ala Val Gly Ala Val Gly Ala Gly Thr Gly Ala Ala Val Ala  
 100 105 110

Thr Gly Ala Ala Asn Val Asp Thr His Met Gln Ala Ala Lys Val Leu  
 115 120 125

Gly Leu Ala Gln Glu Met Ala Asp Arg Leu Thr Ser Glu Ala Arg Ser  
 130 135 140  
 Glu Ser Lys Ser Met Leu Asp Glu Ala Arg Glu Ala Ala Glu Lys Gln  
 145 150 155 160  
 Ile Glu Glu Ala Asn Ser Thr Ser Asn Arg Thr Leu Glu Asp Ala Arg  
 165 170 175  
 Ala Asn Ala Glu Lys Gln Ile Ala Glu Ala Gln Asn Arg Ala Asp Thr  
 180 185 190  
 Leu Val Asn Glu Ala Asp Ala Lys Ala Lys Asn Leu Val Ser Glu Ala  
 195 200 205  
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## APPENDIX A: DNA SEQUENCES

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>RXA00407-downstream

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>RXA00414-upstream

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>RXA00414

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>RXA00414-downstream

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>RXA00415-upstream

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>RXA00415

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>RXA00538-upstream

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>RXA00538

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>RXA00543

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>RXA00543-downstream

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>RXA00544-upstream

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>RXA00670  
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>RXA00672  
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>RXA00699  
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&gt;RXA00706-downstream

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&gt;RXA00709

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>RXA01149-upstream  
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>RXA01149  
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>RXA01157-upstream  
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>RXA01255  
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>RXA01279  
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>RXA01280  
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>RXA01334  
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>RXA01343  
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>RXA01356-upstream  
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>RXA01356  
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>RXA01374-upstream

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>RXA01374

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>RXA01423-upstream

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>RXA01424-upstream

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>RXA01424

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>RXA01424-downstream

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>RXA01453  
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>RXA01453-downstream  
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>RXA01480-upstream  
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>RXA01480  
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>RXA01481-upstream  
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>RXA01481



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>RXA01581  
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>RXA01594  
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>RXA01661  
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>RXA01682  
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>RXA01682-downstream  
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>RXA01683-upstream  
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>RXA01683  
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>RXA01684

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>RXA01688

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>RXA01689

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>RXA01713-upstream

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>RXA01713

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## &gt;RXA01718-upstream

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## &gt;RXA01718

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## &gt;RXA01718-downstream

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## &gt;RXA01735-upstream

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## &gt;RXA01735

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## &gt;RXA01736

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>RXA01739  
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>RXA01740  
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&gt;RXA02145

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>RXA02369-upstream  
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>RXA02369  
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>RXA02370

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>RXA02371  
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>RXA02389  
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>RXA02419-upstream  
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>RXA02420-upstream

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>RXA02463-upstream

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>RXA02463

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>RXA02468-upstream

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>RXA02522

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>RXA02522-downstream

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&gt;RXA02533

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&gt;RXA02533-downstream

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&gt;RXA02615-upstream

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&gt;RXA02633-upstream

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&gt;RXA02633

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&gt;RXA02635-upstream

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>RXA02635

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>RXA02657-upstream

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>RXA02657

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 GCTACTCCCTGTTTGGCGCCCTGTCCAACAGGAGCAGCAGCGTGTATTATGACCCGCAC  
 TCTGGTCGACGATTGTGCTTTCCACCAATATCGCAGAGACATCCCTGACGGTTCCGGGC  
 ATTCACTACGTGGTTGATACCGGTACCGCGCGTATCTCTCGTTATTTCAGTGCACCAAG  
 GTGACGCGCTTCCGATTGAGAACAATTTCCAGGCGCAGCCCAACAGGCTTCTGCTGCT  
 TGTGGTCTGTGCGAGACGGTATTGCGATTCTGTATTTCGAAGATGATTTCAAATCT  
 CGCCAGAGATTACCGATTCGGAATTTGCGCACCAACTTGGCGAGCGTTATTTTTGGCG  
 ATGGCTCGTCTGCGTCTTGGCGATATTAAATGATTTCCCTTCTGCTCAAGCCAGAGCAA  
 CGCTCCATCGAGGATGGTATTTTGTGCTCCACGAGTTGGGCGCACTCACCCAGCACACC  
 CAAGCCGATGGTTACCGCGAGCTCACCCAGATCGGTAAAGACTTAGCCACATCCCGAT  
 GATCCCGCATGGCCCGCATGCTCGTAGAAGCCAACTCTAGGCTGCCTGCATTTCTGTG  
 ATGGCTGATTTGTTCGCTCTGACGATTCAAGATGTTTCGCGAACGCCCTTGGAAATTCGA  
 GCGCAAGCTGATCAAGCCACCGTAGGTTCAAGGACACCACTCAGATTCTTAGGCTTT  
 TTGAAACTGTGGGATGACATCGCCGATCAGCGCAATCAAAGCAGCGCAATTCCTTCCGC  
 AAGCAGATGAAAAAAGAAATTCCTCACTACATGCGTATCCCGACTGGTGGGATTTGGTGT  
 CGCCAAATTAGAGCAGATTGGCCAGCAACTTGGTTGGGCAAGAAAGGAGCAGGTTGCGAGC  
 ACCGCCAGCCCTGACATCATCAACCAATCTTGTCTCAAGGCTGTCTCGCAAAATCGGT  
 TCCCGTGTATGGTGGAGCAAGAAATTCATGGAGCCAGAGGTACCAAAATTTTGTGCTTT  
 CTTGGTCTGCGCTAACCAAGAACCGCCACAGTTCATATGGCTGGCCAAATTTGGTAGAA  
 ACCTCACGTTTGTGGCTCGGATGTAGCCAAAGATTGAACAGAGTGGGTGGAAAAAGCA  
 GCCCGCCCAATTGCTCAAGCACAATACTCTGACCGCTATTGCTCTCAAGCGTGGCGGC  
 TGCCATGGTGCACCGCAAACTCAAGCTCTTCTGGTGTGACAATTTGTTCGCTCAAGGTAGT  
 TCCCTACCAACCGT

## &gt;RXN03166-downstream

TGATCCCGTGCTGCGCGGATA

## &gt;RXN03175

GTCCGCGCAAGCGAAAAAGACACCGCCACCGCACTGCAATCCGCCCTTAGATAACGGATGG



CACTACATTGGTGCCCCAGCAGCTGCCAAGGGACGTGCCGGTGTGGCATTTTGTCTAGG  
 CATGAACCTGAAGATGTGAACATCGGTTTGGATCTTTCCTTGACTCCGGCCGCTACATT  
 GAAGCAACCATCAAAGACACCACCTGGATGTGCCAGTAACCGTGGCATCTCTTACCTC  
 CCCTCAGGTTTACGCGGGACCGACAAGCAGGATGAAAAGTACCGCTTCTCGATGAATTC  
 GAAGGGTTCTTGACACGCGCGCTAAAGAACGCTCCACATGGTCATCGGTGGCGACTGG  
 AACATCTGCCACCGCGCGAAGACCTGAAAAACTGGAACCAACCAAAAGAAATCCGGT  
 TTCTTCCCCGACGAACGCGCATTCATGGATTCACTCTTTGACACCTTCCAGATGAGGCA  
 ACCAGGTTGACGGGCGCGGACTTCTTCGGTGCCGTGGCATATGAAGGAACGAGGCGT  
 CGAGAAGCAACTACGACCTTGCCTGGTTCCAGCTTGACGTCGCGCTGCAACCTGAAGGC  
 GACGGCCCTACACTTGGTGGACCTACCGCGAAAGCCTTCGACACCGCGCGGATGG  
 CGCATCGACTACCAAGCAGCAACCGCAGCGATGCTCGAACGCGCAGAACGCTCTGGGTA  
 GACAAAGCGCTGCATACGATTTGCGTGGTCAGATCACTACCACCTGAACGTGATCTAC  
 TTC

>RXN03175-downstream  
 TAAAAATGCTGCTGACAATTCCTAT

>RXN01389tr  
 CAGGACGGCGATAAGCTCGCTGGCCGCCACGGTAACAAGGGTGTGTGCGTAAATTTTG  
 CCTCAGAAAGATATGCCATTCTCTCCAGACGGCACTCTGTGACATCATCTTGAACACC  
 CACGGTGTTCACGTCGTATGAACATTGGTTCAGGTCTCTGAGACCCACCTTGGCTGGCTG  
 GCATCTGCTGGTTGGTCCGTGGATCCTGAAGATCCTGAGAACGCTGAGCTCGTCAAGACT  
 CTGCCTGCAGACCTCTCGAGGTTCTCTGCTGGTTCCTTGACTGCAACTCTGTGTTCGAC  
 GGTGCGTCAAACGAAGAGCTCGCAGGCTGCTCGCTAATTCAGTCCAAACCGGACGCGC  
 GACGTCATGGTTAACGCGGATGGTAAAGCAACGCTTATCGACGGTGGTCCGCTGAGCCT  
 TACCCGTACCGGTTTCCATCGGCTACATGTACATGCTGAAGCTGCACCACCTCGTTGAC  
 GAGAAGATCCACGCACGTTCCACTGGTCTTACTCCATGATTACCCAGCAGCCACTGGGT  
 GGTAAAGCAGTTCGGTGGACAGCGTTTCGCGCAATGGAGGTGTGGGCAATGACGGCA  
 TACGGCGCTGCCTACACACTTCAGGAGTGTCTGNCCA

## APPENDIX B: AMINO ACID SEQUENCES

> RXA00050 (1-2196, translated) 732 residues  
 MSNTENVNGD VEQPNNVISS ESQETPQGDS ASADFALETP TNTVEDAPAS EGSEETITRVA  
 DTSDEDASAD ADNANNVINE NEDSSEGANQ PSNESSSTEA KSGFDALGLP ERVLDAVRKV  
 GYETPSPIQA QTIPILMEGQ DVGGLAQGTG KTKAFAALPI LARIDKSVRPS PQALVLAPTR  
 ELALQVADSF QSFADHVGG L NVLPIYGGQA YGIIQSLGLRR GAHIVVGTPTG RIIDHLEKGS  
 LDISGLRFLV LDEADEMLNM GFQEDVERIL EDTPDEKQVA LFSATPMVRI RLRSKOYLN  
 PAETVTKSET RTNTNITQRF LNVHRNKM D ALTRILEVTE FEAMIMFVET KHTEVEVAEK  
 LRARGSFAAA INGDIAQAQR ERTVDQLKDG RDLILVATDV AARGLOVERI SHVNFIDIPN  
 DTESYVHRIG RTGRAGRTGE AILFVTPRER RMLRSIERAT NAPLHEMLP TLQVQVDMFRK  
 VKFADSIYKS LEDKQMDLFR TLVKEYSQAN DVPLEDIAAA LATQAQSGDF LLKELPEPPR  
 ERNDRRRDRD FDRGRGRGRD RDRGRGRGRG SRFRDRDENL ATYRLAVGKR QHTRPAIVG  
 ALANEGGLNS KDFGRITIAA DHTLVELPKD LPQSVDLNL DTRISQGLIN IERDSGGRRP  
 RREFRDRRG RGGFRGRDRD RGRGRDRD RGRGRGRG RDRDRDRGRG GFRGRDRDRD  
 RGGRGYRG RD

> RXA00060 (1-2457, translated) 819 residues  
 VTEKTDQQLM LIDGHSMFR AFFALPAENF STSGGQATNA VYGFSLMST LLKDEQPTHV  
 AVAFDVGRKT FRTDMFPAYK AQREATPPEF KGQVEILKEV LSTLIGITIE KIDFEADDVI  
 ATLSVAAKPL GFKTLIVTGD RDSFQLVNDT TTVLYPMKGV SVLHRRFTPEA VEEKYGLTRV  
 QYEPFAALRG DPNDLNPIN GVGEKTATKW IAQYETILDNL LDHADEIKKG VGASLRERIE  
 QVRMKNKITE MVDKLEPLG PDDFEMKFPVQ VAEVAAKFD LFEFTNLNRER VLAVVKAEGS  
 AAPVEVEAE QVVVDTQSLA QWLPARAGQA LALALAGVAK PAAGDTYALA IADTKRHAVL  
 VDVADISAE EKALATWLAS EDPKMLHGAK AAYHMLAGRG FELHGVVHDT AIAAYLLRPG  
 QFYELADVY QRHLQRQLST NDNGQLTL D DAADDQSLVD DVIAILELSE BLTKQLQEIQ  
 ARTEYHDL EIT PLSGILARME AIGIAVDVAT LEEQLKTFIC QVAQEEAAR ELAEDPTNL  
 SSPKQLQVVL FETFGMPKTK KTKTGYSTAA AEIEALAIKN PHPELDHLA HRQYQMKKT  
 LEGLIREVAP DGRHHTTFNQ TVASTGR LSS TDPLNLQINPV RTEAGRKIRS GFVVGEGYET  
 LLTADYSQIE MRVMAHLSQD PGLIEAYREG EDLHNYVGSK VFNVPIDGVY PELRRGVKAM  
 SYGLVVGSLA FGLSQQLSIP AGEAKQIMES YLREIFEGVQR YLREIVEEAR KAGYTETLFG  
 RRRYLPELTS DNRVARENAE RAALNAPIRE LPQTSSRW

> RXA00061 (1-210, translated) 70 residues  
 MIRVORLKEA AAVKSRVLLQ VHDELVVEVA AGELEQVREI LEREMDNAIK LSVPLEVSAG  
 DGVNWDAAAH

> RXA00066 (1-813, translated) 271 residues  
 VTDPLSALD SGRINHAYLF SGFRGCGKTS SARILARSLN CVEGPTSTPC GVCNSCVALA  
 PGGPGTLDTV ELDAASNNGV DDMRELREIRA NYAPAESRYR VFIIIDEAHMI STQGFNALLK  
 IVEEPPAHLI FIFATTEPDK MIGTIRSRTH NYPRLLTPG DMKRVLKNV DGEVGVHDS  
 VYPLVIRAGG GSFRDLSIL DQLIAGSGPE GLTYERALPL LGVTSFTLID DSIHALASKD  
 NASMFTTIDN VIEEGLEPRR FTIDLPDSPL R

> RXA00095 (1-2289, translated) 763 residues  
 MNTSPPTFGS PDLIDGLNEQ QRAAVEHIGS PLLIVAGAGS GKTAVLTRRI AYLMRYRGVH  
 PQQILAITFT NKAAEEMRER VSQLVGPAVE RMWVATFHSV CVRILRQQAQ LVEGLNNTET  
 IYSDSDSRRL LTMIAKDLLE DIKKFSARTL LGAINSLKNE LVTPOEALAD AERTHNRYET  
 VVARAFSEYQ SRLRRANAVD FDDLIGETVR IFRHPPVAE YRRRRFRHVL IDEYQDTNHA  
 QYELISLTVG KPDQDPSEL C VVGDSQDSIY AFRGATIRNI EFERDPSNA RTILLEQNYR  
 STQTLISAAN AVISQENNRK PKNLWLTALGE GEQIIGYVD NEHDEARFIA SEIDNLVDHG  
 MSYSDIAIMY RTNNSSRALE DVMFRTGVPIY KVVGGTKFYE RKEIRDI IAY LRVLENPDOT  
 VNLRRINTP KRIGIDRAQA FIALHSENNQ ISFGQALLDA ALGKVVDLLGA RGNKAAIKFN  
 ELFDALRSEL PTMVNEVTGL PDIGQVISRI LDITGYKAE EASNDPQDGA RDLNLDNELVS  
 VAREFSSDAA NRMVNEVPEG EAQPGSLQAF LERVSLVADA QDIPDSNGV VLNTLHTAK  
 GLEFFIVFIT GWEDGQFPHL RSLGDAKELA EERRLAYVGI TRAKRLYMT RAMLRSSWGN  
 PVTNPFSERL QEVPALIDW RREPQMSSA WAFRRTSIP TRKRTNNKQL DLSVGDVRNH  
 DKYGLGTVLV SDGSGPRATV TIDFGSSGKV RLMLLGGVPM EKL

> RXA00103 (1-4560, translated) 1520 residues  
 MAKSIISRFR PQVAEWFDRV FASPTPVQEG TWEAVSKGKN ALVVAPTSGS KTLAAFLWAL

DSLTEQTGQQ VLDGTGTPVPV RGGKVKVLYI SPLKALGVDP ENNLRAPLGT IARTASRMGL  
 DVPNITVAVR SGDTPSAERA RQVRKPAHIL ITTPESAYLM LTSKAGATLS DVDVVVIDEI  
 HAMAGTKRGV HLALTLERLE KLVGRPVQVR GLSATVRPLE TVAGFLGGGR PVIIVAPPAE  
 KKWDLTIVPV VEDMSDLVPQ EPGSTIGELV MDDPLGITGE SALPTQGSIW PHIEQQVYNQ  
 VMSAKSTIVF VNSRRSAERL TSRLNEIWAM EHPDESLSQP LRRDPQAQIMS SADVAGKAPQ  
 VIARAHGGSV SKDERATTET MLKEGRILRAV ISTSSLELGI DMGAVDLVIQ VESPSPVASG  
 LQVRGRAGHT VGATSIGSFY PKHRSDLVQT AVTVQRMKEG LIEEIHVPKN ALDVLAAQOTV  
 AAVSIKDVQV DEWYETIRKA YFYRDLAREV FDSVIDLVSG VYPTDFLAEI KPRVVYDRVS  
 GVLEGRGFSQ RVAVTSGGTI PDRGMFGVEL VGDGPRRVGE LDEEMVYESR VGDVFTLGS  
 SWRIEETIRD QVLVT PAFGH TGRLPFWTGD AAGRPAELGK ALGAFRRSTL TDPSSSGLEG  
 WAHDNLIAPL QEQEESTGVL PDEKTLVLER FKDELGDWRI VLHTPYGRGV NAWALAYGA  
 KIAETEGMDA QAVAGDDGIV LRLPEGDEDP SAALFMFEAE EITLVTEQV GNSALFASRF  
 RECAARALL PRRNPGKRAP LWQQRQRAAQ LLDVARKYPS FPIILETVRE CLQDVYDLPA  
 LKNLIEDLQL RKVRIAEVTT QQSPFFASAL LFNVTGAFMY EGDSPPLAEKR AALALDPAAL  
 LAKLLGEVEL RQLLDPIIA EVHQQLRRQG DRAARNNEEL ADSLRILGPI PLDELGEHIT  
 FENPDLETRA MTRVINGREH LAQVLDAPLL RDALGVVPPP GVPAQVETIT DALEQLVNRW  
 VTRTGFFPTAN DLAAEAGLGI ATAITALQSA PVIEGRYRGQ VDVQYECATE VLSIIRRRSL  
 AARQKOTRPV SOSAFARFLL DWQOIAFVGA TPELRGVGDT YTVIEQLAGV LRPASAWEDL  
 VLPRRVADYS PIHLELTSN GEVLIVGAGQ AGSRDELWISL LPVDYHQAQVL GEASTMSMPL  
 QDAVLDQLRA OGAFLESDIL EENFGYTTAQ LQEAAMWGLVE AGLVSPDSFA PIRARLASGT  
 TAHRAKRRPA RSRLRTRTSF ASDVPPDMRG KWTLSVQPAD ATSRSAHGE CGLDRFVGLIT  
 RGSVVAEDIV GGFALAYKVL SGFEESGKAM RGYFIEGLGA AQFSTPAID RLRGHDSDF  
 VEGWPSGATD PDVYLIAAAD PANPYGAALP WPEQGSPRAA GAMVVLCDGL LLAHLTRGGR  
 TLTVESDNIP KIATALITYE RLTVEKINGD NVFDSPLLEQ FRKHGATITP KGMRFRRPVA  
 RETPSDTLPT RTFRGGFGR

> RXA00157 (1-1263, translated) 421 residues  
 ARIVAEQREA EAVEKKVQTE AAIANSEQL NVLTNRSFT VAQRDGAERN LAIARAQADN  
 LQCRAREYEE FQQAQARIQ AEAEAAQAAE EKRRADAAA QAAEAQEA QQAQAEAAQ  
 AAQAETAQA QAAQAETQA AQAAQAQAEA NDRAAAQORA AEQAQAQA QREADAQAAN  
 DAQAQALREQ ALTAASIAAA ALIAASQSSH ATTQNPYPTD EDADPTDIAD IQGPTQPGTG  
 ESGDSQSNSS PDLSTGNDST GSDSSSDSSS GNDSSSEVISG DRSAQIETIV ARAMSQLGVO  
 YAWGGSGNANG PTLGIRDGGV ADSYGDYKNV GFDCSGLTLY AFAGVGISLP HYTGQYQHG  
 TKVSPSEMQR GDLIFYGPGA SQHVAIYLGD GQMTAEPNSG SVVKISPVWR SGMTESVVRL  
 I

> RXA00163 (1-561, translated) 187 residues  
 LDQAQGLDSVE LLALRDVEAY DEPIEDGRTF ADNAQIKARA GVTHGTIATI ADDSGIAVEE  
 LNCMFGVLSA RWSGAHGNDT ANNELLQAQ EHVDPERRNA AFVSVCVLAL PDGQSEVQEG  
 RWEGQLLRGP KGENGFYDYP LFIPEAEIDG QGRSSAELSA EEKDALSHRG QALRGLVEKI  
 AQAVAAS

> RXA00208 (1-849, translated) 283 residues  
 MNTPAKRKR EMKIKTATVT GVRQISPDLI RFSFDCPEIV GADLGFTDHY IKILFVPAGA  
 DYSVPFDMAE IAETQPRELQ PVRRTYTFRT VDTVAGTFDI DFVAHGTDLG AGPWAQQAQV  
 GDIWAFGGPG GAETKPETTYE HYVLAGEAEE APAIFAALEH LPAGTTAKAF TEISSNEARF  
 NAPASDNIEV VWVPRDGATH GTLLIDALRG DGYPTKKT SW FIGHVAMVKV ETRKFLFVVG  
 NVDKADASIE GYWRGLGMTD QWQASKREFN EQNEAEELAL SKA

> RXA00212 (1-1560, translated) 520 residues  
 MNILCLLCKW FAVRCSSLWR ISQEVNAQRI ADGGKPFANP RNAAAGSLKV KNIEDVKKRR  
 LRMSHGIGF TEGFSPASQH DAYLALAAWG LPTSPYTEAV TDPEDEVKKV SYEDWHRHDA  
 LHEMDGLVIK VDDIASQRAL GSTSRAPRWA IAYKYPPEEV TTKLLDQVQV VGTGRVTPF  
 AVMEPVVLAV STVSMATLHN QSEVKKRGVL IGDTVIRKA GEVIEPVLGP VVELRDGTER  
 EYIFPTLCPE CGTRLAPAKA DDVDWRCPNM QSCPGQLSTR LTYLAGRGAF DIEALGKGA  
 EDLIRTGILL DESGLFDLTH DLLLSSNVYT TNAGKVNAGS KKLLDNLQKS KQTDLWRVLV  
 ALSIRHVGT AARALAGRYH SIQALIDAPL EELSETDGVG TIIAQSFQKW FEVDWKAIV  
 DKWAAAGVTM EEEVGEVAEQ TLEGLTIVVT GGLEGTFRDS VKEAIIISRG KASGSVSKKT  
 DYVVIGENAG SKATKAEELG LRILDEAGFV RLLNTGSADE

> RXA00213 (1-573, translated) 191 residues

VTEDNAQLRR TWNDLAEKVR YHRDRYYNEQ FEIPDADFDA LFKQLQQLLE DHPELAVPDS  
PTMVVGAPVA EQSSFDNVEH LERMLSLDNV FDEQELRDWL GRTPAKQYLT ELKIDGLSID  
LVYRNGQLER AATRGDGRVG EDITANARVI EDIPHQLQGT DEYFPVPAVLE IRGEVITITVE  
DFPGGQRAAH C

> RXA00214 (1-711, translated) 237 residues  
MNSPSPNSPT VPSLDTTKML SFDLETTGVN PFDTRIVTSA MVTITSKGAE PIELLADPGI  
EIEPEATAVH GITTEHARAN GRPHDEVLAIE TISRLRAGWQ AGLSVIVFNA SYDLTVLRNH  
DPSFTIDGLV YDFFVIDKVK DRYRKGKRTL TDMCAHYDVQ LGNAHAETSQ ALAARIAWAK  
QVRLWPFLTK MTGEELMEFQ AVNYYEQQS FRSYLIGQGR DASDVNTSWP VQTDPAAS

> RXA00313 (1-939, translated) 313 residues  
MAGNDSRRGG LRKTNKKGAT KGSGGQVRRG LKGKGPTPKA EDRTYHAHAK RKVERDRRDR  
GRHQREMPLE VVGRNPVLEC LHAHVPAATL YVAEGAANDE RLSEAVHTAA GRNLPVLEVN  
KLELDRTMGN GMHQGIGLAI PPYEYADVHD LIANAASAK PMGFVLIDNI TDPERNLGAIV  
RSVGAFFGGNG VIIPERRSAS VTAVAWRTSA GTAARVPVAK ETNMTRVVKE FQONGYQVVG  
LDAGGDHLD TYDGDNDVVI VVGSEGGKIS RLVRENCDTI MSIPTEGWVE SLNASVAAGV  
VLSEFSRQRR IKG

> RXA00341 (1-1407, translated) 469 residues  
MKLYAAVLDF EPVAQEFQVE RGFDPHIHDE AASSVDRYAQ EREDLLHMPF VTIDPVGSRD  
LDQAVLIEEI DSGFRVHYAI ADVAAFVEPE SELEKISLHR GQTIYLPDPS ARLHPPEELSE  
DAASLLEGQT RPAVVSIDL DERGEVTATK VRRGLVKSRAL RLDYDQAQID AENGRLHPSI  
SLLPKVGQLR QESALRREAV NLSIPSQRVV KVPNDAGEH YEIVIEPRPH IMDYNSEISL  
LTGMVAGEMM VKAGHGLLRT LAPATKESEA TFRSEAAQALG FEIAPEQPIG EFLQSVDPNT  
PKGMATQREA QKLLRGSGYA SVKNGDSEVH SGVGGYIAHV TAPLRVLCRAI FATEHCLATA  
SGTDVPEWNT RVEEQVLDTM KYSSILASQV DNACLDLITE TVLKYEWEQGN FNAVUVASEP  
EKNSARLFVY KPPVLAKCIG APEQNTQDV TLVTANLKKR EVLFAWPAE

> RXA00361 (1-1848, translated) 616 residues  
MTTSETAPSK ASLYELLEGV SLSDERTFRR RLSKARAPKA LGAIKADIDK ARLLIDEKSO  
LHPSITYPEN LVSSRRDDI AEAIRDNQVQ IIAGETGSGK TQIPIKICL LGRGRRLGIL  
TITQPRRLAR TVAERIADLE QGDIGESVGY AIRFDLDRVSS HTSVKMLTDG ILLAEQRDR  
FLNAYDTTII DEAHERSLNI DFILGYLRQL LPKRPDLKVI ITSATIDPER FAEHFADASG  
KPAPIEVSOG RTFPVEIYR PLEVLDGDKI IDTDPLDGLC SALEELMAEYD GDILCFFAG  
ERDIRDAMEA IEARRWKVE VTFLFGRLSN QEQRHVFSFH SGRRIVLSTN IAETSILTVPG  
IHYVVDGTGA TRISRYSVRTK VQRLPIENIS QASANQSGR CGRVADGIAI RLYSEDDFNS  
RPEFTDPELT RNTLASVILR MASLRLGDIN DFFVQAPQ RSIIRDGILL HELGALTDDT  
QADGSPQLT IGKDLANIPV DPRMARMLE ANTLGCLHSV MVIVSALTQI DVRRERPLEFO  
AQADQAHARF KDTTSDFLGF LKLWEYIADQ RNQSSGNSFR QMKMKEFLHY MRIREWDLV  
RQLEQIGQQL GWAKKE

> RXA00407 (1-576, translated) 192 residues  
LNVAQVEALA RAGAVDCLGV GRRQALWQAG VAATEKPGML PGLSVIEAPA LPGMSAFELM  
ATNISATGVT ADYQPMALIR ERMEELGIVP ADRLLEVEDG TRLRIAGIVT HRQRPQTASG  
LTLFGMEDET GLMNMVMSVG LWQRQRLAR NAKALIIRGI VQNAQGVATV VADRLEPLDM  
GEFLSRGSRD FR

> RXA00414 (1-420, translated) 140 residues  
MQGEASVPFA ELHATSSYNF LTGASDPSDV VVQAKKLGLA ALSVMDRDGF YGAVRFAEAA  
AEGMHTVYG AELSLEQGVLT TVLCKNPEGY KKLSHLISDA KMARGEKGKF AIRRCQWLLN  
MLQGIGWSLQ VFGGWTKSTM

> RXA00415 (1-1962, translated) 654 residues  
MVAEHAAGDW VVLGAFQWLD KIDYVIDCFK PENIVLEFGS TMTPEDADRN EYLRRTOAKF  
QLRGILSTNP ESAARGSVRL AGAKQALARK MPLADAESL HPMGTTWMSR GDTLLKAHPD  
YADLIATTVL LAEACFTLD LVAPNLPKWD TPEGHEMSW LAHLVSTRID TRYVGRSADI  
KARAAQTIQY ELGVIEKLG FGYFLVNNLD VEFCDRSDNIL CQGRGSAANS AVCFVLGITN  
AEPISAGLIF ERLFSPDRDG PPDIIDITES GRREEVIGYV YEKYGRDNAA QVANVITYRT  
KGMAMRAARA LGYPQGAADA WAKGTSEPPD DVLELAAQFK GQPRHLGHS GGMVICDRPI  
ADVVPVEWAR MDNRNSVQWD KDDCATAGLV KFDLLGLGML EAIHMLDLV AEHRGKKINL

WELDLAEVEF YDMLCKADAV GVQVESRAQ LSTLPRLKPR TFFDLVVEVA LIRPGPIQGG  
SVHPYLRRRA GEEAITYDHP VLEKSLGKTL GIPLFQEQLM QVAVDAAGFS GGEADSLRRA  
MGSKRSRPER AALRSRFFQG LKDTNGIVGE TAEKLWNKIV AFAAYGFPE HSQSFASTIVY  
FSAWFKYHAP AEFVCGLLRA QPMGFYSPOQS LISDARRHGVS SILPITVND S GVEA

> RXA00460 (1-378, translated) 126 residues  
MPEHPLHVIF DNPVIPPNTG NAIRMCAGTG AHLHLVEPLG FELTEKHLRR AGLDYHDLAD  
VTVHATFDEA MAAPVGRVFA FTTTANTRFT DIAFEPGDAL LFGTEPTGLP QEHEVHSRIT  
SELRIL

> RXA00538 (1-1269, translated) 423 residues  
MSRISARTLA IALAGATAAS LAVVPAATAN PAGTAPVINE IYEGGNSGSG LFSNDFIELY  
NPTSGDISLD GWSVTYYAAN GNSGGTTNLT GNIPANGYYL IQQRAGSNNT GALPTPDATG  
NLAMGASQGS VALTDNSGLT ADLVGFGGTS MFEGTAAAP TSNKLSVQRK EVGADSDNNS  
VDFETGAPT P TSSGGSPAVD PGEPEFPVNP GETVSIQAQI GTGLATPLEG QTVTTEGIVT  
AVYAEGGFNG YYIQTPGSGT APKVAGDASD GIFVYVSGNG SYPELGASVT VTGKATEHYE  
MTQLGNSQNT VSDTAFFEPVT PLELDTVPTG DDIREAYEKG LLKPTGAHTV TNNYATNTFG  
EIALAFGNPE LYQATQMVAP GAEAIAYEAE NVAQKITLDD GRSGNYTRGD SSTPMAWLVQ  
DGG

> RXA00542 (1-519, translated) 173 residues  
ALFLTVNVWR QAAENVAESL SKGMRVIVTG RLKQRSYETR EGEKRSVFVE EADEVGPSLT  
FAKADVQRTP RGGNSGGNYG GGNQGGGLGG NQGNQGGGFS NQNSGGGFGN QGNQQSQNSQG  
FGGNGNQSQ GNNFFGGGFG GGSQAAPDN DFWNASAPPAG SGGFGGADDE PPF

> RXA00543 (1-426, translated) 142 residues  
MKLILTAAVE NLGVAGDIVE VKNGYGRNLL LPRGLAIVAT PGAEKQIEGI KRAQEAREIR  
DLDHAREVKK ALEALEGVTI AVRTSESGKL FGSVKTDDIV DAVKAAGGPN LDKRAIVLPK  
NLVKTGKYQ VEAKLTDGIV SA

> RXA00544 (1-1530, translated) 510 residues  
MATDTHAASF DDDYVPPQEP SDSFADDAHV DVPAPAFEDF SPAQAFQGT RGGDSQGFKK  
RGRKDESREY RDRFQPPYDN DAEMGVLGAM LLSPTTVIDI LDILTPEDFY RPSQLIFQA  
IIDLFSDNDR IDPVIUSGRL DRTNDLDRVG GGAYLHOLIQ SVPTAANARY YAEIVSEKAV  
LRLVLDACTR VVQLGYEGDE GAEIDAVIDR AQQEVFAVSQ KNQSEDIAYL ADILDETMAE  
LEMLNDGGIA TGITPGFKDL DDLTNGLRGG QMIIVAARPG VGSKTIALDF MRSASIKNNM  
ASVIFSLEMS KSEIVMRLLS AETEIRIADM RGGKMDETAW EKMVQKLDKV AQAPLFIDDS  
ANLTMEIRS KARKLKQKHD LKMIVVDYLQ LMSSGKRVES RQQEVSEFSR QLKLLAKELD  
VPLIATISQN RGESESRDKR PQLADLRESG SLEQDADIVM LLYRPSQDQK DDERAGEADI  
ILAKHRGGPI DTVQVAHQLH YSRFVDMARG

> RXA00545 (1-255, translated) 85 residues  
MIILDSQDE RTVAPSCLKF LEVVRKDKGD VVKVDVWGKR RLAYPIDKKE EGVYAVVDLK  
CESATVLELD RVNLNDGV L RTKVL

> RXA00562 (1-630, translated) 210 residues  
MDADPLIED VSGAEVKDSS DEPLLALTRY VFDRGERPVT RGLFHQVAAI LSIVSGSVLS  
TYAWMLVWM QALGVMYAL AMLGLFAVSA AYHRGPWRRL HTVAWWRKAD HSTIAVFIAA  
TYTPLCLIVL EPGTAAMMLG IAWVGAIOSV IYNNVWVNH P RWSLVLYLA LGWLIVPLVP  
QLWSGAGPTV VWLLLAEGIV YSVGALVYGF

> RXA00625 (1-339, translated) 113 residues  
SDHDPIKVG NLSEETTEPTI PVEPTDPAEP TDPTTPVKPT DPVETTDPS PTDPAEPTDP  
AETPDPEETH KPEEPKNPFS SNGSSQYATI AATIAAILGA IALAFQFFHS SSN

> RXA00670 (1-489, translated) 163 residues  
MPTPKKARL GGSASHQKKI LSNLAASLFE HGAIKTTDAK AKALRPYAEK LITKAKSGSV  
ADRRNVLAIV PNKEIVAYLF NELAPKFENR PGGYTRIIL ENRKGDNAPM SQISLVLEET  
VSAEASRATR ASASKAAEE AETEEVVEAP AEETATEEAA EEK

> RXA00671 (1-1014, translated) 338 residues

MLISQRPTIT EEFVNNARSA FVIEPLEPGF GYTLGNSLRRL TLLSSIPGAA VTSVKIDGVL  
HEFTTISGVK EDVSDIILNI KGLVLSSDSD EPVVMQLVKE GPGVVVTAGDI QPPAGVEIHN  
PDLHIATLNE TAKIEIELIV ERGRGYVPAT VTATGGEIGR IPVDQIYSPV LKVSYKVEAT  
RVEQRTDFDK LVIDVETKNS ITARDALASA GKTILVELFGL ARELNIAAEG IEIGSPQOET  
EYIAAYSMPI EDLDFSRSY NCLKREDIHT VGLAERAES DLLDIRNFGQ KSINEVKIKL  
AGLGITLKDA PEDFDPSTLE GYDAETGGYI DVEAEDSE

> RXA00672 (1-603, translated) 201 residues  
MARYTGFPATR KSRRLRVLDLV GGDMAFERRP YPPGQAGRAR IKESEYLLQL QEQKQARFIY  
GVMEKQFRRY YAEANRRAGK TGENLVVLE SRLDNVVYRA GLANTRRRAR QLVSHGHFTV  
NGKAIDVPSF RVSQYDIINV REKSQKMWF EEAQDNLADA VVPAWLQVVP ENLRILVHQL  
PERAQIDIPL QEQQLIVEFYS K

> RXA00673 (1-90, translated) 30 residues  
LQAAGLEIGS ISDVTQPQHN GCRPPKRRRV

> RXA00694 (1-396, translated) 132 residues  
MTMTDPIADM LSRVRNAGNA HHDTVSMPS KIKANIAEIL KQEGYIANYT VEDAKVGKTL  
SLELKYSNTR ERSIAGLRAR SKPGLRVYAK STNLPQVLGG LGVAIISTSQ GLLTDRQATE  
KVGGEVLAY VW

> RXA00695 (1-534, translated) 178 residues  
MSRIGKEPIT IPSGVETKID GQLVEVKGPK GTLNVNVPPEP ISVAVEDGKI VVTRPDDHRT  
NRSLLHGLSRS LVNNLVVGVV EGYTIKMEIF GVGYRVALKG KDLEFSLGYS HPVLEIASEG  
ITFAVDGNKT LSVSGIDKQK VGQVAIVIR LRKDDPYKKG GIRYEGEQIR RKVGKTGK

> RXA00696 (1-402, translated) 134 residues  
MSNTENKQKR VSVGKDIATR RRVARARRHF RIRKNLRGTP EAPRLVVHRS SRMHVQIID  
DVAGHTLAAA SSIEAEVRAT EGDKKAKGAK VGQLIAERAK AAGIEQVVFED RAGYKYHGRV  
AALADAAREG GLKF

> RXA00697 (1-633, translated) 211 residues  
MPGRERRDGG RSADDNKQND RNERRGGRR DRRNRQQQDE RSQYIERVVT INRVSKVVKG  
GRRFSFTALV IVGDGKGMVG VGYGKAKEVP AAIQKGAEAA RKNFFRVPMV NGTITHPVQG  
EKAAGIVMLK PAAPGTGVIA GGAARPVLEC AGIQDILSKS LGSDNAINVY HATVDGLKQL  
VRPEEVAARR GKTIEEVAPA RILRARAGQE A

> RXA00698 (1-183, translated) 61 residues  
MALKITQIKG TVGTPKPKHRE NLRLSLGLKRI RHTVIRPDTF EVRGMLAVR HLIVVEEVAG  
E

> RXA00699 (1-444, translated) 148 residues  
MSEPIKLHDL RPAAGSNKAK TRVGRGEASK GKTAGRGTGK TKARKQVSAA FEGGQMPLQM  
RLPKLKGFFN PNKVDYQVNV IADLAEKFPQ GGDVSIADIV AAGLVVRKNEL VKVLGNGDIS  
VKLNVNTANKF SSGAKEKIEA AGGSATVA

> RXA00706 (1-267, translated) 89 residues  
EFLDRLLTVA LPRIRDFRGL SDQQFDGHGN YTFGLTEQTM FYEIDVDKID RPRGMDITVV  
TTAVTDDEGR SLLRELGFFP KGEDGNRQQ

> RXA00709 (1-339, translated) 113 residues  
VADNTGAREI LCIRVLGGST RRFAGIGDVI VATVKEATPG GNVKSGEIVK AVIVRTKKET  
RRADGSYISF DENAAVIKN DNEPRGTRIF GPVARELREK KFMKIVSLAP EVI

> RXA00710 (1-312, translated) 104 residues  
MKVHKGDMLV VISGPKDGAK GQVIAAFPKT EKVLEGVNR IKKHVANSAP ERGAESGGIV  
TQEAPIHVSN VMVIDSDGNE TRVGYRFDEN GKKVRVSRRN GKDI

> RXA00711 (1-156, translated) 52 residues  
MTENYIPRLK TRYQDEIRTK LQGEFEFENV MQIPGVTKIV VNMVGVDAAAR DS

> RXA00717 (1-960, translated) 320 residues  
 VTTPARRDGT PDKQSNRSRG GYRSSRVGRYK PGSSRPNTRO QPQKKDEILL SNAKPAKKON  
 VKSDDDDWSMG FLNRNDSGDV RLQKVLAQAG VASRRHAEIL IDQCRVEVND RIIVTQGVVRV  
 DPNNNDVIRVD GVRIHINEDL EYFVLNKPGR MHSTMSDELG RPCVGLDVSE KTASGQRLFH  
 VGRLLDADTEG LLLLLINDGEL ANRLMHPKYE VSKTYLATVR GEATNKLVA LRDGVELEDG  
 PAKADFAQII DVFOGKSLLR IEIHEGRKHI VRLFDDELGF FVERLVRTKL HTVQLGDQKP  
 GSLRALNSSE LTSLYKVVQL

> RXA00789 (1-243, translated) 81 residues  
 MTNPDIIVSG QGNDSEFPEVA QLSYERARDE LVEIVKILEL QQMGLDESLK YWERGEALAK  
 RCEHLHAGAS ARVEQALNQA E

> RXA00790 (1-1026, translated) 342 residues  
 RNRPTPLKDG DRVIVYGKPA FYAGRGTFSL WVTDIRPVGI GELLARIEEL KRRLAAEGFLF  
 DPARKKRLPF LPNRVGLITG RGSAAERDVL SVAKDRNPEV QFEVINTAVQ GASAVPEIIE  
 ALRVLDQDPR DVVIIIARGG GSVEDLLPFS EEALQRAVAA AQTPVVSATG HEPDTPVLON  
 VADLRAATPI DAAKRVVPDV AEERMLINQL RSRSAALRG WVQREQQALA AIRTRPVLD  
 FMTPIINRRD EIAQAVGLIR RDVTHLVKTE QALVASLRAQ VSALGPSATL ARGYSVVQVI  
 PRDGSAPPEV TTIEQSPPGS QLRIRVADGS ITAASMGTTQ AN

> RXA00798 (1-2355, translated) 785 residues  
 DYWDLSAEFN ARENGKADSD NPSSFARLS TIDGNRVAQG RDNFNRGELT SEAVVVDKQR  
 AEALAEALEG QEMAVVGVEE KPYTRRPYAP FMTSTLQQES GRKLHYTSTR TMRAQRLYE  
 NGHITYMRTD STLSLSEQGMK AARDQALELY GAELYSPSPR TYDRKVRNSQ EAHEAIRPAG  
 ERTFATPGQLH QGLDAEEFKL YELIQRQTV A SQMADAGTS MKVTIGGTAK TGEKTEFNAT  
 GTLLTFEGLL RAYVETRTTA DGRDVADNAE KRLPLLSEGD LKVLISLEAD GHSNTPARY  
 TEASLVKKME DLGIGRPSY ASIIKTIQDR GYVYSRGNAL VPSWVAFAV GLEEFANFSL  
 VIDYDFTSSME DELDNIAAGR EGRTWELNGF YFGDAEADQS MAESVARQGG LKALVDANLE  
 HDHARSVNSL KLFFDDEGRA VNVVRVGRYP YIERIVGTTA EGEPEFORAN LPEETTPDEL  
 TLEVAEKLFRA TPQGREGELI NPANGRMVVA KECRFGPYVI EQVTDSEQR AEAQAEVEVA  
 AERKAEDQRA ATDGMRPKNW ETKTAANQKE KRINQLVEEN LKPATASLFS GMEPAATYLE  
 EALKLLSLPR EVGVDPDSNE VITAQNGRYG PLYLKGSDSR SLNSEEQIFT LTLEDEARRI  
 AEPKRRGRRA AQPLLKQLGD NDVSGKPMTV KDGREGPYVT DGTTNASLRK GDVPESLTDA  
 RANELLSERR AKEAADGGAP AKKTSTKKTIA AKKTAKKTT AKKTVRKAPP KTTKNVVKAG  
 AKKKS

> RXA00807 (1-1119, translated) 373 residues  
 VFDSLGSAGT VSKTLFDDAAS SARALVRART TERARARAEH QNFAMIHDSG FAQSWLFTGP  
 VGSGRSVAAK VFAATLVCSN PDVVGGCGQE DCRAAMGGSH PDIEHIVPQQ LSGIVDDAARE  
 VIKAAAVSPV AGNWRVVEFE NADRLTMQAA NALLKTVEEP TESTVMILCA PTDDPRDIAI  
 TLRSRCRHLY IPTPSIAEVA RILVAEGNVS QADAELAAAH GAHIGRNVY LAHNNAQRRI  
 RASILNLAEI IFHGDVAFRS VNTLVKMWET EAKDSNKEKE EGDLEAVRIS LGMAAKGKGV  
 HKAVRGGAGD KFALEDQKQL RRTFRFLRDSL DLALVDLAGI YRDIIISQQ AQVGLTHPDM  
 EGLSQELATK VSKQ

> RXA00809 (1-510, translated) 170 residues  
 LITPDFFESE QAMRPSFGE ELAAIVSKRY SESTLTHMVT LPASKAKYVD WPSWVPASLR  
 DALVNRGINK LFSHQEQTAL LAWNQHVUV ATGTSSGKSL GYQLPLSAL GTDPTACALY  
 LTPTKALGSD QLTSTSTLLR DIPDFHPINP APYDGTPTSE ARSGIRDLRS

> RXA00817 (1-1710, translated) 570 residues  
 FYGSHPTVIL ASATSSDPEI HASRLLGAPV KAVTEDGAPT GERTVLLWEP GFIEGAEGEN  
 GAFVRRRAST EAANIMATLI SEGARTLTFV RSRQAEIIVA LRAQEELSTL GRDPFARRVA  
 SYRAGYLAED RRRLERLDD GTLLGVASTN ALELGDVGG LDVAVVTAGFP GTVASFWQQA  
 GRAGRRGGQS LVVLVARDEP MDTYLVHHPA ALLEKPVVEA VFDPTNPVHI RGHVYCAVE  
 KPLTEAEVAV FGAQKVVEKL ELEGLLKKRF RGWFAVEKPM SEDPDELSDP SAHQQVSLRG  
 GSGSEFMVVD ITDGRLLGTI DSAKAMSQTH PGAVYLHQGE SFVIDELDL ENLALARPEL  
 PDYTTYARS D TDIRITSAFL EDEVFDAGGG LWVANVEVQV TDRVTGYVTR LSDGTTLDAI  
 GLYLPPLQILQ TRAVAYTIDP LALEAMGIPA ADIPGALHAA EHAAGIMLPL LAGTCRDWDIG  
 GVSTALHADT GYPTVFVYVD MDGGAGFADT GFRRFQWIE ATFEVVRSCS CESGCSQCVQ  
 SPKCGNGNNP LDKAGAIKLL GAMVTLTGTS

> RXA00823 (1-780, translated) 260 residues  
 MGSITPQKRP RVGSHIANKG QETDIGRKRK ARRINRRLTV AYPDAHCELD FTNPLELTV  
 TILSAQCTDV RVNQVTPALF KRYPTATDYA NADRTLEEF IRPTGFYRNK ATSLIGLGEA  
 LISLHDGQVP GTLEQLVELP GVGRKRTANV LGNAFGVPGI TVDTHFGRVL RRLKLTDEED  
 PVKVEKVMNE LIEKPEWTFM SHRLIFHGRR ICHSRRACG ACMLAADCPG FGLEGPSDFP  
 EAQKLIKSDD REHLKLMAGM

> RXA00890 (1-1275, translated) 425 residues  
 LSIATVVALL FSGLLGAVES ALSSVSRARV EQMLKDEASG SASLLRVIDE RALHINMLIM  
 LRTLDDASAA VFAAGIAVNV MDSWANGIVL AIVVVSLLTF AVVGVFGRTV GRKNPYSVML  
 RSVAVLSGLA KILGPIARGL IWIGNIAPG PGFRNGPYAT EVELREMVDI AQEHGIVEIE  
 ERRMIQSVFD LASTTVRQVM VPRPEMIWIE SGTAGQATA LCVRSRGSRI PVIGENVDDI  
 IGIIVYKLDVL QKTYATDGG KSVLVDEVMR EATFVPDSKS LDALLQEMQE DHKHAIALVD  
 EYGGVAGLIS IEDILEEIVG EIADEYDARE VAPIEKIGDR TYRVVSRSLR EDLKDHIIEE  
 LDLEIEFEGDE IEDQVDTVGG LIAFELGRVP LPGATVETCG LKLTAEGARN RRGRLRMHSA  
 VVEVG

> RXA00898 (1-789, translated) 263 residues  
 MRIVNVNVS ARTRVDRMVD FLRLHDVDVL AVQETKCKDE QFPTERTFEI GYEVAFHGLN  
 QWNGVAITSR VGIENVETHF PAQPGFNKDI TKEQSIARA IGARCGGVQV WSLYVNGRE  
 IADPHYDYKL RWLFSLRNVY IDTLEYRPEE KLVLLGDFNI APTDIDVWDI AAFEGKTHVT  
 EPERAAFDGL IEAGLKETTP GPGTYTYWDY KGARFLKGG MRIDFQLASP ALAATAGETF  
 VDVEERSGTG ASDHAFVIVD YKV

> RXA00967 (1-363, translated) 121 residues  
 MPVQDAGERN NNDPRVPMGE ILREEFMEPL GLSQNGLARA IGVPPRRINE IVHGKRAITA  
 DTLRALAAYL GPDQFWLNL QTHYDLSVTY LDARTLLEAI KPYDRQQNVA RTLNPLQESS  
 Q

> RXA00990 (1-453, translated) 151 residues  
 VATDIAARGI DVDDVSLVHV VDPPEAKKAY LHRAGRTARA GTSGTVTVTL MDEQIKEVRE  
 LFQKAGVTAA EVKVNENSE LAKITGARR SGVALPAPGQ QQPKREKQNT HNRSDSRGSS  
 RNPERRGSGS SRSTGRSNPR RQTSRKDGPK S

> RXA00994 (1-342, translated) 114 residues  
 MTTFLELKL DEIVRELRSG GITEAFPIQE AAIPDALAGK DVLGRGPTGS GKTFTFGLPM  
 ITRLARSGAS KPGRPRGLVL VPTRELAAQV RERLDDPARV MGLRVLEVVG GVNI

> RXA01030 (1-1176, translated) 392 residues  
 MTSTTPQGGT PELSADTHSE PWDVIENTL EPFQKVVRQF IIDRPYSGIF LTMGGGKILT  
 TLSALYIQPG PGHILVVAPL NISRLTWPEE VRKWNIPVNA ISLITNERGT KLTRAKRLKL  
 YEETATTPPT LYYITINLLE DIVNYFGDRW PFWTVIIDE QTISDISSK TRALFSVRPY  
 IGRLLILTPT SANKFDSIY AQVAVLDYGA SLGDNDIVFR ARWCAPDIIT DKQVRWRKPA  
 NKQAEAEVYR TISHLVMSAV NTDIKLPLH FVDVEHVMSD DEHRDYELFK KDVAIALLD  
 MAEENEGGEG ADDTDAADSA TTFPASPQ TPNPAIPAGL QAIQQTQDNT GRAIAPVTTA  
 ELDFHEDLPV QRQEDLGTIV VISAVHASDS AA

> RXA01064 (1-636, translated) 212 residues  
 MSLSISFHKI ALSATILLGA VAISACALVT QAPPINAAVP TGSSSLSFTL DLGTTTPTSI  
 DTVKLTQQAQ NQAAPRVAAS LVVRVVDGDI VVNYQGAQKT VRMIGDSPE TKHPTKPVGF  
 YGPESSQNL TMLRGATITL EFDSTQARED QYGRLLAYVW YTKGDSGLKL ANLEQTASGS  
 AAESYFDTRY NHRNIFLRAQ TLAKASSLGM WG

> RXA01149 (1-258, translated) 86 residues  
 VVAPQSRKPQ HPGEILSERF LEPGRISHYD LAKTLHITEA TIANFVEGRT DLTIGLAVRL  
 SRSFDLSTQE WIALQRTFDQ AHRRA

> RXA01157 (1-1605, translated) 535 residues  
 MSFSAEKGTH LSEFIADLGF DLDEFQIKGC HAVEEDHGVLC VCAPTGAGKT IVGEFAVSLA  
 LSRGKCFYF TPICALSNQK YHDLVARHGS DAVGLLTGDV SINHDADIIV MTEVLRNMI



YAGSFALERL SHVVMDEIHF LADASRGAVM EEVILNLDD S VNIIGLSATV SNSEEFGEWL  
 TTVRGDTRVI VTDHRPVPLD QYMMVQRKVM PLFEPGTDGR VNKELEATID RLNSKQSEGG  
 RAAYRSGEFG RARSKGDKQD SRTGKPREQD RHRPLGRPEV LSILKGINML PAITTFISRA  
 GCDGALYQCL RSKLVLTDOA ESEETARIVD AGVVGPIPED LQVLNFKQWR AALMRGFAAH  
 HAGMLPAFRH IVEELFVKGL VRVAFATETL ALGINMPART VVLEKMYKFD GEGHVDTLTPG  
 QYTQLTGRAG RRGIDVLGNA VVQWSPALDP RWVAGLASTR TYPLISTFPQ GYNMSVNLK  
 TIGYEPSLRL LEKSPAQFQA DGSVVGDVRE IERAEAKVAE LRAQLNKEIA ATNPA

> RXA01238 (1-1401, translated) 467 residues  
 VIAAYGASIS LDSTLTITISY SPLLAALS S SAQSESVDLT QVSGVSVQDP TAFTHGFLNL  
 EGVKSI AFA PNSSADLAAL AADIDAVLKG EKPQHLGGGA PVVSPAPSTV AGLNFGVFDV  
 ETANDDWGSI CQIGLVKYVD GVEESSESWL CTPPESLNFF NEINIGIHGI TPENVADQPR  
 FADLVFKMVE FVGDLPLVAH NAQDFDTALS RACAAAGIDV PEMIYGCSIDV LARNEKLQVE  
 NHKLPTVASH LGFELKNHHD AAEDARACAA ITIALAKRHS FEFGSFVDFVH SRGFTMGTVT  
 NARVYPVLKD RSGANVALQR RNFGLDAGKT EYVPQAPVDP AWETPKAEKP QKSGRAAPWD  
 KVATPEVIPP PNPADAPSSI LYQNVNLTG DFEPYKCAL WQRIADQGL IGKNVTKKTT  
 ILVAGPWATI TSKQKRAEL KEKGQDIQIW DEKQLFTALG LDEQPPF

> RXA01255 (1-1080, translated) 360 residues  
 MSTTSESQDH AARIEAERQE AIEAAPFVS S SIQSSGIHPS TSRMVTIDLV TSPNLEPVE  
 TFHAVLDKST DPGFHLHGV TEEEFASAKR FGQILKSLDR LIDGRTLH NAARSWGFIV  
 SEAKRAMNDA ARANRNSNRG NRRGGRGRRR QRVGHIKPKL VIVDTLASAR RQAIALDDVR  
 IRGVAHTLGL DAPAAEASVE RAQVSHRQLC REETLLVARL YGALKQSGPL AEIDPQSLRA  
 DKFGLQRSTI RQVQGEASPT LVNPGTYEPG KTLIAGMEVV VAPEIEMDPD IIQACVDAD  
 LSYSEKLTRQ TSVVVCNQTR DIDGKAMHAQ RKGIFLLSDV AFLAAVKRVK EGKKVDVKEK

> RXA01279 (1-465, translated) 155 residues  
 MRKSAAPKRP VVQDPVYKSE LVTQLVNKIL IGGKSTAEK IVYGALEICR EKTGTDVPGT  
 LEKALGNVRP DLEVRSRRVG GATYQVFDV RPERANTIAL RNLVTFTRQR RENTMIERLA  
 NELLDAAAGL GASVKRRRED HKMAEANRAF AHYRW

> RXA01280 (1-366, translated) 122 residues  
 MPTIQQLVRK ARHDKSDKVA TAALKGSPQR RGVCTRVYTT TPKPKNSALR KVARVRLTSG  
 IEVSAIYIGE GHNLDQESMV LVRGGRVKDL PGVRYKIVRG ALDQTQGVKDR KQARSRYGAK  
 RG

> RXA01286 (1-654, translated) 218 residues  
 MSENKIKGIL GTKLGMTQIF DEENRVIPVT VVEAGPCVVS QIRTVETDGY NAIQIAYGEI  
 DPKRVNQPLT GHFKKAGVTP RRRHVTEIRM DVSQHYEVQGD VTVEIFNDIK FVDVTGTTKG  
 KGYAGAMKRH GAGQGGAGHG NQAAHRRVGG IGAATPGRI FKGRMAGRM GNDRVTTQNL  
 KVQKIDADAN IILKGAIPG NRGGIYVTKT AVKGGAHA

> RXA01287 (1-303, translated) 101 residues  
 VAGQKIRIRL KAYDHEAIDA SARKIVETV TGRARVGVFP PLPTEKNVYA VIRSPHYKDK  
 SREHFEMRTH KRLIDILDPT PKTVDALMRI DLPASVDVNI Q

> RXA01305 (1-1866, translated) 622 residues  
 MRPSSRPLGL VLCTALASTI ITVPAASAE PALLDASAIA PHTASYGYVV DAWDNTVSTD  
 LNPSSNAAVG VLEEMLEWT PGEENWTVK VDPFTVLDNSI AQSWAISQQA TDAQQUERAW  
 LDRRNQNYTA TDGLGAYADS YRETAQVGT IPDVVPADAT TVKYNDGGNV NGNWAETGGE  
 LGSTVDLIEA IRQHAATSN AKAYYQYPRF YRWTESIEPE AWGEGVDME YANPLRKDES  
 EAASDGGFPS GHTSAGGMAT NGLAYAFPOQ YDKLLMTAAE IGESRIQLCM HSPLDVIGGR  
 VLSTAITAGA LNDPNLDSVK AEAFFDAQAW ISNQSDITT TROFDEQLAE YTNFLTGFGE  
 QSGDPTQDMR VPKGAELALE TRLPYLDDEQ RRWVLHSTGL ESGFPVLDDA EGWGRNLNYA  
 AQAGSADFDT NVDVTMNAID GGYNAKDNWQ NDIEGAGSLT KNGSGELTSL GDNSTYTGTT  
 ITAGTLVAAT ESALGAGDLT INDGATLKIT QPVTVDGTAN LGGTLHVALP VGTNHVTVID  
 AASISGEFDE VIVDGAVDQA VSYDNGSVVI TTGAPSDDVK ETGSSAGGIL AIVAAALGGIA  
 ALIFGAFTQF GPPPAIKEMF DL

> RXA01334 (1-384, translated) 128 residues  
 MAKLTKEDELI EAFKEMTLIE LSEFVKEFEE VFDVTAAPV AVAAGAAGG EAAAAEEKDE

FDVVLEDEAGA KKIGVIKAVR ELVSGGLKE AKELVEGAPK AILEGANKDD AEAAKAKLEE  
AGAKVTLK

> RXA01335 (1-513, translated) 171 residues  
MANPRNEAAL AELKARFAET DTVVLTLEYRG LTVAQTTTELK KALGFVDVQYS VAKNTLVKIA  
ANEAGVEGLD DLLTGPATAV FIKGEAVDTA KVLKKFGEEN KAFVVKGGYM DGNALTAEQV  
NAIAELDNRE TTLAKLAGAM KGS�AKAAGL FNAPASQVAR LAVALQDKKD A

> RXA01343 (1-651, translated) 217 residues  
IYSPLEAANL VKETSSKNYD ASIDVAIRLG VDPKKAQDLV RGTVSLPNGT GKTVRVAVFA  
QGEKATEAEA AGADFPVGTDE LVEKIQGGWT DEFVAIATPD QMAKIGRIAR VLGPRLMFMN  
PKTGTVTNDV AKAIIEVKGG KISFRVDKAS NLHAAIGKAS FDAKKLAENY GALLDEIIRI  
KPSKAGGIYV KRVTLSSTTG PGVEVDTHVT KNYEEA

> RXA01353 (1-339, translated) 113 residues  
MNILDKIDAA SLRDDVPAFR AGDTLDVHVK VIEGTTTRTQ LFGKVIVIRQ GGGIRETFTV  
RKVSFGIGVE RTFPVHSPNI EKIEVIRRGD VRRAKLYLRL ELRGKARIK EKR

> RXA01356 (1-627, translated) 209 residues  
LSRNLGPVAA GVDEAGRGAC CGPISIAACI LPDKPIQELA ALTDSKKLAS STREKLMPLI  
KKHALAWSVI VISAQDIDRF GIQHANISGM RRAVALGTQ PGYVLTDMK VPGETVPYLP  
IIGGDASARC IAAASVLAKQ TRDDIMTOMA NDYPHYGLEI HKGYSTKIHM DAVRHHCASP  
EHRYSYANVA KAHQEWLHAA DNDTTEGGA

> RXA01363 (1-699, translated) 233 residues  
MSSLIPVHAA GSIQEGITEY LITSFSLADK QVATELKKRFL GHGDSGMFHH PYVVARLPYA  
QAQEWENVLV WLPENFVPHY HQKAAFORLS SLDNRGKDRR PDPTLVVGTG GSGKTESFLY  
PILDHALRIL KRCQQGKIAL LLYPMNALAN DQADRLARLI HNNPALKGVY AGIYTGEAKG  
NRMQGGEREL INDPQAMRVV PPDILLTNYK MLDQQLLSV DREMWMQKAT SLQ

> RXA01374 (1-882, translated) 294 residues  
MSESGALSST DLSLPGVTIE VRDEIWLVTB VTRSTDGFRV KARGLSYVR DHEATFFTAL  
DKDLKVIDPT QVTVSLLDSS NYRRTLRLWE ATMRTVPVPL YQESLSVADQ MLADPLEYQL  
AAVRKTLSSA NLRPRVLAD AVGLGKLTLEM GMILAEILRR GRGERILVVT PRHIMEQFQQ  
EMWTRFAIPL VRLDSVGIQV VRQKLPASRN PFTYFPRVIV SMDTLKSPKY RAQLEKVHWD  
AVVIDEIHNA TNAGTQNNEL ARTLAPTAEA LILASATPHN GDPESEKIL RLLD

> RXA01423 (1-141, translated) 47 residues  
MAKGKRTFPQ NRRRRARVHG FRLRMTRAG RAIVAARRRK GRAKLTA

> RXA01424 (1-309, translated) 103 residues  
VHLWDSAESL DGETKQGEVA SFGGPRFGLV VSKAVGNNAV RHRTSRRLRH ICASIAEKSP  
ELLSPTHHVV ITRLAGAGNA TSAELERDIR YGLGKASVR TNK

> RXA01453 (1-297, translated) 99 residues  
MAQKLYPPH PGEILMEDFI KGFGLTQNKV AVSIGVPPRR INEIVHGKRS ITADTALRLG  
RYFGIDPQFW LSLQTQYELE LDRDAGAATY AQITPLKVA

> RXA01480 (1-1893, translated) 631 residues  
MAKGRIPES IQAIRERTPI EEIVGDYVOL KSAGADSLKG LSPFDEKTP SFHVRPNRGY  
YHCFSTGKGG DVFSFLMEME HISFPPEAVEV CAEKIGYQIN YQGGGPGRRR EPGTRQRLIL  
ANKAAHQFYR EQLETPEAQP GRELLQRGF QQGHYHFFEC TKHLLKGFGE  
FKELEAAGLS KMGKRGPIQ FQRLLWPIK NLSGDVIGFG ARKLFDDDKM GKMNTPEPIL  
LYKKSXVLFG LDSAKKAIAA GHQAVVVEGY TDVMMHAAAG IDTAVASCGT AFGEHLQML  
RRMLDDNYF RGEIYTFDG DEAGQKAAMR AFEGDQKFTG QSFVSVAPEG MDPCDLRLER  
GDAVVRDLVA RRIPMFEFVI QSISEYTLT TVEGRLAALR RAVPIVADIR DKTQSEYAR  
LLSGVGVGWS DSEVLQVHE EARRPKRDKK PVRAKRFDPQ LEDQSLRPTL ALPNPRNPVL  
WQERESLkia LQYPELAGSY FDGLPTDSFT NPAYRMVRDA ISAAGGCERA LDGTDWLPAV  
SENMTDILGT SLVSELAMEP TEVEAQDLES YTDGVLRLQ ETRVGNGQIAI LKGQLQMRMP  
SEDEQAYNSL FSDLVALEQA RRELLARAFR G

> RXA01481 (1-492, translated) 164 residues  
MONSCKTLGG VLGIVIVLAA AWFIDGLSTS GEATSQASSS ATTTTITSSN TPTSESISSN  
SDLDGDSCSM SELPQEADEV VDDILAGGPF DYPDNDGVRF GNYEGVLPE SSNNYREYTV  
ETPGLSHRGP LRIVTGGSNP TDPEVWYITS DHYETFCALT DAEN

> RXA01487 (1-267, translated) 89 residues  
MALTSEQKKS ILSEFGLHET DTGSPEAQIA LLTNRIINLT EHLKFHKHHD HSRGGLLLV  
GRRRGLLKYL ADNNVDYRD LIARLGLRR

> RXA01495 (1-447, translated) 149 residues  
MADNARAARM AKRIQTIIVAS AIERDIKDRR LEFVTITDVT MTGDLHDAKV FYTVRGASIE  
EEPDLAEAAA ALHRRARGQLR KIVGQQLGVR FTPILTYSID TVPEASAHME ALLDRARKRD  
EELAKLREGA APAGDADPYK TSSKSESE

> RXA01563 (1-810, translated) 270 residues  
QIFDLHLKLG HGSEDSWKRK LPESWLNYYA LDVEMLLELA DVMAEILDQQ GKLPWAEQEF  
VHIVDQFATM TEPSSETSWQD LKGLSTLKRK DQLVVAREMW LERDSFAASR DLAPGKVLN  
KVIVEVARVL PRTPAELAQV KGFPGRSQGA TKRWFRITR ALKSPRRNWF KPQQRKDGIP  
DRRAWASYYP EEHEVLQEUR ALIDDLAADI NVPGENILQP STLRAVAVMMA KHTGEIHNAAE  
TLNAVLIDYQ ARQWQIDQTF PILSANLLKL

> RXA01568 (1-435, translated) 145 residues  
WDNITYLMRA ARKGTVVPMV IELDGRFVGQ LTIGNIQHGG ISDAWIGYVW SSAVTGRGIA  
TAACALGVDR AFRRIGLHRL TATYLPSPNA SGKVLGHSGF RPEGYLIRNL HIDGQWMDHH  
FVALLADEYS ITAVERLTRE GRLRR

> RXA01581 (1-813, translated) 271 residues  
MALDFNEAET ERTPRIVNAA KLHRAAQRKK DKRFLVEGEN SVEAAVATGA ATDLFVTESA  
AERFEIIVRT AGYMNVTYTHA ITDKAAKHLIS DTVTTTGIFA LCDVFLNSVG KAITGQPRVL  
SVPVETREPG NAGTLIRVSD AVGADAVVFA GESVDPLGAK AVRSSAGSLF HIPVARNNNI  
ADVLGQLRSK GLQILATSAD GEVDLDDADE LLAKPTAWLF GNEAHGLDES LLAQADHRVR  
IPIRGRAESL NLATAASICL YESSKALFAG E

> RXA01594 (1-744, translated) 248 residues  
MIRGRRVFVA GMLALKPATV VEPEVSIRVE EDASEDWASR GAHKLLGALE SFEPLGLKVK  
GRRVLDAVAS TGGFTDVLRL REASEVAVVD VGYGQLIWRL QNDDRVVRVD RTNIRYMTLE  
DTGGECCMMV GDLSFISLKL TLPAIAKVLIS DGADLLPMVK PQFEVKGKDLR GSGGVVRSPE  
LRAEVTADVA KFAATLGLSL KHVVASPLPG PSGNVEYFLW LVKDGGAAMP DDQQLSAMID  
TAVKEGPO

> RXA01637 (1-309, translated) 103 residues  
VREASVEKQP ASSDPLETIR SRWSELNRIV EKQSVRTSIM LTEARVLGLR GDTLVLGHST  
GALAARLNAA DHNGILVKVL AEETGLQLKV ECTVGTNPAA AGF

> RXA01661 (1-666, translated) 222 residues  
LDSNTPGPT EWGESRVGKG PWEEENFGVP RPTSPLEFDTV LLNEGDRNRV VDAYRYWTRE  
AIVEDIDTRR HSLHVAIENF ENDANIGTVV RTANAFVANT VHIVGRRWN RRGAMVTDRY  
QHLMHEDVD SLLAWAIAER LTIVAIDNTP GSVPLETAEI PKNCLLLFGQ EGPGVTEAAR  
AGALMTCSIA QFGSTRSINA GVAAGIAMHA WIRQHADLSQ AW

> RXA01682 (1-234, translated) 78 residues  
RTKVDYAKSQ KRGGKGVCGA ELKQDDIVRH FFVSSTHDWI LFLHQLRSRV PPQGIRTSRG  
IPHRTWTARG QPSGIPTW

> RXA01683 (1-750, translated) 250 residues  
VYRLKAFELP EASRTARGQH VANLLEFPQG EQIAQVIQLE SYNDFFPYLVL ATAHGRVKKS  
RLLDYESARS GGLIAINLNE DDRLIGAALC GEEDDLLVS EFGQSIRFTA DDEQLAPMGR  
ATAGVKGMRF RNDQQLSMS VVRDGEFLV ATSGGYGKRT PLEDYSTQGR GGLGVVTFKY  
TPKRGRLVSA IAVEEDEIF AITSAGGVVR TEVQKIRPS RATMGVRLVN LEEGVELLAI  
DKNVDDQGEA

> RXA01684 (1-873, translated) 291 residues  
 GDTAIYDTLV RMAQFWSMRY PLVDGQGNFG SRGNDGPAAM RYTECRMTP L AMEMVRDIRE  
 NTVNFSPNYD GKTLEPDVLP SRVNNLLMNG SGGIAGVMAT NIPPHNLNEL ADAIFWLLN  
 PDAEESALE ACMKFVKPGD FPTAGLIIGD KGIHDAYTTG RGSIRMGRVT SIEEENRTV  
 IVITELPYQV NPDNLISNIA EQVRDGLKG I SKIEDESSD RVGMRIVVTL KRDAVARVVL  
 NNLFKHSLQ ANFGANMLSI VDGVPRTLRL DQMLRYVVAH QIEVIVRRQT Y

> RXA01688 (1-564, translated) 188 residues  
 QFEGQTKTKL GMTEIKSFVQ RMANEHGHGW LEANPAEAKV IINKAVGSSAQ ARLAARKARD  
 LVRRKSATDL GGLPGKLADC RSKDPEKSEL YIVEGDSAGG SAKSGRDSMF QATLPLRGKI  
 LNVKARLDK VLKNAEVQAI ITALGTGIHD EPDINKLRYH KIVIMADA DV DGQHIATLL  
 TLLFRFMP

> RXA01689 (1-726, translated) 242 residues  
 FDSDSYAVSG GLHGVGISVV NALSTRVEAD IKLHGKHWHYQ NFEKSVDPDEL IEGGNARGTG  
 TTIRFWPDAE IFETTEFD FE TISRRLOEMA FLNKGTLTIL TDNRATDEEL ELEALAEQGE  
 TATELSDLEI DNETELVEET TDAPKKPKKR EKKKIFHYPN GLEDYVHYLN RSKTNHPSI  
 VSFARKGDH EVEVAMQWNS SYKESVHTFA NTINTREGGT HEEGFERSALT SLMNRYAREH  
 KL

> RXA01713 (1-354, translated) 118 residues  
 MVSDLLQPRD GIPPLLSTPG EFTAAADLLA SGTGPFPAIDT ERASGFYDD RAFLIQIRR  
 GSGTLLFDPE QFRPELTQAL KPVNLGQEWI IHAASDTLPS LAWLDLHPGL LFDTEL AG

> RXA01718 (1-486, translated) 162 residues  
 LLTAVLSLIA GLUVIGIIV LNGYFVAQEF AYMSVDRLNEL RALADSGDKK ARRALSITKR  
 TSFMLSQAQL GITVGTLLVG FVAEPLVGNA LGVLLGSGVG PAAVSISVGT VLALAISTVV  
 QMIFGELFPK NYTLATPLKS ALALAFSTTW YLKPRLWLVDH IL

> RXA01735 (1-282, translated) 94 residues  
 VANTEHNYDA SSITILEGLE AVRKRPCHYI GSTGPRGLIH LIWEVVDNSV DEAMAGHATK  
 VEVTLLLEDGG VQVVDGGRGI PVDMPHSPAG TVQV

> RXA01736 (1-2868, translated) 956 residues  
 TVSTYDSYAG TLIREYGLLL PVEPSARLIT QTELYHIARN VVNNYDGELT ATQTPATVTE  
 YLLKLVSMD NMVMTAEDIR EESDPFIKLF DELPKGKGQR DNLNAEMTKW RDTQVARLQY  
 LPLVKALKEE LHNQAVVTFG EQMSKAAHLA STHPQVGYSO RRRFRVVMLO EYQDTSHSQR  
 VLLSSLFEGT DPGTLVNAV G DPMQAIYGRW GATAANLENF VDDFPVHLD GKTRAPKNEL  
 TTSNRNPPEV LTIANAVSRE VLGSPPAPTR TVQPLQPREG APTGEVSLWG FTGAAQEREF  
 VADEMVKHWN AREKGTFTA AVLVRRKRRS APMAEELTKR GIPVEIVGLS GLLDIPEIAD  
 LISLATMLVR PHDNRAALRI LAGPHVGLGV ADLQRLQGRA RNIAGRVSRE RREKNPDPLA  
 ELDAIEEAT AIEPEAVVGL ADAVADLGG DFRSEGLSR LKRLATQLRY LRKYSLGRSV  
 ADIFADIETV FNIRTEVLSR QDPHADGAAG TVHLDKFAEE VASHGGIELP ELLDYFELAK  
 DQEEGLEPGE VTVRSRVRQI LTVHKAKGLE WDIVSVLHAD ASTYDAKAST WLKNVTMIPS  
 SLRGDAGTGA PEMDTSEAD RKALEDSGKE YTSEVREGLR EENSRLFVYG ITRSERVLLV  
 TSGALDESGT KAKVPYGHLE ILRDKAPECV VSWWEGEEGD VEKQKPAEAG FPQLLAADSS  
 GADLVGRGPA EPNNEGGLES LWKEVSALI DEHRRLSNPI VEVEPTREL ATDLVSMKNN  
 PQPFARMRR PVPKPNNTYA KRGTLFHQWL EDRFGSTALL DETELPDGIDE DYSDDAFIEL  
 RDAFLGSTWE NRTEPFVEHP FEVTIGEHVI RGRMDAVFHT DGTWMMVDWK TGRTPTGPEM  
 DAAIIQLAVY RLAWARKLGL EPEEVRAAFH YVANDHTFEP NDLPQTQEELA RLLSQE

> RXA01739 (1-597, translated) 199 residues  
 VINLQDLED QRIASAPRG PVCILAGAGT GKTRTITYRI AHLIDQGFVS FNRVLAVTFT  
 SRAAEGMRHR LNLGMIGVQ ARTFHAAARK QLLYFVPQVA GNLFWRLLDN KFQLVGRAVR  
 GARLESQTEK VRDLIGEIEW AKASLITPEQ YPDLGTRTP PAPAIEAEV YQRYENMKAT  
 PEGMLLDFDD LLLHTAGAL

> RXA01740 (1-1422, translated) 474 residues  
 VAEEFQQYR SFVDEYQDV TPLQQRVLA WLGDRDDLTV VGDANQTIYS FTGATPEFLL  
 NFSRKYPEAT VVKLQRDYS TFQVTALANT VIGQARGRVA GTRLELQGM R IAGPEPEFSA  
 FDDEPTARE VAGRILLTLK NGVQASEIAV LYRINAQSAV FEQALADAGI VYQVRGEGEF

FTRPEIRQAL SQLIRTSQRD VDES DLVRLT QRTLVPLGLS SEEPSGAQER ERWQSLNALV  
DLVKDLVKAT PDLDDTLGLL KLRRERQEAH PPTVEGVTLA SLHAAGKLEW DAVFLVGLVD  
STLPISHAIK SGDEAIEEER RLFFVGVTRA REHLHCSWAL ARQEGGKRKR KSRFLDDGIV  
VEMASEGTP RSNRPKNCRV CGSVLSSPAE KAVGRASCAP IQADERVFEQ LRTWRNDTAK  
RENKAAYMVF SNATLMAIAE MNPTNENELL SVPGVGFPMKI ENYGGDVLAI LGAL

> RXA01772 (1-2364, translated) 788 residues  
FKKAPFKQSE ALGIVYTPVE IVDFILRAAD DVSKKHFGRG LSDKDVHVLD PFTGTGTFMV  
RLQSQGLIKP EDLARKYANE LHATEIMLLA YVVAVNIEY TYFGLLEGRA LRNGEDAPVY  
EPFDGIVGLD TFQMYEDDDK LDDLVFTANN DRMERQRLTP VQVIVGNPPY SVGQSSANDN  
NANLKYPTLD RRIEDSYAKY STATNKNSLY DSYLRAFRAW TDRIHTQGVV AFVSNNGWVD  
GNTADGVRLS LAQDSESELY FNLGRNSRTG GDIAKREGGN FVNVRVGTQI IVAVKNPQLS  
GCRILYKDIG DNLSADAKLN EIAVATIEGA EWQTISPNEY GDWISQRSVD FDTWPLVGLK  
KNKSALKVFP TFSAGLKTGR DAWCYGPTSA QVKTINITRL ETYEQAQQRF NSWVVDNGVT  
SPKEADVNOF LKQNPDLADS KKISWDSNLK MSLSRGDTFS FDPSSIQMSL YRFFFPQQTY  
FHVSLNORRY QLESMFPTPE HDNQGFIYVN PGSAKPFSTL ATNLLPLDAL WGSNAGQFFT  
RWTWEPIETR EGLEDGFGNL FSTTPKKGVE GEILDGYYRV DNITDEILKL YQSSLGEDVT  
KDDIFYFYVA QLHDPAYREA YAADLKKMLP HIETPTDRAR FDHFVTAGKE LMDLHINAGD  
VEPWDVEVKV KEKADPTDRE TWRVTMKMWA KVRDEPETKKL VEDHTTLYN SMTISGIEPE  
EAENYQLGSR SAIAWLIDRY QVKKDKASGI VNDPNDWADE VGNPRYIVEL IAKVTRVAVE  
TMRIVEEL

> RXA01786 (1-441, translated) 147 residues  
MRAAKITRGF TSNPAGSVLV EFGNTRVMCT ASVELGVPRF KRDSGEGWLT AEYAMLPAAT  
AERNRRESMA GKVKGRTHEI SLIGRSIRA AVDLSQLGEN TTAIDCDVLQ ADGGTTRIASI  
TGAYVALADA IKVLQERGVV PGSPLLA

> RXA01797 (1-708, translated) 236 residues  
GSLAWIDLTP EDRSAYDDQV RQGSWMGMRR SAMLSPTRRL TSAKMORILE LFEEAEEHGR  
KALIFTYFID VLDELEKHLG ERVIGRISGD VPATKRQLLV DALSHSKPGS ALIAQITAGG  
VGLNIQSASL CIICEPVKPK TIEQQAARV HRMGQTATVQ VHRILIGDETA DERMLEILAG  
KTHVFVDYAR LSETAEIPDA VDITESQLAA RVIDEERARL GLTESTGPKD EETALS

> RXA01824 (1-822, translated) 274 residues  
MKETDNLLRE NSHDRDISEI VATITALDHP SPSSLRLFTAF VPGSANNPVW AEANVAIRLY  
LSEEFDDATR VYTVRSFDAA TESIVVDVVQ HHESFPMMRW SDTVKINDTL VLTGPRPHFV  
IPEGEQAALF LDDTAIPALA AILDQWPTDL RGKGWVVTDD PAADFELPSI DGLELNLAP  
GSDPTVQFLA QQAYDLENPE TYVVAAGER DEIKSIRRH F RKQVGLEKDA VAVFGYKYN  
TTNTQIDAVR KENYMKMLSE GLQLENFDDL SLEI

> RXA01832 (1-894, translated) 298 residues  
MATSNRIANA MNSLAKLDSS MQRGLDNALA FVFRGRVUPA ELEELLKQEA EDNVVHTEFG  
YVEAPNVFKV SVSPNDFSNL VDRFPDQPAR FGQDMKFCR NSGWTLVGFV IVLIEEDSL  
HTGQLKSVSE KDPPDPLSSG YLPLEGDGIL PVAESESKNV SDSSPYTGTPE FLPAQSADRP  
LVQGVQPSQV DANQAAAMPK AGPTVTLLQL DGSRSRTYLRV EGSNIIGRNS DADLLPPTG  
TSRQHVEITV DGRDAILVDL KSTNGTTVND TPVDNLLAD GGVITVGHSN IEVRIVSP

> RXA01866 (1-321, translated) 107 residues  
LKPGRHDDGV TVLPIPIVLG GLDTGEFDWL VPGLRLDLVT ELIRTMPKAL RRTVVPAFPF  
AERVLPLLRP YMTPLTTQLA DALHTLGGQG INASDFDPAK LPDHLRI

> RXA01867 (1-492, translated) 164 residues  
PEWVEKAAGP LLKHQYSEPY WSSKRGAAWP HRKSTLFGVT IVAVKVVPYH TVDFVAARDM  
FIRHALIEGD WSTHHRFYHD NVAKLEAIGE LEAKARRRDI VVEDLTLDFD YDAKLFSNAT  
TTRNFDWWK KTSRVTPDLL DFPDPSLIKE DAGALRRSL RQVD

> RXA01876 (1-1473, translated) 491 residues  
IIGPNKTFLE YISHVLPELG ETGVVLSTVG ELFPVIGVPTG SEDTLTREIK GSEEMASILA  
EAVKAYQVLP ERTKIVSVSDG IEISIDEKTV AKSRTRARRA RQSHNSARPI FREHLVEQLA  
HQMAQTIGAD PLGGKNLLSA ADIDQLHDDL LDDAALQSVI DDFWPELRPQ DVLHDLTISE  
ERINVAAGY DEETKSALLR GELDFWAPSD AALDELALL IGLDFPEEAR EKAEAKWREQ

IDDAQEVLVD LSSSQSSDID DVTEAEVLSA FDVIDAETLA QRQTVTDNRT TAERAQADHKK  
 WAYGHVIVDE AQELSPMEWR MVFRSPSRW MTLVGDIAQT GWPAGVDDWA ESLWPFVEKR  
 FRHHELTVNY RTPAEIMSA NELLTQINPD IAPAMAIRES GREVVNLPLD ADLSAVMDSL  
 REEDSQRTIA VISSRRHHES DFYLVDDIKG LEFDHVIVVD PAGIVEESPQ GLQDLYVAVT  
 RATQSLTILG E

> RXA01893 (1-555, translated) 185 residues  
 MIDEILFEAE ERMTATVEHT REDLTTRITG RANPAMFNGV MAEYGVVPTP ITQMSGITVP  
 EPRMLLIKPY EMSSMQVIEN AIRNSDLGVN PTNDGQVLRV TIPQLTEERR KDMVKLAKKG  
 GEDGKIATRIN IRRKGMQQLK KLQKDGSDAGE DEVQAAEKEL DKVTAGFVAQ VDEVVARKEK  
 ELMEV

> RXA01912 (1-771, translated) 257 residues  
 MRRFIFTERN GIYIIDLQQT LTYIDQAFEF VKETVAHGTT VLFVGTGKKQA QEAVQVEADR  
 VGMPYVNHWR LGGMLTNFQT VSKRLNRMKE LQAMDAEANG YEGRTKREVL MLTRERTKLE  
 RVLGGAEMT RVPSALWIID TNKEHIAVAE AHKLNIPVVA ILDTNCDPDV VDFPVPGNDD  
 AIRSTALLSR VISTAVEEGK KAREERQLAA AKDAAGDAKP EAEAPAAAE AEEAPAAEAE  
 EHLQSLKPL TAVSAVS

> RXA01948 (1-603, translated) 201 residues  
 SVELPAEIFD REVSVALLHQ VVNAQLAAR QGTHSTKTRG EVRGGGRKPF RQKGTGRARQ  
 GSIRAPHFTG GGISHGPKPR DYSQRTPKKM IKAALYGALS DRARNARIHV VSELVPGQTP  
 STKSAAKATIE RLTERKSVLL VVSREDINAQ KSANNLPGVH ILAADQLNTY DVLKSDDDVV  
 SVEALHTFIN RASGAQEEQ N

> RXA01949 (1-303, translated) 101 residues  
 MATIANPRDI IIAPVVSEKS YGLMEQNVYT FFFVSTDANKT QKIAIEEIF GVKVASVNTV  
 NRAGKRRKR TRGTRKATK RAYVTLREGS DSIDIFSGSV A

> RXA01950 (1-384, translated) 128 residues  
 MAIRKYPKPT PGRASSVSM FTEITRSTPE KSLRLPLSKT GGRNSHGHT TRHRGGGHKR  
 RYRVIDFRRN DKDGVLAQVA HIEYDENRTA NIALASLLRW REALHPRTG PDPGHRVVR  
 RCSRHQGW

> RXA02037 (1-330, translated) 110 residues  
 GKGKPLYAPN VDCGDHVIIV NADKVAVTSN KREREMRYRH SGYPGGLKSM TLGRSLDLHP  
 ERTIEDSIWG MPMHNKLTAA SAKKLHVFSG SEHPYAAQKP EAYETKKVAQ

> RXA02038 (1-309, translated) 103 residues  
 MSEPIQNEV ESNVADAADI AATAATEEF TNTIGDAIAT ASEETIEAA PVVLGDPQIT  
 VGRKKRAIVR VRLVAGSGEF KCNGRTLEEY FPNKLHQQLI KAP

> RXA02041 (1-714, translated) 238 residues  
 RLGITSDWKS HWYADKSYAD YVAEDIKIRE FLGSKGLDRAG IADVVIERTR DRVVRDIHTA  
 RRGIVIGRRG AEADRIRREL EKLTKGQVAL NILEVKNVDA NAKLVAQSLA EQLTNRAVFR  
 RAMRKALQSA MRQPQVKGK VVCSGRLGGA EMSRTERYHE GRVPLHTLRA EIDYGTYEAH  
 TTFGRIGVKV WIYKGDVVGG RRESEINAPA ERGRGRDNA RPRRGQRRQ RAEQKQEG

> RXA02042 (1-414, translated) 138 residues  
 MLIPKRVKYR RQHRPTRSGI SKGGRVTFG EYGIQALEPA YITNRQIESA RIAINRHVRR  
 GGVNINIFP DRPLTKPLG VRMGSGKGPV EKWVANIKPG RILFEMSYPD EATALEALRR  
 AGQKLPCQVR IVKREDQL

> RXA02043 (1-141, translated) 47 residues  
 MAIGTPAHEF RELNEELVT RLNEAKEELF NLRFLQATGQ LTNNRRL

> RXA02077 (1-396, translated) 132 residues  
 MLGKCELLTE GRSKDSILAD TTEALFGAIF ROHGFETARD VILRLFAYKI DNASARGIHQ  
 DWKTTLQEL AQRRKPMAYE SATSVGPDHD LVFTAIIVTLE GEEMGRGEGP NKKLAEQEAA  
 HQAFKRES RA

> RXA02145 (1-1617, translated) 539 residues  
 MSLATVGNL DSRVTASGI RRQINKVFPT HWSFMLEGTA LYSFIVLLLT GVYTLFFDFP  
 SITKVIYDGG YLPLNGVMS RAYATALDIS FEVRGGLFIR QMHWAALLF VVSMVLVHMLR  
 IFFTGAFRDP REANWIIQVV LIILGMAEGF MGYSLPDDLL SGVGLRIMS A IIVGLPIITG  
 WMHHLIFGDF FPSDMLDRF YIAHVLIIPA ILLGLIAAHL ALVWYQKRTQ FPGAGRTENN  
 VIGIRIMFLF AVKAVAFGLI VFGFLALLAG VTTINAIWNL GYPNPSQVSA GSOPDVYMLW  
 TDGAARVMVA WELYLGNVTI PAVFWAVAML GILVLLVTVY PFIERKFTGD DAHHNLLQRP  
 RDVFPVTSLG VMLVIFYILL TVSGNDVYA MQFHVSLNAM TWIGRIGLIV GAPIAYFITY  
 RLICIGLQRS REVLEHGIET GIIKQMPNGA FIEVHQPLGP VDDHGHPIPL PYAGAAPVKQ  
 MNQLGYAEVE TRGGFFGPDF EDIRAKAKEI EAHNHIEEAN TLRALNEANI ERDKNEGKN

> RXA02179 (1-828, translated) 276 residues  
 MTRTVISDP ADPRLDDVRD LNHSDSRPDL PGKGVLVAE GPLVVGRLLE SRYPVRAIVG  
 FKNKLDSDFL SIDASLVEGI PVYEVSRELL AEVAGFDMHR GLLATADRT EASVAQVLEN  
 ARTVVVLEGV GDHENIGSMF RNAAGMGVDA ILFGNGCADP LYRRVRVSM GHVLRPFPAH  
 LEGTYTTWRQ SLEQLKEAGF HLVSLTPDPE AEHLEDALAG KDKVALLVGA EGPGLTEHAM  
 RATDVRARIP MAPGTDLSNL ATSAALAFYE RDRSQR

> RXA02190 (1-1458, translated) 486 residues  
 MPNNAPQVA INDIGSAEDF LAADITIKY FNDGDIVELT VVKVDRDEVL LDIGYKTEGV  
 IPSRELSIKH DVPDPEVVEV GQIDALVLT KEDKEGRLIL SKKRAQYERA WGAZEELKEK  
 DEPVGTGTVE VVKGLIIDI GLRGFLPASL VEMRRVRDL D PYIQOELEAK IELDKNRNN  
 VVLSRRAPLE QTQSEVRSEF LHQLQKGQVR KGVVSSIVNF GAFVDLGGVD GLVHVELSW  
 KHDHPSEVV TVGDEVTVVE LEVDLDRERV SLSLKATQED PWRVFARHTA VGQIVPGKVT  
 KLVPPGAFVR VEEGLEVLVH ISELAQRHVE VPDQVAVGE EVMVKVIDID LERRRISLSL  
 KQADEYTEE FDPSEYGMAT SYDEQGNIFY PEGFDNETNE WLEGFDEQRC AWEARYAESE  
 RRTTAHTAQI ERRRQQAEEA AAEAPAGNYS TDSAEDAPAA EAVEESAGSL ASDEQLAALR  
 EKLGN

> RXA02241 (1-2028, translated) 676 residues  
 VARVPLLLGL PHLDRLFYDR ISEDQHDVVQ PGVVRVRVFG GRLVDVAIMS RTAQTSGEKL  
 LMWLDRIVIS IVVYPPQTA LIEQLSDRYG GVRSDLIARS LPARHAGAE ADTSTWESL  
 GEVKEPDLSS WSAYQGQSF VDAVLAGTTA RASWQIAPGD DWALALASLA VKVVKDGGGA  
 LLVVPQQRDL DRLEAALRGL VAAKQITVIN SGLGQARAYR RFLSVLSGGQ RLIIITRSAA  
 FAPVKDLKLA VILNDGDDNL VDPRAPYAH REVLTTRSSL EASSLIAGH ARTAETQLLV  
 ESQGMWNHIA PRDTIRTRMP RIQAVGSDSF QMERDPMARS ARLPGIAFHA VRSALREDQP  
 ALIQVPRKGY VPTLACGNCR TPARCHCNG PVGLPQGSDD LAGVPTCRWC GRPDSFKCQ  
 NCGSPKLRV VLGERTAE LGRAPFSVRV ITSNGNKVVD SVENRASIV STPGAEPFVA  
 NSPERPEKSE KPEHKGAYGA LLLLDTWAL GRQDLRAME ALHKWAAAT LVHSHHQEQ  
 VIVVADPSFP AVQSLIRWDM AGAAQELAS RREVMPFSPV HMAAIDGATA ALESFLDLAE  
 LPDHAENVLGP VDLPPGVSLP GEYDEQRFGP PQRLIRITPL GPRSELGRAL RSAQVARAVR  
 KNDPLRIQM DPPIHG

> RXA02293 (1-2388, translated) 796 residues  
 MSSRIGNFLI NRISTGLPVE NIIPHLQEA SAGPKNLVQI APPGTGKTTL LPPLVANILC  
 NEGAGNATPT KVLVTAPRRV AVRAAARRLA QLDDSQLGT KGVFSVRGEHI SGSHVQFMTP  
 GVLIIRQLLNN PELPGIGAVI IDEVHERQLD SDLLGLMLAE LSQLRDDFSL IAMSATLSDS  
 KFAALLDAQV LSVAEIIFPL DISYAPARAP RLNAKGVVDV FLDHMAQKTH DAVTHSEHSA  
 LIFVPGVREI DRVMSTLKL GHNNVFFLHG QLSFTEQDRA LAPSQQRII VSTPVAESSL  
 TVPGVRIGVD SGLSRSPKRD SARGMTGLIT SSCAQASAGQ RAGRAGREGP GQIRCYSEE  
 DFSHPFRFVT PEISSADLTQ AALWLAQWGT SPADLPLDQ PPHAAKTAQ QILRLIGALE  
 GDAITSLGHR LSTLPLCPQL SASLLRFGQ SAKILAVVSE NPGQDEVEKQ POKREVERLR  
 RLAPASVGKA SAGQIVGAAP POLIGRKIDN GEYLLASGR ARLMDSDLKD AEWISVAAIN  
 RSQNSAIIIRA AARISDDAI DIIIGVVEETR AIFVNGKVQA RKVKAAGTAE LSSPTKPTTP  
 AEASATIATA LAKGGIDLPH FSDKAASLRD RLKFIHEHRG EPWPDITAD PHWLSPPEIE  
 ALSHGTRLNN IDMPALQRL LPWPEATNE EFAPSHLSVP SGNQHLRDIS SGRPVIRVKL  
 QECFGLEESP QLCGIPVQFH LLSPAGRPLA VTDDLRSFWS GPYSQVRAEM GRGYPKHPWP  
 EDFWTAPATA RTKNRM

> RXA02357 (1-1203, translated) 401 residues  
 NSSRPEEITD LSAVPDWTFL EKRPENTLGS QLEIRFRVML RRALKNRHAK LVDRVWNSNS

YVDIEMSSGV RWRMSEQVDR GYTRPDFWFE PLNGNYPTVA VFTDGAFAHI SSANYRLDGD  
 IQRMKLALD PDNLPWNIT SLDLDRFSNP AAQGEPAWF SPIGRQLSKA NLILDPOQSTA  
 LLAATPMDQL LAFLDNPAAW SWKEFAHIAA AHMLGHNPKQ NGDGVGTGTFR NKSILRATMV  
 NRELRAQLW LAPTTPEELE VDTWTAFLNL ANLMWLAPES VYVSTNGSPH KIDIVPAPAA  
 PLVVVEPELW APILDGTAD EDEBAEGALQ ILAKEHALVP ETTGDELSSI PTIATWPSVK  
 IALLYESDPP DELEDDLKAE GWTLFLFANDL ETSIDIPALR P

> RXA02359 (1-1869, translated) 623 residues  
 VELPSPGEAL AHAGHTPEVL EAEGLIDPAA TRIVLELASE DDIAAALPSS PTWEKDALIG  
 LVAGLSIBDI RESLAIPAPS TEPDTRSED TRLIAGLKTPA AQMDFAYLDT PNSNDLRRVI  
 ETEGFSWRV YIDPSQRSVL TRNFSGSGRV FCGAGTCKTV VVVHHRANRLV TDSGHLETDD  
 KTRPVLLTTY TRGLADALKS SMNALNPFTF EAEKPGSPGL WISGIDALAN KVALANTAVE  
 REAAATATLG RAAGRITPFI GNGEQEFWD AIISADPDLG SEEISNTTEFL AQEFETVILA  
 RGITQEKDYL RAPRPRGRTG LNRVQRKKVW AIIOQFMSTC AREGKMSWA LSSIAANTLE  
 QRAAAGQRL FDHVLIDEAQ DFHAGHWLLL RAAVAEGPND IFLAEDSHQR IYQQHVLVSR  
 FGISTGRAS KRLTINRYRT AENLSYALGM LTGEWTDAG ETDITIEHYS ARKGPKPHLY  
 QFSESTRFE AEALIKVWQ DRTTDVIRGI LARTPLINK VVNALSEQGI DAVKTNQABL  
 AAHETVSVMT MHGAKGMEFT HVILGMGRD LIPLQYTMQG LGEAERNDAQ QRESSLVYA  
 ASRRARDLVL THTPESELL PRV

> RXA02363 (1-4900, translated) 1600 residues  
 MSNAPKKFS DFFSPLATET ETTITLSAIE VEKVNKTEV TRNIDPVEAA EQISRDRYRY  
 LKTLISPSNK TIAAEFNREI DESENLYVGP ILQLTPPYAP GKSPAQLIDE GVLSPNFSSL  
 DAALPKDRPL YQHEDALRK IASGRNLIVS TGTSGKTES FLIPIDQLL RQQAGELNRP  
 GVRALLLYPM NALANDQEKRL LRELLADTPE ITFGRYTGD TQTREEAEKY FKLINGRNAT  
 PLRANELLRD EMQENPHIL LTNYAMLEYL LLRPADNAFF DDAYSNNWKF LVLDDEAHVYA  
 GAQGTVEAMR MRLRLKDRVQR GNPLOCIATS ASLEGTKEAI MTFGQDLFGE PFEFVNEFPS  
 RDSQSVHRLR KLPKTFTWSL PDELFDPQLE SDGLFQALQE RGGDQYEELS KEEHIVKLEP  
 LQSQSSTRVE DIGKGLWPNV TDKASMHRTH MLVNLGSGVL SHDGPVPSLA RYHMFVNSN  
 GAFGLYTEQG KPVLSDLRQV TLGDTARPMY EMGACIKCGT VHISAHDNQE FLVPPENSVR  
 FDEQQLKWVV LDDTFETADI DEDDLETDAD ENNVKLELQK LCTACGKLNG KNSLLSCGGS  
 SHHDQFIDVK ILEPRNGSQL TCTRCGGREK NLIRRLRTDS NAAPSVLTLS LFQLLPESAD  
 QSTRKIGAG RKLTLFSDRL QAAAYAAPYL QASYTRLLER RLIETLRDE EFTEGASIER  
 RHRSASEVAK NNRVLANNLN PRETLEQTGN WVFPDLASTV RSSSTEGLLG AKIELTPEAL  
 SQLSRFKPLG EMFGDPPAAD AFNLFQAQEF RHKGAINCPD VYNLEDERFG PRRGQHEFTK  
 DGGKRKSTRRL YSWIPQRTGN NRKDFITKVL NRIGQAGDEG ENITTLHLHL WNDYTNSEIL  
 KVPGEKAEGY TLYNSLQVS PGKQHSWYEC DTCRNTTPFN VLGLCPHGFC GKKLKEIDTF  
 LPBYATNHYR KLATSLLEIL LSAKEHTAQW TPTEAAEVQK EFIEGKINVL SCSTTFEELVG  
 DVGDLQSVMM RVNVPRTANY VQRAGRAGR SGSAFVLTF AKRSSHDLAV KNPMTQMDG  
 EMTVPFLHIN NARIARRHTY SIALAAFFRE QAAQNRFKKK AGEFFLGTDA APYLRAPAVE  
 QEATEILEEF LSPVPNYITE ALRRVPFESL HEDLDIENQG WVKQLEIFD FTKLEIDTF  
 QTLKKMQGRA LGSEQGGKAD AFKRTITTL DQDLGLGYLAK KNMLPKYSFP VDTVDLQTNF  
 SEAGNKVSLR RDLQLAITDY APGAELVAGG KLWKSAGIRH LAGKKVETFF WTTCTECKHT  
 ETSRFGTSE DVCSCQSAPI SLGKKNKFLI PRFGVADPN PRFEGTAPP VNSRNLFEVK  
 PKFKNDDSEE FSNSDGTATA QVLTSSWSRT EMGALETGPN KNGFWYQCTG GGGTPNGAEI  
 QSGHNRNPRT QQCQTYYLEP HSLGHTYQTD IATVAVPSAY NLDFFEGWAF MYAIIIEAAE  
 CLEINRDLN GTMAKHDRNP TMVLFDTVPG GAGITRKVRE NFPQVLEAAI RRVETCSGCI  
 DTSCYACLR FSNQRFHLDL RRDIALDLLH HMAVAMPKSE

> RXA02369 (1-2289, translated) 763 residues  
 VPNNAKVAE ISPSAVLAAE FDRDSLSEKT RVHQLAKRLG MYSKDVVVVAL DGIGLVKVAQ  
 SNLSKEEVEK LLDALSQPVL NAAPAAVPDV EPVEKIRRV EKNVENEIHA IEKVEVERELA  
 AVAQPTDFAA AAREEATAEL LEDIVPEITP APVEASVYTP IEVAPAVVPT ENVQDTDDQ  
 VRERTAKRRR GRGCTGRGRG AEAEVTEVS EEAESTVEEE VNEPIGIKGS TRLEAQRRRR  
 TEMREENKKY RHVVSTQEFM ERRESMERRM IVREQRHHD PLQVTQGVVL EDDQLVEQFV  
 TSDAQMSMGV NIYLGVRQNV LPSMEAADF IGKGRNGVLY AGEVDWKAAG LGGGRGRIEQ  
 ALKAGQDQVL QSKDPLGHK GARLTQISL AGRYLYVYPG GRSAGISIRKL PGPERKRLKE  
 ILGRVVPAG GTIIRTAAG VSEENIAADV NRLTLWEQI KERTAEEKKS RGSKPIITMYE  
 EPDFMLKVIR DLFNEFDTSL IVDGDRAWNT VRAYIQSVAP DLVSRVEHFN RADFDGKDAF  
 EAFDLNTQLE EALSARKVNL SGGSLIIDRT EAMTVIDVNT GRVTGKGGGN LEETVTLNNI  
 EAAEEIVRQM RLRLDGLGMV VDFIDMVLP E NQELVLRLN EALENDRTRH QVSEVTSGLL



VQMTRKRIGA GLETFSSPC EHCEGRGIIV HVDPVDTVDE RVEAKAEERS RRHQRSNSTN  
KAAAEHPMVV AMRDLVESDE HDLDQEFEEEL AASMIVLDDS DLL

> RXA02370 (1-792, translated) 264 residues  
MTPIYYDVND DKLDPEPERIL AESTVEPEEG PRMRARRRQRO ESAADDIAAI AAAAVDIASE  
EDPDEPSGSS YVSDFEAEPI APVVEKAAEP VAEPTADYEK ARAEFEASPR RRRKTGNSR  
SDHAPKPEDF APVVEEVAET PVKTPARKAP RRNRPELSS GAPSSAPSTR NRRRAVRROL  
VEAPETVVEI APEAAPEQVA EPQVEFDQPD NRRKRRRAVR VTAAPVEKIV ASTSNARAPK  
KEPQAASTTN PGRRRRATRR GPRS

> RXA02371 (1-270, translated) 90 residues  
MYAIVKTTGKQ QYKVAEGDLV KEVKIEGEPG ASVALTPVLL VDGADVTAA DKLASVSVNT  
EIVEHTKGPK IKILKYNNKT GYKKRQGHKQ

> RXA02389 (1-261, translated) 87 residues  
MANIKSQIKR NKTNEKARLR NQAVRSVART EIRKFNAIE AGDKDAAQAO LRTASRALDK  
AVTKGVFHIN NAANKSNMA TAFNKLK

> RXA02419 (1-192, translated) 64 residues  
MKNKTHKGTA KRKVTGSGK LVREQANRRH LLEGKSSTRT RRLKGIVEVD KADTKRMKRL  
LGKA

> RXA02420 (1-381, translated) 127 residues  
VARVKRSVNA KKKRREILKS AKGYRGQSR LYRKAKEQWL HSMTYSYDR RARKSEFRKL  
WIQIRINAAAR MNGITYNRLI QGLRLAEIEV DRKILADLAV NDFATFSAIC EAKAALPED  
VNAPKAA

> RXA02463 (1-114, translated) 38 residues  
MTYVHCXGRT GRAGHNGTAV TLVGFXTXK WTXDXNEX

> RXA02468 (1-531, translated) 177 residues  
VEITDALEAL GINRTFAIQE YTLPIALDGH DFIGQARTGM GKTYCFGVPL LDRVDFSADV  
AETDGTPRAL VIVPTRELAV QVGDDLQRAA TNLPIKIFTF YGTFPYEEQI DALKVGVDDV  
VGTPEGRLDL HKRGAISLKD VAILVLDEAD EMLDGLFLPD IEKILRALTH QHQTMLF

> RXA02522 (1-543, translated) 181 residues  
MWARDINFLY MSTEQELQIG KVKKSHGIRG EVVVELSTDD PDIRFAIGEV LNGKQAGKEH  
SLTIDAARMH QGRLLVKFAE VPDRTAADS LRGTRFFAAPL EDEDEDGFGY DHELEGLRVI  
HEGEDIGEVT GVMHGPAGEI LEVRLTSGKE TLIPFVHAIV FEVDLEEGTA TITPPEGLLD  
L

> RXA02533 (1-567, translated) 189 residues  
MEDDLAALV KALFDARTQR RLSISALAES SGVSRAMISR VENAEAQPSA ALLGRLSGAL  
GMTLSLIAQ AEGGYDRGAR RSKQSVWTD ATGYTRRAVS QPSESPLVLV EVMLPPGAEV  
GYPADAYRFM DQVVVVLEGA VRITEGEEVH ELSTGDCLRF GPPRDTDFAN PTTVATRYLV  
ALDKRVFRA

> RXA02615 (1-636, translated) 212 residues  
MQFAQNPRIT NDAVILEPLS HQWTQDLQEA VASQELWRHW FVALPTPEGM AEEIDRRALAE  
HADGLCAPWA IISAATGRAV GMTSFHTLDH ANKRLEIGRT WMAAHVQGTG INPSVKFLQL  
QRAFEDLGVN AVEFRTNWHN HRSRAIERL CAQKQDGLVR HRIHPDGIVR DTVIYSITND  
EWPVAVKITLM ERLYRHMQVP IIPNEASLFD AS

> RXA02633 (1-264, translated) 88 residues  
MKKDIHPDYH AVVFQDAGTG FQFLTSTAS SDRTVSWEDG NEYPLIVVDV TSESHPFWTG  
AQRVMDTAGR VEKFERFRGG MARRKKKA

> RXA02635 (1-234, translated) 78 residues  
MSAHQQTGR KPSEKGSVSH SHRRTSRWN PNVQRKFYV PSEGRITITL VSTKGLKVID  
RDGIEAVVAQ IRARGEKI

> RXA02636 (1-162, translated) 54 residues  
MARNDIRPII KLKSTAGTGY TYVTRKNKRN NPDRIISLMKY DPVVRKHVEF REER

> RXA02637 (1-303, translated) 101 residues  
MKAKSKIAKN EKRRKEIVARY AERRAELKAI ISNPNTSDED RLDAQFELNS QPRDAAAVRV  
NRNDSHDGRF RGYLRKFGLS RVRMREMAHR GELPGVRKSS W

> RXA02657 (1-3582, translated) 1194 residues

MARLSHMAQK SSFVHLHNHT EFSMLDGMK IDMLADEVKA QGMPAVGITD HGNMYGSNFF  
YRKMTGEMGI PIIGLETYMA PESRFFKERV RWGEPHQKSD DVSQSGAYLH QTMLAENTTG  
RLNLFYLSMM ASDYEGQLGW PRMDADIIAE HAEGIIATTG CPSSGDVQTRL RLQGFDEALE  
AAMWQDIYG RDNYFLELMD HGLDIETVRV SELLEIGRKL NLPLVITNDC HYVLESQAQA  
HEAMLVCVGT KTLHDEDRFK FGGTGYVYKS AEQMRALWDD MYPDGCNTL WIAERVQSYD  
EIWEESHSDR MPIADVPEGY TPTTWLHHEV MAGLEDRFSG QQVPEDYIER AEVEISVIDM  
KGYPSYFLIV AEIHKHARS I GIRVGPGRGS AAGALVAYAL TITNIDPEMH GLLFERFLNP  
ERPSADVIDI DFDRRRRGEM IRYAADRWGE DKIAQVITFG TVTKTKQALK SARVQMGQPG  
YQIADRVKE LPPAIMAKDI PLSGITDPDH PRFNEAGAVR QLIEDDPDV RIYDTARGLE  
GVVRQSGVHA CAVIMSSVPL LDCIPMWKRP ADGALITGWD YFACEAIGLL KMFDFGLRNL  
TVIGDAIENI KANRDGEVLD LENLAIEDDEE TYKLLGRGET LGVFQLDGGG MQELLKRMQP  
TFGNIDRAAL ALYRPGPMCV NAHWYDADRK NGRKPIPIH PELEEALEEI LGETYGLIVY  
QEIQIMRISQK VANYTAGQAD GFRKAMGKKK PEVLEKEFAN FEGGMKANGY SDAAIKTLWD  
TILFFAGYAF NKSHAAGYGL VSFWTAYLKA HYAPEYMAAL LTSVGNKDKK SAIYLSDCRH  
LGRVLSLSDI NESSINFLPV GTDIRYGLGA IRNVGAEVVD SILDTRKEKG LFKDFSDYLD  
KIDTLPCKNR ITESLICKGA FDSLGHARKG LMLVFEDAVD SVIATKKAAD KGQDFDLFAAF  
DSNDDNDVAS FFGQITVPDE WDRKHELAL REMLGLYVSG HPLDGYEDAT AAQVDLTALT  
IVAGELKHGA EVTVGGIISG VDRRFSKKDG SPWAIVTIVD HNGASVELLV FNKYYSIVGS  
MIVEDNII LA KAHISIRDDR MSLFCDDLVR PELGPGNGQG LPLRLSMRTD QCTMSNIAKL  
KQVLVDNKG SDVYLNLDIG DNSTVMILGD HLRVNRASAL MGDCLKATMG GILG

> RXA02682 (1-327, translated) 109 residues  
MSYHDSDIE YLKKIGANSF DAFKAFVHFD EALRGPNKK IPRNYTEMIA LAVAFITTQCA  
YCIDIIHTAA KKEGVTTTEL AEVALIAAAL RAGGAMTHGA LAMKLYDEN

> RXA02752 (1-495, translated) 165 residues  
MAVKIKLQRL GKIRTPHYRV VIADARTKRD GKVIENIGIY EPKAEPSVIK INSERAQHWL  
SVGAQPTAV AALLKVTGDW QKFKEGIEAG GTLRVAEPKP SKLELNFQAL SEANNGPTAE  
AITEKKKKAR EDKEAKEAAE KAAAEKAAA ESEEAPEAEA AAEAA

> RXA02755 (1-1995, translated) 665 residues  
MSAPESPTNT TPDPLNASTE ELLTAAVEAL GGARRAGQEA MAKAVTKAFD TERHLAVQAG  
TGTGKSLAYL VPSIRHAQKS DSTVIIVSTAT IALQRLVNR DLPLRVDALE PIMERRPTFA  
IMKGRSNLYC MNKVARQEEL NQEDALIEQE DISWLGHKIV RLNEWANETE TGDRDLDDPG  
VPDLAKQVS VTARECIGAS RCPHGDECEA ETARGKAKEA DVVVTNHALL AIDALSQVSV  
LPEHDVVVID EAHLEDGRIT AVASAEITVN SLNLAARRAS KLDSOKREER VQEIAGDLET  
LLQTMQPGWR NDMDEGSKGT LVALKDALWA LRAQIAGAPE GEAAANDPERF AERQNLNSHL  
MEIHDDANRVI LEVFAEDPS KQYDVVWNH DRRGDSLVN APLSVAGLLH ELQFIENTVY  
LASATLTIGG NFNMAASWG LPKGSWDSMD AGTPFPDPAKS GILYTAHRLP DPGRDGLPEE  
TLDBIYELLIT AAGGRTLGLF SSKRAAEQAT KAMRLRLPFD VLCQGDNDNTA ALVKKFSDVS  
NTCLFCTLTL WQGVDPVGRS LSLVLIDRIP FPRPDDPLLQ ARKEAADAE RNFMEVAAT  
HAALLMAQGA GRLLRHVGDR GVVAVLDHRL SKTRYGGFLR FSPRWFETT NPETVRAALK  
RLVTK

> RXA02764 (1-2784, translated) 928 residues  
MSEYKPPPI DPQVRLIKPT SKLRPSWEG EVSHLVKQST GLWRVTGSEV SGVSSAVVDV  
VLERIRGWE PSSMLVVATS KEAASRLRQE ISESVQMDY VSEGLVQRV HSVAFALIRD  
ASDDDDRLIT GAEQDAVIRE LLRGHADDGR GGWPQEQREG LRMVGFARQL RDFLLRAVER  
GVGPDELVEL GERFERANWV AGEFELREYK QVMKLSGAHS FSASELVTEA LRGPSPVYKY  
RGVFTDDAQH LDPKSSELVS RFFPEAELAV VAGDPQOSVF RFRGANPDPL TKLSVDHEVY  
LKGRKASTS IIVVAETESA ADLLADTVRR AHLIDGRWS EIATIVRSAG MIAPITWRTL  
AAGVPVHISP TDVVLAEQRI VAAMILGLRA LTESLNAIEL EDLLGPIGG ADPVTLRLL  
RGLRQAEKMK GGQRRATEVL RSLAESDAE MLGFLTDREL NLLERVRSVL EAGREALEAH

GSIEEVLWAL WSATDLSNSL SAISLRGGAS GSQADRLDA MMALFDAAGD YVERYPSAGV  
 RSFIHISEQ ELPTGMRRER GAIPAEVEVL TAHATTGREW KRIVIAEVOE GSWPSLGETG  
 TLLGQEEFVD LVDEGIDPDI IISRSARLA EERLLFYLAT TRSTESLLVT AVNSPDSDEV  
 REPSRFLELL SQPIVVLGE EASAIAPPEE IGRHLLSIPA MVAELRRVNV DRPDPRFKQA  
 ARQLSRLAEA GIPGANPAEW TNLRTPTDE ELIKGAVSL PSRIEQLLNC FLRAVLDRLD  
 SEEEPTIAML KGTLVHFAE AVAGGVDAAL AEEKVTSAYM QLANVPSQAM ESTEIAFRRI  
 LSRTDTWLKT SRADTEVTGT EMDVSVTIDD SVSIRGRMDR LERNKSGELV VVDFKTGKTQ  
 IAAKMDGHP QLFAYQLALS KGVLHGDK

> RXA02785 (1-3855, translated) 1285 residues  
 PVSYPLVEDI EVVLDTIATA QHEDDYAQLC FRVFCERVWL CEADLHAAS AYAADHLTAA  
 ILQHAADSTP LSRRDQDEV T ALPELVLGAT ERILGEVKAA EFISHALAM AFVRAEYGVK  
 AAWGAKRLPG VETHLWVREV SRIDRALGVG DEQSMFRWSD DGPPEADANTQ QWLPAICYRS  
 CGRSGWMVSL EQGTNIPVLE EQKIRLNSPE QPHKORALL ATSEQRAAIE QGRSVAGPFG  
 VDGTSAVLWF HSASNELSTR QPSPEEEQSG SSIAVLTHFG PEADDLSAQ TCPCSGDVDS  
 IRYIGSGDST LLSVSLSNLF GMADLDSAEK KTLVFADSVQ DAAHRAGYVQ ARSRAPALRT  
 YTRRAVGNINE VTLPSISRAL MDNATSGRTR YELLPPDLTD LDYIKPYWHF DASKAERREA  
 SRNVHKLRSF DLALFEGQRA DLPSRLATG ALSAFVDPK GVALSAAAEA LYAEVPTLD  
 IEDENLRLR VQGALELLRA RGGINHEWFG AYLRTDGNPY MLNRRQARAE GIPGFVRGGA  
 PEPFRVGSAL SGLRSSTGT TPLGSPRGY ASWTSQVLGI STHDAATAT LKFDALSNRS  
 ILSSISTDSG GKIIYCLEAER IRIFSEDHPE VLECSVCHAQ TGVIDHVRDF LDGAPCFSPS  
 CGGVLHIEEV EDNYRRLYS AIEPRTVIAR EHTSMLKKKD RLALQEVSFRG GEGSAKQSD  
 APNVLVAPT LEMGIDIGDL STVMLASLPT SVASYVQRV RAGRLSGNSL VLVAVRGRGV  
 TLPRLNQPLS MIKGAITPPV AYLASEILH RQFLAYVIDC LDTRAELPKL ETADIVFDNA  
 AGKTPVIALL KAQIHAGLDP LLEEFTVRLN MQISIDNIFE LRTWASGNST DSLALLET  
 QKQWMEERRS LTARGELEK IFDKLDARND AHDEELKEEK RKTAAASKAV KQIRLDLGE  
 FWIAALERYG LLPNFTLVDD SVELNVAVTS FNPQVEEFTD KNHAYSRGIS AALFELAPGA  
 TFYAQGIKAA VDSIEIGEHG SAIEQWRCLP VCSHSEILQP GVSTPGSCPT CGSPAFADKG  
 QILEVQMKR VSSAVEKTRA AISDDRDRF STRFNQHVFS VVPPDGHGKS WYLNDFGFIGE  
 HLPKVELRWL NLGIGNGQKR RLGGFEVTPS TRFNVCRCCHG LDSEAGANSR WDHREPCPHR  
 YEQKEDTVSF ALGRITLKTQ VMLLPPEYFG SEADSMVVT S LIAAIKLGFR EVLGGDPDHL  
 DVTSVQVPT SGGGALDALL LHDQV

> RXA02819 (1-612, translated) 204 residues  
 KLQIGDVIAM PGRKRPVLAV VMTPANQSRD PRPVTWTEG WSGRVDAESF TNPPITIGHM  
 RLPQQAIEEP RRNARRVQEL FRREHFKRPN KMREFARVRP NEAVTKLRNA IRDHEAHHWP  
 DREHLARTAE RMIRKERDLA KLTGNVDKAR ETLGRTFERI LSLLEMDYV DYSNPDNPVI  
 TDEGERLAKI HSEADLVAQ CLKR

> RXA02826 (1-399, translated) 133 residues  
 MAPKKKKKVT GLIKLQIQAG QANPAPPVGP ELGAGGVNIM EFCKAYNAAT ENQRGNVVPV  
 EITVYEDRSF DFKLKTPPAA KLLLKAAGLQ KSGSVPHQTQ VGKVSMAQVR EIPATKNEDL  
 TLAISTLLRR SSL

> RXA02833 (1-579, translated) 193 residues  
 TRVLSLRMGR SFSLAVSVEP QEIPKPQLK QEFKYQPDAL VFSSNKAPOK YEVGGRGEAS  
 TSDGWEGTHS APAPEHPAP IADREPELAT PQRIPRETPA HNPNRVSLN PKYTFESFVI  
 GEFNRFANAA AVAVAESPAK AFNPLFISGG SGLGKTHLL AVONYAQELO PGPRIKVSS  
 EEEYHQLHL RAR

> RXA02883 (1-912, translated) 304 residues  
 MSFHITSVNV NGIRAAVKQR SETNLGFLEW LEETRPDVLV LQEVRASEKD TATALQPALD  
 NGWHYIGAPA AAKGRAGVGI LSRHELDVN IGFSGFLDSG RYIEATIKDT TLDVPTVAS  
 KYLPSGSAGT DKQDEKYRFL DEFEGFLDQR AKERSHMVIG GDWNICHRRR DLKNWKTNQK  
 SGLFLPDERA FMSVFGTFP DEATQVAGAG DFFGAVDYEG TRREATTDP AWFDFVARRLQ  
 PEGDGPTTWY TYRGKAFDTG AGWRIDYQAA TAAMLRAER SWDKKAAAYD LRWSHSPFLN  
 VIYS

>RXN00061 TRANSLATE of: rxn00061.seq check: 8093 from: 1 to: 2667  
 VTEKTDQTLMLIDGHSMAFFAPALPAENFSTSGGQATNAVYGLSMLSTLLKDEQPTHV  
 AVAFDVGRKTRTDMFPAYKAQREATPEPFKGQVEILKEVLSTLGITTIETKIDFEADDVI

ATLSVAAKPLGFKTLIVTGDRDSFQLVNDTTTLYPMKGVSVLHRTFEAVEEYKYLTPR  
QYPEFAALRGDPSDNLPI PGVGEKATKWAQYETLDNLLDHADEIKGVGASLRERIE  
QVRMNRKLTEMVKDLPLGPDDEFMKPVQVAEVAARFDDLEFGTNLRVRVAVVKAEGS  
AAPVEEVAEQVVVDTSQSLAQWLPARAGQALALAGVAKPAAGDTYALAIADTKRHAFL  
VDVADI SAEDEKALATWLASEDKMLHGAKAAYHMLAGRGFELHGVVHDTAIAAYLLRPG  
QRTYELADVYQRHLQRLQSLSTNDNGQLTLLDAADDQSLVDDVIALELSEELTKQLQIEI  
AFELYHDLIELTSGILARMEAGIADVATLEEQLKFTFGVQAQEEEAARELAEPDPTLNL  
SSPKQLQVLFLETFGMPKTKTKTGYSTAAAEIEALAIKNPFPDHLHLAHRQYQKMMKT  
LEGLIREVAPDGRHTTTFNQTVASTGRLSSTDPNLQNI PVRTAEGRKIRSGFVVGEGYET  
LLTADYSQIEMRMVAHLSQDPGLIEAYREGEDLHNYVGSKEVFNVPIDGVTPELRQKVAM  
SYGLVYGLSAGFLSQQLSI PAGEAKQIMESYFERFGVQRYLREIVEEARKAGYETETLFG  
RRRYLPELTSNDRVARENAERAAALNAPI QGTAAIDIKVAMI RVDRLSKEAAVKSRLVQV  
HDELVEVVAAGELEQVREILEREMDNAIKLSVPLEVSAAGDVNWDAAH

>RXN00066 TRANSLATE of: rxn00066.seq check: 6030 from: 1 to: 813  
VTDPLSAALDSGRINHAYLFSGPRGCGKTSARILARS LNCVEGPTSPCGVCNSCVALA  
PGGPGTLDVTELDAASNNGVDDMRELREARANYAPAESRYRVFII DEAHMISTQGFNALLK  
IVEEPPAHLIFI FATTEPDKMIGTIRSRTHNYPFRLLTPGDMRKVLKNAVDEGCVHVDSD  
VYPLVIRAGGSGPRDLSLIDLQIAGSGPEGLTYERALPLLGVTSFTLLIDDSIHALASKO  
NASMFTTIDNVIEEGLEPRRTIDFLSTRSG

>RXN00103 TRANSLATE of: rxn00103.seq check: 3594 from: 1 to: 4560  
MAKSILSRFRPQVAEFRDVFASPTPVQEGTWEAVSGKGNALVVAPTGSGTKTAAFLWAL  
DSLTEQGTQQQLDGTGTPVVRGKGKVKVLYISPLKALGVVDENNRAPLTGIARTASRMGL  
DVPNITVAVRSGDTPSAERARQVRKPPDILITTESAYLMLTSKAGATLSVDVVIIDEI  
HAMAGTKRGVHLALTLELERLEKLVGRPVQRVGLSATVRPELTVAGFLGGGRVPEIVAPFAE  
KKWDLTVTVPEEDMSDLPVQEPGSTIGELVMDPDLGITGESALPTQGSINPHIEQQVYVQ  
VMSAKSTIVFVNSRRSAERLTSRLNEIWAMEHDPESLSPQLRRDPQAQIMSSADVAGKAPQ  
VIARAHHGVSQKDERATTETMLKEGRLAIVISTSLLEGIDMGAVDLVIMQSSPPSVAQSG  
LQRVGRAGHTVGATSIGSFYPKHRSDLVQVAVTVORMKEGLIEEIHVPKNALDVLAAQVTV  
AAVSIKDQVQWEYETIRKAYPYRDLAREVFDSDVLDVSGVYVPSDFAELKPRVVYDVRG  
GVLECRPGSQRVAVTSGGTIPDRGMFGVFLVGDGPRRVGELDEEMVYESRVGDVFTLGA  
SWRIEELTDQVLTVPAGHTGRPLFWTGDAAGRPaelGKALGAFRRSTLTDPSRSSGLEG  
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KIAZETGMDAQAVAGDDGIVLRLLQCGDEDPSSAALFMFAEIEITLVTEQGVNAAALDPA  
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FENPDLEDRAMTVRINGREHLAQVLDAPLLRDALGVPPVPGVPAQVETITDALEQLVNRW  
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AAARKQTPRVPSQSAFARFLDQQIAPVGATPELRGVDGTYYVIEQLAGVRLPASAWEDL  
VLPRRVADYSPHIDELTSGNEVLIVGAGQASRDPWISLLPVDYAAQLVGEASTMSPL  
QDAVLDDQLRAGGAFLESDILEENFGYTTAQLQAMGLVEAGLVSPDSFAPIRLARLSGT  
TAHRAARRPARSRLRTRTSFASDVPEDMRGRWTLVSQPADATSRSAHGEGLVDRYGVLT  
RGSVVAAEDIVGGFALAYKVLSGFEESGKAMRGYIEGLGAAQFSTPAIIDRLRGHDSRGP  
VEGWPSGATDPDVYLIAAADPANPYGAALPWPEQGSRAAGAMVLLCDGLLLLAHLTRGGR  
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>RXN00163 TRANSLATE of: rxn00163.seq check: 899 from: 1 to: 618  
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FVSVCVIALPDGQEFVQEGRWGSQLLRGPKGENGFYDPLFIPAEIDGQGRSSAELSAE  
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>RXN00407 TRANSLATE of: rxn00407.seq check: 2077 from: 1 to: 2664  
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QLRGRLSTNEAARGSVRLAGAKQALARKMPLADAEEHLMGTWTMRSGDGLLTKAHPD  
YADLIATTVELAAECAFTLDLVAPNLPKWDTPGEHTEMSWLHLVSTRIDTRYVGRSADI  
KARAAQTIDYELGVIEKLGFFGYFLVVDNLFVFCRDSNLCQGRGSAANSACVFCVLGITN

AEPISAGLLFERFLSPDRDGPDDIDIDIESGRREEVIQYVYKEYGRDAAQVANVITYRT  
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 WELDLAEPEVYDMLCKADAVGVQVESRAQLSTLRLKPKRTFFDLVVEVALIRPGPIQGQ  
 SVHPYLRRRAGEEAIYDHPVLEKSLGKTLGIPLEFQEQLMQVAVDAAGFSGGEADSLRRA  
 MGSKRSPERMAALRSRFFQGLKDTNGIVGETAEKLWNKIVAFAYGFPESHSSQSFASLVY  
 FSAWFKYHYPAEFVCGLLRAQFMGFYSQSLISDARRHGVSILPITVNDSSGVEADAPNGA  
 IRLGLNLVKGGLGHDAORIEDNAPFDSIPDLSSRADLNVAQVEALARAGAVDCLGVGRKQ  
 ALWQAGVAATEKFGMLPGLSVIEAPALPGMSAFELMATNISATGVTDYQPMALIRERME  
 ELGIVFPADRILLEVEDGTRLRIAGIVTHRQRFQTASGLTFLGMEDETGLMNVMVSVGLWQR  
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>RXN00414 TRANSLATE of: rxn00414.seq check: 6909 from: 1 to: 354  
 MQGEASVPFAELHATSSYNFLTGASDPSDVVVQAKKLGAALSVMDRDGFYGVAFVFAEAA  
 AEGMHTVYGAELSLQEGVLTVLCKNPEGYKKLSHLISDAKMAREKRGSSLSAAANGC

>RXN00460 TRANSLATE of: rxn00460.seq check: 909 from: 1 to: 471  
 MPEHPLHVI FDNVPI PNTGNAI RMCAGTGAHLHLVEPLGFELTEKHLRRAGLDYHDLDAD  
 VTWHATFEAEMAAVPGRVFAFTTTANTRFTDIAFEPGDALLFGTEPTGLPQEHVEHSRIT  
 SELRIEMLPGRRSMNLSNSAAVATYEAWRGLGVFGVV

>RXN00542 TRANSLATE of: rxn00542.seq check: 3719 from: 1 to: 675  
 MAIGDTNIIVGNGIVADPELRFTPSGAAVANFRIASTPRSFNRQTNQWEDGEALFTTVNV  
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 TPRGNSGNGVGGGNQGGGLGNGNQQGGGFSNPNQSGGFGGNGQNGQSGGFGGNGQ  
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>RXN00545 TRANSLATE of: rxn00545.seq check: 1627 from: 1 to: 267  
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>RXN00562 TRANSLATE of: rxn00562.seq check: 810 from: 1 to: 723  
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 TYTPLCLIVLEPGTAAMWMLGIAWVGAI DSVIMNMVWINHPRWLSVLVLALGWLIVPLVP  
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>RXN00625 TRANSLATE of: rxn00625.seq check: 6900 from: 1 to: 942  
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 FKSXGVTGRDADTG DGGGNNANVRVAQAQALIDHLENQDDWASKPIFILGDTNSYAKRT  
 AMTTLYGAGYTNIAETFDAGYSYQFSGRIGSLDHALGNEAAKMHVIDAEVVDINADEAIA  
 FEYSRRLNNTSDVFNENVFRSSDHDPIKVGFNLSSETTEPTIPEVPTDPAETDPTTVPVK  
 TDPVETTDSEPTDPAETDPAETDPEETKKEPEEKNFGSSNGSQYATIAAIAAILG  
 AIALAFQFFHSSNN

>RXN00673 TRANSLATE of: rxn00673.seq check: 3349 from: 1 to: 402  
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 QPHNGCRPPKRRRV

>RXN00706 TRANSLATE of: rxn00706.seq check: 3516 from: 1 to: 573  
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 GLSDQQFDGNGNYT FGLTEQTMFEYIDVDKIDRPRGMDITVTTAVTDDEGRSLLRELGF  
 PFKGEDGNRQQ

>RXN00709 TRANSLATE of: rxn00709.seq check: 7555 from: 1 to: 366  
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>RXN00714 TRANSLATE of: rxn00714.seq check: 3128 from: 1 to: 561  
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KDLGPWGVYLRDRPSEFVGVGVELIDGKVDLKYLRPLDWNGYATEISNAATLATKR  
IDDSLPLTARVTTNHPASFRILEKGLTPVWEGRRVGTEDDPNEPDVRIYSDRPLSDEIL  
EMLKQRP

>RXN00724 TRANSLATE of: rxn00724.seq check: 5366 from: 1 to: 1977  
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CTRALFTGKVVFERNPQLSHPEFIVIPDPGSGRRLLATGGMKSLAAAYGDVEVALRLVD  
REYIPIACTATMTTWRIMAARVQVLETFVKEFLSVVPEGMPSPFDEAIRGHDHPGHE  
PSTFINRLKYNEALSATVMAIRRADTKNRKAPPMPRALKGHQHMLIDALNFOLTVGQKQ  
VIREISADIEQVPMRLLQGEVSGKTIIVSLIAMLQAIDSGRQCAMLAPTEVLATQHAR  
SLSKTLLDDAGLDINVVLLTGSMPTGAKKEALLEIISGDADIVVGTALIQTVFEDFLG  
VVVDQHRFGVEQRDLRTKGREGLTPHLLVMTATPIPTIAMTVFGDLAVSLTRELPGG  
RREIQTSTVI PDHKPGWVKRGWERIGEVLAGROAYVVCPRIEGEGGVLEI HAYLSEQVYF  
GLNVGMLHGRMDTDLKDSVMQFAAQGEIDILVATTVIEVGI DVANATVMLIREAREFGVS  
QIHQLRGVRGRGQHDSLCLLHTTFDEDS PQQRGLAAISTTDDGFLQELDIQVRQEGDVL  
GTRQSGSDTKLRHLSFISDQKIIERALIDATELVAAASRALELVSDTAMINQVEYLEKS

>RXN00790 TRANSLATE of: rxn00790.seq check: 8140 from: 1 to: 1062  
MSVQLTCTPTDIIIRNRPTPLKDGDRVIVYGKPAFYAGRGTFSLWVTDIRPVGIGELLARIE  
ELRKRILAAEGLFDPARKKRLPFLPNRVGLITGRGSAERDVLSVAKDRWPEVQFEVINTA  
VQGASAVPEIIIEALRVLDQDPDVVDVII IARGGSGVEDLLPFESEALQRAVAAQTPVVSIA  
IGHEPTPVLDNVADLRAATPTDAARVVPDVAERMLINQLRSRSAAALRGWQVREQQA  
LAAIRTRPVLDPMTPINRRRDEIAQAVGLIRRDVTHLVRTQALVASLRAQVSLAGPSA  
TLARGYSVVQVPIPRDGSAPFVVTITIEQSPGSQLRIRVADGSITAAASMTQOAN

>RXN00807 TRANSLATE of: rxn00807.seq check: 4862 from: 1 to: 1242  
VFDSLAGSKTVSKTLFDAASSARALVRARTERARARAEHQNFAMIHDSGFAQSWLTFGP  
PGSGRSVAAKVFAATLVCSNPDPVVGCGQEDCRAAMGGSHPDIEHIVPQQLSIGVDAARE  
VIKAAAVSPVAGNWRVVI FENADRLTMOAANALLKTVEEPTSTVMILCAPTTPDRDIAI  
TLRSRCHLYIPTPSIAEVARILVAEGNVSQADAELAAASGAHIGRARYLAHNNAQRR  
RASILNLNLAELIFHGDVAFRSVNTLVKMVTEAKDSNKEKEGDLAVRISLGMGRAGKGV  
HKAVRGAGDGFKALEDQQLRRTFLRDSLDLALVDLAGIYRDAIIISQAQVGLTHPDM  
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>RXN00817 TRANSLATE of: rxn00817.seq check: 6901 from: 1 to: 2394  
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ATSSDPEIIEASRLGAPVKAVTEDGAPTGERVLLWNEPGFIEGAEGENGAPVRAASTEA  
ANIMATLISEGARTLTFVRSRQAEI VALRAQEELSTLGRPDFARRVASYRAGYLAEDRR  
RLERLLDDGTLLGVASTNALELGDVGGDLAVVTAGFPGTVASFWQOAGRAGRGQGSVL  
LVVARDEPMDTVLVHHPAALLEKPEVAAVDFPTNPHVIRGHVYCAAVEKPLTEAEVAAFG  
AQKVVEKLEIEGLLRKRPRGWFAVEKPMSEDPELSPDSAHQVSLRGSGSEFMVIDIT  
DGRLLGTIDSAKAMSTHPGAVYLHQGESFVIDELDLLENALARPELPDYTTIYARSDTD  
IRITSAPLEDELEVFDAGGGLWVANVEVQVTDRTVGTYVTRLSDGTTLDATPLYLFPQILQTR  
AVAYTIDPLALEAMGIPPAIDIPGALHAAEHAAIGMLPLLATCDRWIDGGVSTALHADTGY  
PTVFVYDGMGGAGFADTGFRFRFAQWIEATEFVVRSCSCSCGCPSCVQSPKCGNNGNPLD  
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>RXN00890 TRANSLATE of: rxn00890.seq check: 1452 from: 1 to: 1299  
LSIATVVALLFSGLLGAVESALSSVSRRARVEQMLKDEASGSASLLRVIDERALHNMLIM  
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RSAAVLSGLAKILGPIARGLIWIGNIAPGPGFRNGPYATEVELREMYDIAQHQHIVEIE  
ERRMIQSVDPLASTTVRQVMVPREMIWIESGKTAGQATALCVRSBGHSRTPIVIGENVDDI

IGIVYLKDLVQKTYTADGGKSVLVDVEMREATFVPDSKSLDALLQEMQEDHKHIAILVD  
EYGGVAGLISIEDILEEIVGEIADEYDAREVAPIEKIGDRTRYVRSRLSLEDLKHIEEE  
LDLEIEFGDEIEDQVDTVGGGLIAFELGRVPLPGATVETCGGLKTAEGAKNRRGRRLMHSA  
VVEVEGPSEDENEG

>RXN00897 TRANSLATE of: rxn00897.seq check: 6537 from: 1 to: 1005  
MTPSLPRFRSQKPAVGDRVARRRIPGANVHWTDVIGHVIGVDPLVVVRPQSVGGMPSDAE  
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SASPLGSPVSGSEPVPMEDISRFYARHDLPVKLHPIPERIGRPAQKVI DADPQKVMVGPIL  
VMTKSLDHVESHELPGGLEFSVDKQPDQEWLGMVHFRGQALPAHALELLRTQIEGRMGFG  
RLTTPAQQTVAITRATITAAEERIFLGYSAVEVDFAPRRQGLGTALGSRIQEWGAEQHAQ  
EAYLQVVAHNEAGIGLYQKLGFEHHRHRYAERKF

>RXN00990 TRANSLATE of: rxn00990.seq check: 3149 from: 1 to: 465  
IPVLVATDIAARGIDVDDVSLVVHVDPPAEHKAYLHRAGRTARAGTSGTVTLVLMDEQIK  
EVRELQKAGVTAAEVKVNENSPELAKITGARRPSSGVALPAPGQQQPKREQKNTHNRSDS  
RGSRRNPRRRQSGSRSTGRSNPRRQTSRKDGPKS

>RXN00994 TRANSLATE of: rxn00994.seq check: 7403 from: 1 to: 351  
MTTFLELKDEIIVRELRSQGITEAFFIQEAAIPDALAGKVDLGRGPTGSGKTFITFGLPM  
ITRLRARGASKPGPRGLVLVPTRELAQVVRERLDDPARVMGLRVLEVVGVMNINRN

>RXN01030 TRANSLATE of: rxn01030.seq check: 392 from: 1 to: 1176  
MTSTTPQGTTPELSADTHSEPDVIVIENTLEPFQKVVQRITIDRPSYSGIFLTMGGGKILT  
TLSALTYIQPPGHILVAPLNIISRLTWPEEVRKWNIPVNAISLITNERGTLKTRAKRLKL  
YEETATTPPTLYIITINLLEDIVNYVFGDRWPFWTVIDESQTSIDISSKRTRALFSVRPY  
IGRILLTLTPSAANKFDSIYAQVAVLDYGLSDGNIDVFRARWCAPDIITDKQVRRWKPA  
NKQAEAEVVRTISHLVMSAVNTDIKLPPLHFVDHEVHMSDDEHRDYELFKKDAVLAAALD  
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ELDHFDLDPVQRQEDLGLTVVISAVHASDSAA

>RXN01066 TRANSLATE of: rxn01066.seq check: 7389 from: 1 to: 726  
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VQLYPGRKLISTIGADTVGYASGIIEDFTRYSCASAILIATHIAGLENDPHLFEETTR  
APKNIQDSPPELILNLDEFMLRAMNHAGWAPSLFDCAACGRPGPHNAFHPGVGGAVCLYCR  
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QA

>RXN01343 TRANSLATE of: rxn01343.seq check: 8146 from: 1 to: 708  
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GTVSLPNTGKTQVRVAVFAQGEKATEAAAGADVFVGTDELVEKIQGGWTFDFVAIATPDQ  
MAKIGRIARVLVGRGLMFPNPKTGTVTNDVAKAIEEVKGGKISFRVDKASNLHAAIGKASF  
DAKKLAENYGALLDEIIRIKPSSAKGIYVKRVTLSSTTGPGVEVDTHVKNYAEAA

>RXN01374 TRANSLATE of: rxn01374.seq check: 3251 from: 1 to: 1242  
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DKDLKVDPDTQVTVSLDDSSNYRRLRLWLEATMRKTPVPVLYQESLSVADQMLADPLEYQL  
AAVRKTLSSANLRPRVLADAVGLGKLTLEMGMILAEILRRGRGERILVTPRHIMEQFQQ  
EMWTRFAIPLVRLDSVGIQVVRQKLPASRNPFYFVRVIVSMDTLKSPPKRAQLEKVVHD  
AVVIDETHNAGTQNNLEAGTLGPTAEALILASATPHNGDPESFKEILRLLDPTAVMP  
DGTIDAEAAQRLIIRHRNSPEVSGFVGEKWAPRNEPQNFLVAASKEENGVAELNHNWVI  
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>RXN01378 TRANSLATE of: rxn01378.seq check: 4647 from: 1 to: 1755  
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VKKNSDTRVIVISERVATLHLWQENLIRDLKMPNPSIAVMHGGPLDQEQMRLVDFEKKTD  
SPIRMITGDVASEGVNLTHTLCHNLVHYDIPWSLIRIQQRNGRIDRYGQTHNESPVTFLL  
DPAEDSKVGEVHVLERLMEREHEAHSLLGDAASLMGKHSEERLEETIREVLGAQNFNDA  
VADPAEVLNPAGLDDIDWLAQIAQADAKAETEAEEAETENQTPADAASNSTGHAQRRLY

AQESSFLYDCLLEGFNNVPEDSINRGGVGFKKHNDNIVELTPTDDLRRLDFLPQDYVAA  
RKVKEDLLLASTLMRGQERLNAARTGEDGSTWPSAHYLGPHFVTSWAAADRALATMPSE  
IPAAAGKVTEPTVLLMSTLSNRGQIVRSFVASSGPFDTVELSDPIQWHLISGLDETAPI  
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TSRTARTAKLIEEQQLSNALEPDRELIRPLAVILPQATLNTVE

>RXN01380 TRANSLATE of: rxn01380.seq check: 8341 from: 1 to: 2199  
LDEGNTVPFPIARYRKEITGGDDTQLRDLLEERLSYLRELEDRKQSILAAIEEQGLKTDDL  
RSLILGCDTKARLEDLYLPFKKRRKTKADIAREAGLEGLVDKLIIDAPSLDAAQAAAFIT  
EGFEDSKVLDGARAILIDRFALDADLVGEVREQMYRAGSMAASVAGKEQEGAKFKDYF  
EFSEFPDKLPSSHRIALLRGENEGVLSLNDAGDDIIYEGLIADRFSLDTHTSSMLAEAV  
RWGWRTKLYVSSGLDVRMLRKEKAEAGALDVFATNLRDVLAAAPAGQSTIGLDPGFRNG  
VKVAVVDTPKGDVATTIVYPHQPNRWKAEVSELANLCAHGVELMAIGNGTATREKFL  
AGEVADMIKAAGGTRPTPVVVSSESGASVYSASPIAAEEFPDMVSLRGAVSIARRLDQFL  
AELVKEIPKAIGVGQYQHDVNOVALAKTLDGVVEDAVNAVGVNLNTASAPLLTRVAGTYS  
TLANNIVAYRNENGSPSSRKELNKPVRPLGPKAFEQCAGFLRISGSTPDLDAVASVHEAPY  
VVRNIAKATGLDVSGLIGNSAVLTCLKPADFADERFGIPTVTVDIIAELDKFGDRPPEFK  
TASFKEGVEKISDLTPGMILEGTVTNVAAFGAFVDVGVHRDGLVHVVSAMSKFTSNPHEV  
VRSGEVVKVYMEVDVDRKRIGLSRLTDEPGAPAPQKGRNRPAPQKQAPQKQSAKPATG  
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>RXN01389 TRANSLATE of: rxn01389.seq check: 5202 from: 1 to: 684  
QDGDKLAGRHNGKGVGKILPKDMFPLPDGTPVDIILNTHGVPRRMNIGQVLETHLGLW  
ASAGWSVPDPEDPENAEVLKTLPADLLEVPAAGSLATPVDGASNEELAGLLANSRPNRG  
DVMVNADGKATLIDGRSGEPYFPYPSVIGMYMLKLHLHVDEKIHARSTGFSYMITQQPLG  
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>RXN01563 TRANSLATE of: rxn01563.seq check: 3710 from: 1 to: 1209  
MVSDDLQPRDGIPLLLSTPGEFTAADLLASGTPFAIDTERASGFYDDRAFLIQIRRR  
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AGQFDHVNLAAMVEQIFDLHLLKHRSSEDSKRLPESHLNVAALDVMELLEADVMAEIL  
DQDGKLPVAAEQEFVHIVDQFATMTPESTSWQDLKGLSTLKRDPQLVVAEMWLERDSFA  
ASRDLAPGKVLNKNVIVEVARVLPTPAELAQVKVGPGRSGQATKRWFLITRALKSPRR  
NWPKPQQRKDGIPDRRAWASYYPPEEHEVLQEIRALIDDLADINVPGENILQFSTLRVAV  
WMAKHTGEIHNAETLNAVLRDYGARQWQIDQTFPILSANLLKL

>RXN01575 TRANSLATE of: rxn01575.seq check: 4786 from: 1 to: 1020  
MKSIDLQLAGTQSRITYQSRKITDEMVARPVHVAIALWEVPWESAKSGKIEGWVIAVDS  
RGRFRVSGQTKNGDAVNRTVSMKLSALKGVRGKAWITVGRQAALRAALVRENYLVGTGS  
AEQNRAGVKASAISSRAEQSALYKAKKIGFEAERAPRVKREQEAHWVPLRSRTQGTAGVL  
RLATDASTDGVPRGAMCFVNASNGDYLLETQDTTASSDELELESITHALYLYLTIGATQAI  
IESDSKALEAIDFILLNRRPRGRWRGITACARNRFRDAWEALIDDCVVELSRVLGHAG  
PLNQAAQDIAYMGMAVIFEQKSAHPTLLKIGIDKALRKAEE

>RXN01594 TRANSLATE of: rxn01594.seq check: 4466 from: 1 to: 819  
MVARRRLDAELVRRKIARSREHAVEMIRGRRVFVAGMLALKPATVVEPEVSRVDEEASE  
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LIWRLQNDRRVRVVDRTNIRYMTLEDTGCEADMVGDLSFISLKLTLPAIAKVLSDGADL  
LPMVKPQFVEVGKDRLGSGGVVRSPELRAEVTADVAKFAATLGLSLKHVVASPLPGPSGNV  
EYFLVLVKDGGASMPDDQQLSAMIDTAVKEGFPQ

>RXN01606 TRANSLATE of: rxn01606.seq check: 3298 from: 1 to: 2676  
MAESNAMDRAQISALLDRAQHTINLAEQANNVRLRLKTPGTATVGDNGTIGTDYILPSR  
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QDAVDFMLVKLDEISSTTHEVSRMLEGVHAAARTRQQQGVALLPFGIHVGVERITYERAQOVL  
ASALGIAGFGAEPWDGHTLAQARRVQRYAQDPNSEYRLKSEAETHLSINELRVQILLE  
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KQEAALRRQNTSIGDEPTQAMRLINVLAREFDQETITPEERARRTRVIDYVEHIPSDDP  
YIVINPATPEFNFTDOLRWIDANPNLPHFQITITPPADIWDDYISRFAPHYQGLATLLG  
RIEGADELLEATTLLQKIRDLTLKTHLTDLHLRGYQSGFARFAIQKTKLLGDDMGLGK



TVQALSAHAALATEKDFRTLVLVVPASVIVNWTRECKRFLNLPVFIAGDNKQDAINAWS  
 NTNGIAICTYDGVTRMDIPAPGLVIADEAHLIKNPSTKRTQALRLKLIDAAPYTLMTGT  
 LENKVVEFVNLVRYIQPELITRGMKMQAENFRERAPAYLRRNQADVDELPTDSDID  
 WIDLTPEDRSAYDDQVRQSGWMGMRSSAMLSPTPRITSAMQRIELFEAEHGRKALI  
 FTYFLDVLDEKHLGERVIGRISGDVPATKRQLLVLDALSHSKPGSALIAQITAGGVGLN  
 IQSASLICIPEQVKPTIEQQAQAVARVHRMGQTATVQVHRLIGDETADERMLEILAGKTHV  
 FQVYARLSETAEIPDAVDITESQLAARVIDEERARLGLTESTGPKDEETALS

>RXN01637 TRANSLATE of: rxn01637.seq check: 3317 from: 1 to: 663  
 MVNSGLDDMRGATSPRLLEILCARLLASNTVACPAVSSSDAAPATPGGLTGIAAAR  
 AKAREYGQKKAAPAPAPTPAPEPVREQSAPTEPTPAAEPTSQPAPEPEPAREPVVEVR  
 EASEVKQPASSDPLETISRWSLELRNIVEKQSVRTSMLTEARVLGRGDTVLVGHSTGA  
 LAARLNADHNGILVKVLAEEETGLQKVEICVGTNPAAEAGF

>RXN01683 TRANSLATE of: rxn01683.seq check: 9344 from: 1 to: 2568  
 VSDNDTQGFDRVNPIDINEEMQSSYIDYAMSIVIGRALPEVRDGLKPVHRRVLYAMFNG  
 YRDRSIVYKSAKPVADTMGNFHPHGDATYDYLVRMAQWPMRYPVLVDGQCNFGSRGNDG  
 PAARMRYTECRMTPLAMEMVRDIRENTVNFSPNYDGTLEPDVLPSPRVENLMMNGSGGIATV  
 GMATNIPPHNNLELADAIFWLENFPADEASEALEACMKFVKGDFPTAGLIGDKGIHDA  
 YTTGRGSIIRMGVTSIEEEGNRTVIVITELPYQVNPNDNLISNIAEQVRDGLKVLGISKIED  
 ESSDRVMGRIVVTLKRDAVARVVLNNLFKHSGLQANFGANMLSIVDGVFRTLRLDQMLRY  
 YVAHQIEIVVRRTOYRLDKAEERAHLLRGLVKALDMLDEVIALIRRSPTPEARTGLMSL  
 LDVDEAQAADALAMQLRRLAALERQKIDELAEIELEIADLKAILASPERORTIVRDEL  
 EIVEKYGDERRSQIIAATGDVSEEDLIARENVVITITSTGYAKRTKVDAKSKQRGGKGV  
 RGAELQKQDIDVRHFFVSSSTHDWILFFTYNGRVYRLKAFELPEASRTARGQHVANLLEFPQ  
 GEQIAQVQLQESYNDFPYLVLAATAHGRVKKSRLLDYESARSGLLIAINLNEDDRKLGAAL  
 CGEEDDLLLVSEFGQSIRPTADDEQLRPMGRATAGVKGMFRDNDQLLSSMVVRDGEFFL  
 VATSGGYGKRTLEDYSTQGRGGLGVVTFKYTKPRGRVLVAIAVEEDDEIFAITSAGGVV  
 RTEVKQIRPSSRATMGVRLVNLLEEGVELLAIDKNVDQGEASAEAVAKGAVEGPASKTAA  
 EETDSVDNGSGDENEGE

>RXN01688 TRANSLATE of: rxn01688.seq check: 5568 from: 1 to: 930  
 QFEGQTKTKLGNTEIKSFVQRMANEHIGHWLEANPAEAKVINKAVGSAQARLAARKARD  
 LVRRKSATDLGGLPGKLADCRSKDPEKSELYIVEGDSAGGSAGSGRDSMFQAILPLRGKI  
 LNVEKARLDKVLKNAEVQAITALTGTGIHDEFDINKRYHKIILMADADVDQHQHATLL  
 TLLFRFMPDLVAEGHVYLAQPPLYKLKWQRGEPGFAYSDEREDEQLNEGLAAGRKINKDD  
 GIORYKGLGEMNASELWETMTDPTVIRILRRVDITDAQRADELFSILMGDDVVARRSFITR  
 NAKDVRFLDI

>RXN01689 TRANSLATE of: rxn01689.seq check: 4148 from: 1 to: 1116  
 VANTEHNYDASSITILEGLEAVKRKPGMYIGSTGPRGLHHLIEWVDVNDVDEAMAGHATK  
 VEVTLEDGGVQVVDGGRGIPVDMHPSGAPTVOQVMTQLHAGGKFDSDSYAVSGGLHGVG  
 ISVYNALSTRVEADIKLGHKHVYQNFESKVPDELEGGNARGTGTTIRFWPDABEIFETTE  
 FDFETISRRLQEMAFNLKGLTITLTDNRATDEELEALAEQGETATLESLDEIDNETEL  
 VEETTDAPKKPKKREKKKIHYFNGLEDYVYHLNRSKTNIHPSIVSFEAKGDDHEVEVAM  
 QWNSSYKESVTHFANTINTREGGTHEEGFRSALTSMLNMYAREHKLLKEKANLTDGDCR  
 EGLSAVIFRARW

>RXN01770 TRANSLATE of: rxn01770.seq check: 9268 from: 1 to: 3765  
 MPTIIDNLNSDDSDSTIGTATEYNPDADLLDAINDADLDGDATISTNATEEGVDAAAE  
 KPKKKRKAPALPKGLTAKFFHRDLTGVGGRITGRLNKNVHPTNPDLISYQPVSDVVTQPSA  
 DHKGIKTRYILTHPTPAVVLSEISINAFHVSTLRNRRNNVNSDSLEAAWBYLYQLDIPQL  
 DQMINVADICDHYFHGYNLWDFTPQTIALRSGKTVLDDGTTASDNTTHVYRVTVHVIA  
 GDGHGSTLLDDQGNQVLRDNDNPSTPSIKRIGAVTDLFDHNPFGFASVNSFAFVDFSDV  
 PATTLVMLNNLSDYLSNHNIIASSPTPIALDMVVLNNESEKSYQLCERVVAQAKLNSN  
 KITAHVSDVIKQANHNILWFTEQMNPGTTNLSEVPISKKSMLPMSRQLRILEHYDVPLTA  
 YSALFTWTVSAIKNESMVQYLVQRNMQLTSSNLDALNSIVSQLVPVDPKDVVAASGYQIQP  
 HFSTQOQREAITTDNPLAIIQAGAGTGKSTVILERIYLCAGNTPEEIAVLFSFTNAAADN  
 ITAKNDKVTSMTISKMVHEIYAHNFPDHEISTIDTINTLDIEYGDQMVTSYDMYQLRDL  
 LYKVMTQGGNANLTALSIFMESHEIAFISVLDQIKQTSLELEIICVYLLDKLIEPHASP  
 KYLIIDEVQDQNSVFEFVALRFAAKHNTSLYLVGDSSQTLYEFRSANPKALNSLEASGVF

GTYRLTTNYSRQELDFANIHLSDIEANQFAGIQLYANSFADPTADSFKKEVLEDMHHV  
SKQSEFTDIPYFMESNKARFDAALNNEQTTIVLAHSGREIRAAQQAALAEYPSITVRNL  
QSDKGFNNTVSTFIKDFWFEVTAVDPAHAATFTTSQVTAHLDKLVGRKQMEQEDVRIRS  
MAAWRENRENDIQGWVQQTQSGAITNEEFFYRLRQCILDEYIRNNRQSMNLNARNANK  
EAVAQEKPLIMVSTIHSKAGLEFDNVIVLQKPPSSDAEMTEEGKRATYVALTRAKKRELI  
AGSTRAYPRIVTDYEQIVDLLEKREDEERKIEEEAALATLAEQETRALAAEAQAQAL  
LLEHNPWLRLSDDEEVTALTEQEIINNVEPALQIEEEEEEARALAAEPAIQYQLSQFAF  
DEFPDDNDNNVVHVAPQILHQAVPADVTQSSAPVTFFVADLEVTTVAQVLEVPGLS  
VAAQPEVDDNLVYSTSPNSHSDVIIVNSDTSENAANVPVLSIDIALRAIFNNQD

>RXN01772 TRANSLATE of: rxn01772.seq check: 5291 from: 1 to: 4938  
MECMSTITDVAISALRTPQSQAQGLAFKLMVNFKSDPTLSTEFDEVHRWVNDPYNNGT  
MEKGLDILVAYNKDDDAYTAIQCKFYLPPTSLAKGLDSFFASGRFTFTEPGTRSFNSRL  
VISTTDKWSNNAEKMLNQTPTNRIGLSAIAESPIWDIAYPGSELTINLQKREYSPFR  
PHQATAIEKAIEGFQTHDRGKLIMACGTGKTFTALRLSEEARLNGNKARLILFVPSITL  
LSQTLKVESTAQKTMDLRPAVAVCSKSVKAAEDIAAYDLEVVPSTDGALIAEKLEHRKRA  
AGTIVTVFTYQSLPAVHAQAEGAEFPDLVICDEAHRTTGITLAGEDPSNTRIHDASAY  
KAAKRLYMTATPRLFDDSVKGAADHSAEVSSMDDEAIYGPFEHRLGFGEAVEKGLLTIDY  
KVVMVTVDQVAAASALTVLGSTPGEELTLDMTSAII GAWNGLAKRSKGEQDQTKTFSSSD  
AAMERAVAFARDIKTSQQAIESFVRVNNAYTTELEVKNDDVDEHNNLNSVACQHVGSNM  
ALERNRSLTWLKAPTQSMETKILTNAARLSEGVDPALDSVIFNFRNSMVDVYQSVGVR  
MRKS PGKNYGYIILPVAVPPGVAPSAALNDSRRFKVWQVNLALRAHDDRNFAMVNSIAL  
NEGNIKDLPEVTEHTGPTSKDRDNAPYDSAESATQYVLFSLQWQAEIYTKLVQDKVGT  
YWEEDWADDVADIAQAQITRIKALLDNASPTIKEEFERFVEGLRGNLINESIDDEAISMLS  
QHLITAPVFDALFAESSFAKONPVSVQVMQRMADALNSAELNSETKLEKFFYDSVIRAAE  
VSAAGKQAVIKDLYERFFKFAFKKQSEALGIVYTPVEIVDFILRAADDVSKHFGFGRS  
DKDVHVLDPFTGTGTFMVRLLOSGLIKPEDLARKYANELHATEIMLLAYVVAANNIETTY  
FGLGEGERALNGCEDAPVYEFDFGIVLGDTFQMYEDDDKLDLDFVTANNDRMEQRTPVQ  
VIVGNPPYSVSGSSANDNNANLKYPTLDRRIEDSYAKYSTATNKSLYDSYLAFRWATD  
RIHTQGVVAFVSNNGWVDGNTADGVRLSLAQDFSEIYFVNLRCNSRTGGDLAQKEGNGVF  
NVRVGTQIIVAVKNPQLSGCRILYKIDIGDNLNSADAKLNEIAVATIEGAQWQITSPNEGD  
VWSQRSDVDFDTPWVLGDKKNKSALKVQFTSAGLKTGRDAWCYQPTSQVQKTNITRLLET  
YEQAQRFRNSWVDNGVTSPEKADVNFQFLKQNPDLADSKKISWDSNLKMSLSRGDTFSFD  
PSSIQMSLYRPFPPQQTYYFVSLNQRRLYQLPSMFTPEHNDQGFYIVNPGSAGPFSTLAT  
NLPLDLAMWGSNAGQFFTRWTEPIETREGEELDFGNLFTSTPKKGVEGELLDGVRVDN  
ITDEILKYLQSSLGEDVTKDDIYFYVYLAQLHDPAYREAYAADLKKMLPHIETPTDRARFD  
HFTTAGKELMDLHINYEDVEPVDVVKVEKADPTDRETWRVTMMKWAQVVRPSSKLV  
DHTTLIYNSITISGIPPEAENYQLGSRSAIAWLDRIYQVKKDKASGIVNDPNDWADEVG  
NPRYIVELIAKVTVAVETMRIVEEL

>RXN01786 TRANSLATE of: rxn01786.seq check: 2034 from: 1 to: 684  
MRAAKITRGFTSNPAGSVLVEFGNTRVMCTASVELGVPRFKRDSGEGWLTAEYAMLPAAT  
AERNRNSMAGVKGRTHEISRLIGSLRAAVDLSQLGENTIADCDVLQADGGTRTASI  
TGAYVALADAIKVLQERGVPVPSPLAPVAAVSVGLVDNVCGLDLPYEEDSRADVDLNVV  
MTEHGEFVEIQGTGEETTFTRAQLNDMLDHAEKCRELVAAQKAAALGI

>RXN01876 TRANSLATE of: rxn01876.seq check: 6935 from: 1 to: 1851  
MARPFYLATVSPGVHRRHIRTGRVTVGVDDVELTGEMADVIEQGGVGSSEVLHQAL  
EQARSGHMRNIVETIQREQDEIIRDTTRGVMMVQGGPGTGKTAVALHRVAYLLYTWDRQL  
AKSGVLLIIGPNKTFLEYISHVLPELGETGVVLSTVGELFPGIVPTGSEDPTLTREIKGSEE  
MASILAEAVKAYQVLPEKTIIVSVSDGIEISIDEXTVAKSTRARRARQSHNSARPIFREH  
LVEQLAHQMAQTIGADPLGGKNLLSAAIDQLHDDLLDDAALQSVIDDWFPELRPDQVHL  
DLLISEERINVAAGYDEETKSALLRGLDPWAPSDAALLDEALLIGLPDPEAREKAE  
AKWRQIIDDQEVLDVLSSSQSSIDDDVTEAEVLSAFPVDIADETLAQRQTVTDNRITAE  
AQADHKWAYGHVIVDEAQELSPEWEMRVFRSPRWMTLVGDIAQTGWPAQVDDWAESLW  
PFVEKRFRHHLETVNYRTPAEIMSVANELLTQINPIDAPAMAIRESGREVVNLPLDALS  
AVMSDLREEDSQRTIAVSSRRHHESDFYLVDDIKGLEFDHVIIVDPAGIVESQGGQLQ  
LYVAVTRATQSLTILCE

>RXN01912 TRANSLATE of: rxn01912.seq check: 1693 from: 1 to: 738  
MRRRIFITERRNGIYIDLQQTLYTIDQAFEFVKETVAHGTVLVFGTKKQAEAVQVEADR

VGMPYVNVHRWLGMLTNFQTVSKRLNRMKELQAMDAENGVEGRTRKREVLMLTRERTKLE  
RVLGGIAEMTRVPSALWIIDTNKEHIAVAEAHKLNPVVAILDNTCDPVDVFPVPGND  
AIRSTALLSRVISTAVEEGKKAREERQLAAAKDAAGDAKPEEEAPAAAEAEAPAAEE  
EAPAAE

> RXN01951 (1-561, translated) 187 residues  
LLHHYDEGKKR YILAFKGLTQ GTVIESGAAA DIKVGNNLPL RNIPTGTTH NVELKPGAGA  
KLARSAGASI QLLGKEGSA YLVRPSSSEIR RVNIRCRATV GEVGNAEQIN IRNGKAGMR  
WKGWRPTVRG VVMNPVDHPH GGGEKSTSGG RHPVSPWGQK EGRTKPKRY SDDMIVRRRR  
ANKNKKK

>RXN01966 TRANSLATE of: rxn01966.seq check: 3341 from: 1 to: 657  
VSESENNTT PAVAADRDRLVWVDLEMTGLDLKRHVIVEAALVTDANLNLVGGVDLVVH  
ATEEELAQMDDFVTNMHSSSGLTEQIRESAVTLKEAEDAVLALIEKHCDPAHPAPLAGNS  
IATDRAFTIREHMPRLDEALHYRMVDVSSVKELARRWYPRVYKQPEKGLAHRALADIVES  
IRELDYRRSEFFVAEPGPTSEQCADDAAVDRFAPYFD

>RXN01979 TRANSLATE of: rxn01979.seq check: 2139 from: 1 to: 1581  
LGHDFRPDYPRIIRDLAGLAPNIPVLATTATANDRVVEDVRAQLEDGTGLFRGGIDRESL  
YLSVGNLNLPTFERPAWLATHLKELTGSGLIYCLTSAADHLADALNSVGNVVAAYTGRT  
AGERERLEHALINNEIKALVATSALGMGFDKPDGLGVVHMGSPSPVSYQQIGRAGRGT  
ARADVILLPGTDEKEIWEYFASVSFPREEVVRQLLAVLTDEAQSIVKLESQVLDLSRSRL  
QVLKVLVDVGDGAVKVRGGVSTGQEWIYDAERYAGLEQARKIEQQSMVNYQNTTECRMRL  
LRKELDDVEATTTCGRCDNCTGKTWGLDTSITLKVQQQLQTPGVKIAPRKMWPTGISV  
RGKTAGLEEGRALGRNLNDIARGPALKALLDSGAYSDDPWARIIEVLKNWOWNTRNPANV  
ALGNTNFGSTEMI IQVAQSTAAVGRMNFAGVLPAAPGAEEVMAQNSAYRVEALLKQWDWS  
QGLQLVPGPILLVTDLIDTGSVTVAGNGIAQRTSEKVLFPALASRG

>RXN02038 TRANSLATE of: rxn02038.seq check: 6905 from: 1 to: 369  
MSEPIQNVESNVADAAADIAATAATEEFTNTIGDATASEEETIEAAPVLVDGPQT  
VGRKRRAIVRVLVAGSGEFCNGRTLEEYFPNKLHQQLIKAPLVLLDRNLQCNIEASIK  
GPK

>RXN02070 TRANSLATE of: rxn02070.seq check: 1536 from: 1 to: 1122  
MTQVTESAVRSALSRVEDPEIGKPI TELGMVKSVSIDGSDVQVEVYLTIAACPMMKTIIVT  
NTEAALKDIDGQVQVHVTVDVMSDEQRRLRVSLRGSTSEPVIPFAQPGSTTRVYAVASG  
KGGVGGKSSMTNLAAALAKRGLSVGILDADIYGHSVPGMLGSDQRP HQVDDMI MPQAHG  
VKMISIAHFTTEGNAPVVMRGPMLHRAIQQLTVDVFWGLDLILLDLPPGTGDIAITVAQL  
IFNAELLIVTTPQAAAAEVAERAGTISVQTNQKVAGVIENMSAMVLPDGTMTDVFGTGGG  
QKIADRLTAVTGEVVKVIGSVPLDPNLRIIGDVGNPITAISEPHSPATAAINEIAEHLAHR  
KVSIVGKTLGLGVK

>RXN02082 TRANSLATE of: rxn02082.seq check: 737 from: 1 to: 2910  
MYLKSLLTKGFKS FASATTLKFEPGICAVVGPNSGSKSNVVDALAWVMGEGSAKTLRGKK  
MEDVI FAGADGRKPLGRAEVTLTIDNSDGLPIEYEVSTTRMFRDGA SEYEINGAKAR  
LMDTIFAGDLSDTGIGREHMIVGQGLKAEILSRPEERRAYIEEAAGVLKRRKKEAKQRK  
LQGMQVNLDRQLDQLTHELAKQLKLARQAEAAQRAATVQADLRARFQIAGFEIVKISEK  
LETSTEREKNI REQAAEQLEAEATTQMEVEMELAEITPQAEAAQQLWFDLSLAERV  
SATMRIAADRSSGAADVPYAGQDDDELGRAEATADKEELEMAVEMTTERLTISQEEA  
EDKAAQAREAREHHAQVRAISDRREGVVRLLASEESLRTQHTSAEEEAERLSEGLEEFI  
GRILDVERERRLTDERKQGVDDTDRAPEEALQKAKHEAAEAATRLLELRTKRSDLKEVS  
RLQSRITETLNQNRPSDAADVDVYQPLATLIRPQRNVNWKALAAALGAHAELAGAAEGL  
VEKLLDAGVARTIIVDGTQAGGAWRLDANI PAGASWLLDHDVLDPAIAGPVNRLADVVL  
VDDPSLGRQAIEDDPRLRVDRNGVLVIGAGWIQVGTETSTVEITAHIEEEEAQLAASAA  
LDDIAGTFDGLHAADNTRVEVAARTAAALRELDMTDRSITRDLARLDKQHEAASEVRH  
VQRLHAAETRREELREQLDIEDRLSRVEDEEDADEPSTTARDQANAEQLQIRAMEAKAR  
LAQRTAEERAGQQRKGDSLRRQAEHERQAKIRHEQAMEARRRTQLAAAVHNGARDVAE  
RVSSVLAQAAIERDQHNRDKALLTSHLAKAKDAVSAARQHLNRLSDNAHSMELARSQAQV  
RMEEAVAKITEQLGIPVAELLRDYPDENFDEKFRARLRKQAEKDLAALGFWNPLALEEF  
KALGRALRVF

>RXN02131 TRANSLATE of: rxn02131.seq check: 894 from: 1 to: 1671  
 VAFGDDGPLIVQSDKTVLLEIDHPQAGEARIALAPFAELERAPEHIHTYRITPLALWNART  
 AGHDAEQVVDMLERFSRFPVQALLIDIAETMSRYGRVRLHRHPAGHLILESCEPAIVE  
 ISRHKKIKPMLGAQVDPETI VVHPSERGRKQELLKVGWPAEDLAGYVDGESHPICLSTE  
 FEDWSLRDYQQMAADSFWEGGSGVVVPCGAGKTMVGAASMARQAATTLIVTNTVAGRQ  
 WKDELLRRRTLTTEDEIGEYSGERKEIRPVTIATYQVVTRTKGEYKALELFDSDRWGLLI  
 YDEVHLLPAPVFRMTSDLQSRRLRLGLTATLVREDGREGDVFSLIGPKRYDAPWKDLSSQG  
 FIATADPEVIRSTMTDAERMVYATAESADRYRLAATAHTKAVVRKLLLEEHAQKPTLIIG  
 AYLQDLQELGAEFNAFVIDGKTPNKKREALFDQFRSGSLSVLVVSKVANFSDIDLEASVA  
 IQVSGTFGSRQEEAQLRGLRLRPKHGDSEAHFYISVSRDITDTEYAAHRQFLAEQGYAY  
 RILDADDILFFLPKKE

>RXN02293 TRANSLATE of: rxn02293.seq check: 2677 from: 1 to: 2388  
 MSSRIGNFLINRISTGLPVENIIPHLQEAFAAGPKNLVVIQAPPGTGKTTLLPFLVANILC  
 NEGAGNATPTKVLVTAFFRVAVRAAARLQAOLDDSQLGTKVGSVRGEHISGSHVQFMTPT  
 GVILIRQLLNNPELPGIGAVIIDEVHERQLDSDLLGLMLAELSQLRDDFLIAMSATLSDSD  
 KFNALLDAQELSVSEAPIFLPDISYAPARAPRLNAGKVDWDFLDHMAQKTHOAVTSEHSEA  
 LIFVPGVIGEDRVMSTLKSGLHNNVFLPHGQLSPTEQDRALAPSQOQRIIVSTPVAESSL  
 TVPGFRGIRGDSLSRSRKDSARGMTGLITSSCAQASQAGRAGREGPGQIIRCYSEE  
 DTFGVHFRFVTPTEISSADLTQAALWLQWGTSPADLPILDQPPHAAWTAQOQILRLIGALE  
 GDAITSLGHRSLSTLPCPQLSASLRLFGEQSAKILAVVSENPQGDVEKQDPDKREVERLR  
 RLAPASVGVKASAGQIVGAAPFQLIGRKIDNGEYITLASGTARRLMSDLKDAEWISVAAIN  
 RNSQSAIRAAARISEDDAIDIIGVVEETRAIFVNGKVQARKVKAAGAIELSSPTTKPTK  
 AEASETITATLAKGGIDLFHFSDKAASLRDLRKFIEHHRGEPWPDIEDAPHLWLSPEIE  
 ALSHGTRLNNIDMYPALQRLLPWPEATNFEEFAPSHLSVPVSGNQHLRSDYSGRPVIRVRL  
 QECFGLSESPQLCGIPVQFHLSPAGRPLAVTDLLRSFWSGPGYSQVRAEMRGRYPKHPWF  
 EDPTWATAPATARTKNRM

>RXN02357 TRANSLATE of: rxn02357.seq check: 4829 from: 1 to: 6300  
 MSSLI PVHAAGSIQEGITEYLTTSFSLADKQVATELKRFLGHGDSGMFHGPYVRARIPYA  
 QAGWENVLSWLPENFVFPYHHQKAAAFQRLSSLDNRCKDRRPDPTLVVTTGTSGSGKTESFY  
 PILDHALRLRRKRGQGGIKALLYPMNALANDQADRLARLIHNNPALKGVTAGIYTGAEAK  
 NRTQMGERELINDPQAMRVSPDPDILLTNYKMLDQLLLRSVDRENMWQKSATSLLQYLVLDEF  
 HTYDGAQCTDVALLLRLRLMLKSKQPPANFLDSDAMHPLGIIITPVATSLTSGSGSDSGSP  
 MLDFAYITIFGERFPADAIVGETRLLEDQWRAEIAQNFAGAPVSEPRELPTVEDIEVNLDT  
 IATAQHEDDYAQLCFRVFCEKVMLEADLHAAISAYAAHDLTAAILQHAADSTPLSRDDQ  
 DEVTALPELVLGATARILGEVKAAEFI SHALAAMAFVRAEYGVKVAANGAKRLPGVETHLW  
 VREVSRIIDRALGVGDEQSMFRWSDGPAEDANTQOQLPACYCRCGRSGWVMSLEQGTNI  
 PVLEEQRILNSFEQPHQRALLDATSEQRAAIEQGRSVAGPFGVDGTSAVLWFHSHASNE  
 LSTRQPSPEEEQSGSSIAVLTHFGPEADDLSAKQTCFSCGVDVSIYIGSGISITLLSVSL  
 SNLFGMADLDSAEKKTUVFADSVQDAAHRAAGYVQARSRAFAALRTYTRRAVGDNEVTLPSI  
 SRALMDNATSGRTRYELLPPDLTDLDIYKPYVWHPDASKAERREASRNHVKRISFDLALF  
 QRADLPRSLALTGALSAFVDLPGKVALSAAAEALYAEIVPTLIDENLRLRISVQGALE  
 LLRARGGINHEWFGAYLRTDGNPYMLNRRQARAEGLPGFVRGGAPEPRPVSGALSGLSRS  
 STGTTPLGSPGRYASWTSQLGISTHDAATATIKFLDALNSRILSSISTDSGGKIYCL  
 EAKIRIFSEDDHPEVLECSVCHAQGTVDHVRDFLDGAPCFSPSCGCVLHIIEVEDNYR  
 RLYSAIEPTVIAREHTSMLKKKDRDLAQSFRCGEGGSAKQSPAPNVLVPTLTEMIGID  
 ICDLTHDQVPGGTGYLNQFADPTKVPELISRAWERSRCQCYDETACPECLLPYTRTD  
 TELLHTRATAEKSLRAILLNNSRFEETDLSAVPDWTFLEKRPENTLGSQELRFRVRLR  
 RALKNRHAKLVDVNGSNSYVDIEMSSGVVRWMSQVDRGYTRDPFWFEPLNGNYPVAV  
 FTDGAAFHISSANYRLDGIQKRMKALDPDNILPWNITSLDLDRFSNPAQGEFPAWFS  
 PIGRQLSKANLILDEQSTALLAATFMDQLLAFLDNPAASSWKEFAHTAAAHMLGHNPPQKN

GDGIVGTFRNKISLRATMVNRELRAQLWLAPTTPEELEVDTWTAFLNLANLMLWLPAPESV  
YVSTNGSPHKIDIVPAPAAPLVVEVPPELWAPILDGFTADEDEEAEGALQILAKHEHALVPE  
TTGDELSSITPTIATWPSVKIALLYESDPDEPLEDDLKAEGWTLFLFANDLETSDIPAAALRP

>RXN02370 TRANSLATE of: rxn02370.seq check: 1226 from: 1 to: 792  
MTPIYDDVNDKLDPEFILAESTVEPEEGPRMRARQRQESAADDIAIAAAAVDIASE  
EDDPDESGSSYVSDFEAEPIAPVVEKAAEPVAEPTADYEKARAEFEASPRRRRTGNSR  
SDHAKPKEDFAPVVEEVAETPVKTPARKAPRRNRPSLESSGAPSSAPSTRNRNRRAVRRLQ  
VEAPEVTVEIAPEAAPEQVAEPQVEFDQPDNRKRARRAVRVTAAPVEKKVASTSNARAPK  
KEPQAASTNTPGRRRRRATRGRPRS

>RXN02371 TRANSLATE of: rxn02371.seq check: 7071 from: 1 to: 315  
MYAIVKTKGQKYKVAEGDLVKVEKIEGEPGASVALTPVLLVDGADVTTAADKLASVSVNT  
EIVHHTKGPKIKILKYKNKTKGYKKRQGHRLPTVLKVTGNQVSFR

>RXN02468 TRANSLATE of: rxn02468.seq check: 4275 from: 1 to: 1224  
VEITDALEALGINRTFAIQEYTLPIALDGHDFIGQARTGMGKTYGFGVPLLDVDFDSADV  
AETDGTFRALVIVPTRELAVQVGGDLQRAATNLPLKIFTFYGGTPEYEQIDALKVGVDVV  
VGTPGRLLDLHKGALSLDKVAIVLDEADEMLDLGLFDIEKILRALTHQHQPLNFSAT  
MPGAILTLARSFLNKPVHIRAETSDASATHKTRQVVPQAHKMDKEATIKLQSKDRGK  
TIIFARTKRTAAQVAEDLASRGFSVGSVHMGQAPAREKSLNAFRTGKIDILVATDVAAR  
GIDVDDVTHVINYQTPDDPMTYVHRIGHTGRAGHNATVILVGDYETLKWTVIDNELELG  
QNPFPQWFSTSPELLETLDIPEGVTERVGPPTKVLGGTAPRPPRTRK

>RXN02727 TRANSLATE of: rxn02727.seq check: 1998 from: 1 to: 912  
VVLPLVLPOLQVQPOLQLPSLLTRQRCARKSKRSAPNTASKLDDASKAAQKQNDKAS  
AQDQLQRAQADAKAARDEAEKAKAEKASASSSTTKAAAVGAVGAGTGAAVATGAANVDT  
HMQAQKVLGAQEMADRLTSEARSEKSMLEAREAAEQKIEEANSTNRNLEDAARANAE  
KQIAEAQNRADTLVNEADAKANLVSEAEKKSAAATLAASTSRAEAQIROAEDKANALQAD  
AERKHETMAAVKEQQNALETIAELQTFEREYRTRLKSLEGLQLEELHARGSSAPTNNK  
PSGE

>RXN02764 TRANSLATE of: rxn02764.seq check: 4873 from: 1 to: 2784  
MSEYKPIPSDPQVRLIKPISKLRPSWEGEVSHLVKQGTGLWRVTGEAGSGVSSAVVDT  
VLERIRQDVEPSSMLVVATSKAEASRLRQEISESVAQMDYVEGPIVRVSHVAFALIRD  
ASDDVRLITGAEQDAVIRELLRGHADDRGGWVQEQREGLRMVGFARQLRDFLLRAVER  
GVGPELDELVELGERFERANWVAAGEFLREYKQVMKLSGAHSFASSELVTEALRGPEPSVKY  
RGVFIDDAQHLDPKSAELVSRFFPEAEALVAVAGDPQOSVFRFRGANPDFTLKLSVDHEVV  
LKGRKAKSTIVVAETESAHADILLADTVRRRAHLIDGRSSSEIAVIVRSAGMIAPWRTLL  
AAGVPVHISTPDVVLAEQRIVAAMILGLRALTESINAIELEDDLGLPIGGAOPVTLRRLR  
RLGRQAEMKMGQRRRAIEVLRSLLAESDAEMGLFLTDRELNLLEVRVSLVLEAGREALAEH  
GSIIEVLWALWSATDLSNLSAISLRGGASGQADRLDDAMMALFDAAGDYVERYPAGV  
RSFILHISEQELPTGMRRERRGAIPAEVVLTAHATTGREWKRVIVAEVQEGSWPSLGETG  
TLGQEEFVDVDEGIDPDIIISRAERLAEEARRLFYLATRTSTESLVTAVNSPDSDEV  
RFPSSRLLELLSQFIVVLEGEESAIAEPEEIGHRLLSIPAMVAELRRVNDPRPRKRQA  
ARQLSRALAEAGIPGANPAEWNLRTFSTDEELIKGAVSLSPSRIEQLLNCPLRAVLDRLD  
SEETPTAMLKGTLVHFAFAEAVAGGVDAALAEKVTSAYMQLANVPSWSRSTETAFPRRI  
LSRTDTNLKTSRADFTVEGTEMDSVTTDDSVSIRGRMDRLERNKSGELVVVDFKTGKTQ  
IAAKMDGHPQLFAQYLALSQVGLHGDK

>RXN02819 TRANSLATE of: rxn02819.seq check: 6309 from: 1 to: 1047  
KLQIGDVIAMPGRKRPLVAVVMTPANQSRDPRPWFVTTESGWSGRVDAESFTNPPTIGHM  
LPRQAITEPRRNARRVQELFRREHFKRPNKMFARVVRPNEAVTKLRNADIDHEAHHP  
DEHRLATAEIRMIRKERDLAKLTGNVDKARETLGRTFERILSLSEMIDYVDSNPDNFI  
TDEGERLAKHSEADLLVAQCLKRGJWDNLDPALLEGAVSMCTFENRRETGGEAQAVTEA  
MADSMNSVERIHWELVEDERRHRLPITRQPEAGFATAIHQWASGAPLGYCMAAAENGAE  
LTPGDFVRWCQVIDLLEQVAKTAYDETETENARQAIDAIRRGVVAIGS

>RXN02826 TRANSLATE of: rxn02826.seq check: 160 from: 1 to: 435  
MAPKKKKKVTGLIKLQIQAGQANPAPVPGALGAHVNTMEFCKAYNAATENQNGNVVVP  
EITVYEDRSDFKLKTPPAKLLKLAAGLQKQSGVPHTQKVGKVSMAQVRETAETKKEDL

NARDIDAAAKIAGTARSMGITVEG

>RXN02833 TRANSLATE of: rxn02833.seq check: 6083 from: 1 to: 783  
LLETWRQVVDLTTLSQQADSGFDPLTPQRAYLNLTKPIAIVDGYAVLSTPNAMAKNVI  
ENDLGDALTRVLSLRMRGSFSLAVSVEPEQEIPEPQAQEFKYQPPAPVISSNKAQKQYE  
VGGRGASSTSGWERTHSAPAPEPHFPAIADREPELATPQRIPRETPAHNPNREVSLNPK  
YTFESFVIGFNFNFAANAAVAESAFAKFNPLFISGGSGLGKTHLLHAVGNVQAELQPG  
PRIKYVSSEYHQLRLHQLRAR

>RXN02943 TRANSLATE of: rxn02943.seq check: 6621 from: 1 to: 1668  
MSRISARTLAIALAGATAASLAVVPAATANPAGTAPVINEIYEGGGNSGSLFSNDFIELY  
NPTSGDISLDGWSVTYIYAANGNSGGTTLNLGNIPANGYLLIQQRAGSNNTGALTPDPTAG  
NLAMGASQGSVALTDNSGLTADLVGFGTSMFEGTAAAPETSNKLSVQRKEVGDASDNNNS  
VDFETGAPPTPTSSGGSAPVDPGEPETPVNPGPETVSIQIQGTGLATPLEGQTVVTEGIPT  
AVYAEGGFNGYIQTGSGTAPKVAGDASDGI FVYVGSNGSYPELGASVTVTGKATEHYE  
MTQLGNSSTFVSDTAFFPVTPLELDTVPTGDDIREAYEGMLLKPTGAHTVTNNYATNFTG  
ETALAPNGPELYQATQMVAPGAEAIAYEAENNAKQITLDDGRSGNYTRGDSSTPMALWLV  
DGGETIKSIRTGDQVEFQAPVIFDYRYDLWKFQFTTPTVGTNTASSDLPTWDDTRAELA  
SINDVAGEFHIASFNVNLNYFTSLGEDEPGCSAYRDIINNTPTVANNVNRGAYTEEALEDQ  
QSKIVEAINRLDVLVDVL

>RXN02981 TRANSLATE of: rxn02981.seq check: 3652 from: 1 to: 366  
MARLAGVDLPFRNKMEVALTYIYGIGPARSKQLEETGISPDRLTNDLDEQIAALRDVI  
EGTWKVEGLDLRQVQADIRKIEIGCYQGIHRRGLPVRGQRTKTNARTRKGPKKTIAGK  
KK

>RXN03093 TRANSLATE of: rxn03093.seq check: 5261 from: 1 to: 1839  
VADTAGTGTSGKKKYLIVESATKAKKIQPYLGNDYIVEASVGHIRDLPARGAADIIPAKYKK  
EPWARLGVDTDRGFAPLYVVS PDKKKKVDLKLKLVDELLATDPDREGEATAWHLLE  
VLKPTVPVRMVFNEITKPAILAAAENTREL DENLVDAQETRRILDRLYGVEVSPVLWKK  
VMPRLSAGRVQSVATRVIVERERERMAFVSADYWLDSAEFNARENGKADSDNPSSFARL  
STIDGNRVQGRDFNDRGELTSEAVVVVDKQRAEALAELEGQEMAVVGVVEEKPYTRPYP  
PMFIMTLQGESGRKLHYTERTMRIAQRLYENGHIITYMRTDSTSLSEQGMKAARDQALEL  
YQAVYVSPSPRTYDRKVNKQEAHEAIRPAGETATPFGHLGQLDAEEFKKLYELTWORTV  
ASQMAQADKTSMKVTIGCTAKTGEKTEFNATGRTLTFPGFLRAYVETTTADGRDVADNA  
EKRLPLLSEGDLLKVLSEIADGHSTNPPARYTEASLVKKMEDLGIGRPSTYASIIKTIQD  
RGVYYSRGNALVPSWVAFVVGLEANTSLVDYDFTSSMEDLDLNIAGREGRETEWLG  
FYFGRCSRSGSVHG

>RXN03139 TRANSLATE of: rxn03139.seq check: 8976 from: 1 to: 249  
MKQRNNAKRVRIEQTRRPKNPLKAAGIEKVYDKINTLRQFISDRHKISRRRVGLTQP  
QQREVATAVKNAREMALLPTSR

>RXN03148 TRANSLATE of: rxn03148.seq check: 7950 from: 1 to: 366  
MVINFIILFMIAITTSFFVASEFALVKIRRSRLQLEKENVKNAKLALHVTTHLDNYLSA  
SQLGITLTGLIIGWVGEVSVAALLEPVIKGLPFSSAISSTISVALGFILVTYVRCGYWRT  
AS

>RXN03163 TRANSLATE of: rxn03163.seq check: 610 from: 1 to: 1497  
MAKTRVPAPEKSVARVLPGLLGLPHLDRLFDYRISEQDQDDVQPGVRRVRFGGRLVDAIV  
MSRTAQTSHEGLKMLWDRVISPIVYPPQTAKLIEQLSDRYGGVRSDLRSALPARHAGA  
EEADTSTSSSELGEVKEPDLSSWSAYQHGQS FVDVAGLTAGTTARASWQIAPGDDWALALAS  
LAVKVVKDGGLALLVPDQRDLDRLEAALRGLVAAKQITVLNLSGLPQARYRRFLSVLSG  
QGRLIITGRSAAFAPVKDLKLAVIDNDGDDNLVDPRAPYAHAREVLTTRSSLEASSLIITA  
GHARTAETQLLVESGMMNLIAPRDTITRTMPRIQAVGDSDFQMERDPMARSARLPGLIAF  
HAVRSALERDQPALIQVPRKGVVPTLACGNCRTPARCRHNGPVGLPQGSSDLAGVPTCR  
WGRPDSRPFKQCNQGS PKLRAVVLGTERTAEELGRAFPVSRRVITSGGNKVVDSENRASI  
VVSTPGAEPFVANSERPE

>RXN03166 TRANSLATE of: rxn03166.seq check: 5429 from: 1 to: 2255

MTTSETAPSKASLYELLEGVSLSDERTFRRRLSKARAPKALGAIKADIDKARLLIDEKSO  
 LIPSIITYPENLPVSSRRDDIAEAI RDNQVVIAGETGSGKTTQIPKICLDLGRGRRLIG  
 HTQPRRLAARTVAERIADELGQDIGESVGYAIRFDDRVSSTSVKLMTDGILLAEQMQRDR  
 FLNAYDTIIIDEAHERSLNIDFILGYLRQLLPKRPLKVIITSATIDPERFAEHFADASG  
 KPAPIIEVSGRTFPVEIRYRPLEVLDDGDKIIDTDLGLCSALEELMAEGDGDILCFFAG  
 ERDIRDAMEAIEARRWKGVEVTLFGRLSNQEQRHVFSPHSGRRIVLSTNIAETSLTVPG  
 IHVYVDTGTARISRYSVRTKVORLPENISQASANQSRGRCGRVADGIAIRLYSEDDFNS  
 RPEFTDPEILRTNLASVILRMASRLGDIINDFFVQAEQORSIRDGILLHELGAITDDT  
 QADGSPQLTQIGKOLANIPVDPRMARMLVEANTLGLHSMVMVIVSALTQDVREPRLEFQ  
 AQADQAHARFKDTSDFLGLKLWEYIADQRNQSSGNSFRQMKKEFLHYMRIREWNDLV  
 RQLEQIQQLGWAKKEQVAGTASPDIIHQSLLTGLFSQIGSRDGSKEFTGARGTKFLVF  
 PGSALTKKPPQFIMAGQLVETSLWARDVAKIEPEWVEKAAGPLLKHQYSEPYWSSKRGG  
 CHGAPQINALRCDNCCRGSSSLPHG

>RXN03175 TRANSLATE of: rxn03175.seq check: 2273 from: 1 to: 783  
 VRASEKDTATALQPALDNGWHYIGAPAAAKGRAGVGILSRHELEDVNI FGFSFLDSGRYI  
 EATIKDITLDVPVTVASLYLPGSGAGT DKQDEKYRFLDEFEGFLDQRAKERSHMVIGGDW  
 NICHRRREDLKNWKTNQKKSGLPDERAFMDSVFGTFPPDEATQVAGAGDFFGAVDYEGTRR  
 REATTDPAWFDVARRLQPEGDGPHYTWWTYRGKAFDTGAGWRIDYQAATAAMLERASRW  
 DKAAAYDLRWSHDSPLNVIYS

>RXN01389tr TRANSLATE of: rxn01389.seq check: 5202 from: 1 to: 684  
 QDGDKLAGRHNKGVGKILPQKDMFFLPDGTVPVDIILNTHGVPRRMNIGQVLETHLGWL  
 ASAGWSVPEDPENAEVLKTLPADLLEVPAGSLTATPVFDGASNEELAGLLANSRPNRDG  
 DVMVNADGKATLIDGRSGEPYPYPVSI GYMMLKLHHLVDEKIHARSTGPYSMITQQPLG  
 GKAQFGGQRFEGEMEVMAMQAYGAAYTLQELL